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OM protein - protein search, using sw model
                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Run on:

September 13, 2002, 09:18:36 : Search time 399.68 Seconds (without alignments)
3.057 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-446-543A-74 47 SRXHXHSMEXR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scarched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

17: 17: 17: 1: \SIDSI\_gcgdata/hold-geneseq\_geneseqp-embl/AA1980.DAT:\*
2: \SIDSI\_gcgdata/hold-geneseq\_geneseqp-embl/AA1981.DAT:\*
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10: \SIDSI\_gcgdata/hold-geneseq\_geneseqp-embl/AA1989.DAT:\*
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18: \SIDSI\_gcgdata/hold-geneseq\_geneseqp-embl/AA1995.DAT:\*
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Pred. Ho. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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Result Ho.	Score	9 Ouery Match	% Ouery Match Length DB	DB	ID	Description
ם	43	91.5	31	18	AAW31384	Rat type G protein
2	43	91.5	31	20	AAW97233	Rat type ligand po
ω	43	91.5	31	20	AAW87614	Rat 19P2 11gand.
4	43	91.5	31	20	AAW95173	Murine pituitary-d
y.	43	91.5	31	20	AAW95174	Murine pituitary-d
O1	43	91.5	31	21	AAB10355	Rat oxytocin secre
7	43	91.5	31	21	AAY87504	Rat prolactin-rele
<b>B</b>	43	91.5	31	21	AAY49292	19 <b>P2 ligand peptid</b>
o	43	91.5	31	22	AAG62524	Rat CRH releasing
10	43	91.5	31	22	AAB90993	Prolactin releasin
11	43	91.5	32	18	AAW31385	Rat type G protein

ĕ	8 AAW31372		ω	89.4	42	U
			ω	89.4	42	4
bPrRp31 pept1de, u			ω	89.4	42	43
			ω	89.4	42	42
Prolactin releasin	2 AAB90991	. 22	31	89.4	42	41
Human CRH releasin			ω	89.4	42	40
			ω	89.4	42	39
19P2 ligand peptid			ω	89.4	42	38
			ω	89.4	42	37
1igand			ω	89.4	42	36
Human oxytocln sec	AAB10		ω	89.4	42	35
Bovine oxytocin se			ω	89.4	42	34
Bovine pitultary-d			ω	89.4	42	S
Human 19P2 11gand.	0 AAW87615		ω	89.4	42	32
19P2 11gan			ω		42	31
			<u>د</u>		42	30
Human type ligand			œ	69.4	42	29
Bovine G protein-c			ω	69.4	42	28
Human type G prote	AAW31		<u>د</u>	89.4	42	27
19P2 11gand peptid			30	89.4	42	26
Bovine pituitary-d			29	89.4	42	25
Bovine G protein-c			29		42	24
11gand	0 AAW97229		1:		42	23
Synthetic ligand 1			::		42	22
Rat CRH releasing			8		43	21
			8	91.5	43	20
type li			8		43	19
type G prote1	AAW3138		83	•	43	18
ine p	AAW9517		8	•	43	17
Rat CRH releasing			ىي	۲.	43	16
OXY			щ	$\vdash$	43	15
			ىي		43	14
Rat CRH releasing	AAG625		ω N	١.	43	13
Rat oxytocin secre			ω	91.5	43	2

## **ALIGNMENTS**

DR DR	X II IX	PA	PR	PR	PR	PR	×	PF	×	3 5	χP	X	SO	×	E ?	ž ž	×	DE	×	3 >	ຄໍ	×	Ð	RESULT AAW31384
WPI; 1997-363672/33. H-PSDB; AAVO2421.	Fujli R, Fukusuml S, Habata Y, Hinuma S, Hosoya M; Kawamata Y, Kitada C;	(TAKE ) TAKEDA CHEM IND LTD.				18-SEP-1996; 96JP-0246573.		26-DEC-1996; 96WO-JP03821.	10-001-1997.	10-711 -1007	W09724436-A2.		Rat sp.	CARCA EPOCH CAP CHICA C	modulation; provinces; convert normone ejecum; panetedo, proprijanetero,	modulator: mituitary, central pervous system; manoreas; prombylactic:		Rat type G protein-coupled receptor ligand fragment 1.	CO 1990 (F14)	On-200 161111 Ontice	AAW31384;		AAW31384 Standard; Peptide; 31 AA.	1384 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a peptide fragment from a novel rat type clipand polypeptide corresponding to amino acid residues 22 to 52 of the sequence represented in AAW3138 and is used in an assay to monitor ligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pitultary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophronia, trauma, growth hormone secretory disease, hyper-and polyphagia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperispidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyper-syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral scierosis, acute myocardial infarction, infaritility, spinocerebellar degeneration, oligogalactia. Assays can also be developed to screen compounds which are activation of the G protein-curied recenter for the G protein-curied recenter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                          Rat type ligand; modulation; prolactin secretion; grotein-coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; kagonz-del Castilo syndrome; rorbes-Albright syndrome; lymphoma; Sheehan syndrome; dysocospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
            Fujli R,
                                                                                23-JUN-1997;
                                                                                                                                                   30-DEC-1998
                                                                                                                                                                                    WO9858962-Al
                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                   abnormai lipidmetabolism; oxytocia.
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                                                                                                                 22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat type ilgand polypeptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
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8; Conser
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               Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              altering
of the G
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                                                                              97JP-0165437
                                                                                                                98WO-JP02765
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                                               IND LTD
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Pred. No.
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              Matsumoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                          Producing a 19P2 pltuitary G prot
of a fusion protein, useful for p
breast cancer, renal failure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autolmmune disease or abnormal pregnancy
                                                                                      WPI; 1999-047884/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 153; 24lpp; Engiish
                                                                                                                                                   (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                               27-JUN-1997;
                                                                                                                                                                                                             25-JUN-1998;
                                                                                                                                                                                                                                             30-DEC-1998
                                                                                                                                                                                                                                                                         EP887417-A2
                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                                                                19P2 iigand; G protein coupled receptor; pituitary;
prolactin releasing peptide; rat; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                Rat 19P2 ligand
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72.7%;
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                                                                                                                     Suenaga
                                       for preventing and treating
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                                         by cleavage dementia,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              senile dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's disease), infectious diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or toxicosis (e.g. hypothyroidism, vitamin Bl2 deficiency, alcoholism, infoxication by drugs, metal and organic compounds), tumourigenic diseases (e.g. brain tumour), traumantic diseases (e.g. chronic diseases (e.g. brain tumour), traumantic diseases (e.g. chronic consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo and hypersecretion respectively, including: hyperprolactinaemia, pitulitary adenoma, chests cancer, infertility, impotence and succimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia, menopausal syndrome and renal fallure (hyposecretion disorders). The 1972 polypeptide/amide is also useful for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Beat Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the rat pituitary G protein-coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAVB3794-95) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and (at high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including:
                                                                                                                                                                                                                                                                                                 Pitultary-derived iigand polypeptide; G-protein coupled orphan receptor; GPRIO; UHR-1; modulator; pitultary; central nervous system; pancreas; tlasue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
                                                                                                                                                                               WO9849295-A1
                                                                                                                                                                                                                                                                   Creutzfeld-Jakob disease; polaoning; schizophrenia; growth hormone;
secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW95173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
 Fukusumi S,
                                 (TAKE ) TAKEDA CHEM IND
                                                                      28-APR-1997;
                                                                                                         27-APR-1998;
                                                                                                                                            05-NOV-1998
                                                                                                                                                                                                                Mus sp
                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                        Murine pituitary-derived ligand mature polypeptide sequence
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8; Conserv
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Pred. No. 0.0
0; Mismatches
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sequence. The polypeptide is a ligard for the G-protein coupled orphan or creceptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with executor containing the ligand polypeptide encoding DNA are used to comproduce a recombinant ligand polypeptide. The ligand polypeptide, and its of fragments, modulate function of the pituitary, central nervous system, cancers and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the camount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia, Alzheimer's, cused therapeutically, e.g. to treat senile dementia, Alzheimer's, comparing the parkinson's or Humtington's disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia, disorders of growth compone secretion; cancer; rheumatold arthritis, epilepsy and many cothers, also to improve post-operative nutritional atatus and as concertions of the surging the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding coffice in the polypeptide encoding the ligand polypeptide. The polypeptide encoding coffice in the polypeptide in the polypeptide encoding the ligand polypeptide encoding coffice and primers; to identify related sequences, in receptor-binding assays; coffice of production of Ab and antisers; in drug development; for gene therapy and condition of the and antisers; in drug development; for gene therapy and an total and antisers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 134; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreas, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide ligand
for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This represents the matured murine pituitary-derived ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-009423/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for orphan G protein coupled receptors - of central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening
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                                 Best Local Similarity
Matches 8; Conserv
                                                   Query Match
                1 SRXHXHSMEXR 11
i srahqhsmetr ll
                                   Conservative
                                           91.5%;
72.7%;
                                  0;
                                           Score 43; DB 20
Pred. No. 0.026;
                                  Mismatches
                                                    20,
                                  ω
                                                   Length 31
                                  Indels
                                 0;
                                  Caps
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Sequence

31 AA;

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RESULT
AAW95174
                        AAW95174;
 10-MAR-1999
                                               AAW95174 standard; Protein; 31 AA.
                                                                        U
(first entry)
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Murine pituitary-derived ligand polypeptide antigenic

epitope.

Pituitary-derived iigand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatold arthritis; epilepsy; vasopressor transgenic animal; epitope

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SUM
                                                                                                                                                                 gene therapy;
(TAKE ) TAKEDA CHEM IND LTD
                            28-APR-1997;
                                                       27-APR-1998;
                                                                                  05-NOV-1998
                                                                                                            W09849295-A1
                            97JP-0109974
                                                       98WO-JP01923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.
Best Local Similarity 72.
Matches 8; Conservative
                                                                                                                                                                                                                                                           Rat; exytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                 06-JUL-2000
                                                                                                                                                                         W0200038704-A1
                                                                                                                                                                                                             Rattus sp.
                                                                                                                                                                                                                                                                                                                                              Rat oxytocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10355 standard;
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                 (TAKE ) TAKEDA CHEM IND LTD
                                                                                             22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                      24 - NDV - 2000
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                          secrotion promoting peptide SEQ ID NO:
                                                       98JP-0369585
                                                                                           99WO-JP07199
                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide; 31
                                                                                                                                                                                                                                             milk production.
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72.78;
                                                                                                                                                                                                                                                                                 comoter; G protein-coupied receptor protein; atomic bleeding; uterine recovery failure; cow;
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                 AAY87504
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                                                                                                                                                                                                                                                         This invention describes a novei oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expuision of placenta uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in vetetinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
AAY87504 standard; protein; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsumoto H, Kitada C,
                                                                                                                                                                                                                                                     promoter.
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                                                                                                           1 SRXHXHSMEXR 11
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                                                                                                                                           Conservative
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Stricker-Kongrad
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                                                                                      22-SEP-1998;
14-OCT-1998;
                                                                                                              22-SEP-1999;
                                                                                                                                              W0200017641-A
                                                                                                                                                                                            Rattus sp
                                                                                                                                                                                                           feeding behaviour; food int
obesity; agonist; cachexia.
                                                                                                                                                                                                                                           Rat prolactin-releasing peptide, PrRP
                                                                                                                                                                                                                                                                            AAY87504;
                                      WPI; 2000-303231/26
                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                              30-MAR-2000
                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                            (first
                                                                                      98US-0101380
98US-0172353
                                                                                                              99WD-US21243
                                                                                                                                                                     Location/Qualifiers
                                                     ,
                                                                                                                                                              /note= "C-terminai amide"
                                                                                                                                                                                                                                                            entry)
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Identifying modulators of body weight by a combination of a cell-free or cell-based assay to identify modulators of GPR10, followed by an in vivo assay for the compounds effect on e.g. feeding behavior -

Exampie

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Page

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82pp;

English

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RESULT
AAY49292
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function applied in clarifying the physiological functions of the ligand and its derivative
                                                                                                                                                         New monoclonal antibodies, studying diseases related :
                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody; 19P2 ilgand; diagnosis; prolactin secretion; pitultary; regulatory mechanism; central nervous system; pancreat
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                                                                                                                               Disciosure: Page 26; 73pp: Japanese.
                                                                                                                                                                                                                                 Matsumoto
                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                        21-MAY-1998;
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                                                                                                                                                                                                                                Kitada
                                                                                                                                                                                                                                                                                        98JP-0140293.
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                                                                                                                                                                                                                                 Hinuma
                                                                                                                                                           to ligand abnormality
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Best Locai
                                                                                                              The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ancitorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                          Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp
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                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                 Kitada C,
                                                                                                                                                                                                                                                                                                                                        (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                              18-NOV-1999;
26-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200135984-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analgesic; hyperaldosteronism; hypercortisolaemia: hypoa-
Addison's disease: adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat;
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   SRXHXHSMEXR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY49290-302 represent peptide fragments of the 19P2 ligand.
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                          Conservative
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                                   91.58;
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0: Mismatches
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AAB90993
                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I)
C comprising a therapeutically active amino acid region (III) and a
C reactive group (II) (e.g. succinimity) and malelmido groups) attached to
a less therapeutically active amino scid region (IV), which covalently
C bonds with amino/hydroxyl/thlol groups on blood components to form a
C peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
C (I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity
in vivo for the treatment of various disorders. Endogenous therapeutic
Deptides are not sultable as drug candidates as they require frequent
administration due to rapid degradation by peptidases in the body.
Modifying snd attaching therapeutic peptides to slbumin prevents or
reduces the action of peptidases to increase length of activity (haif
life) and specificity as bonding to large molecules decreases
AhB90829 to AhB92441 represent peptides which can be used in the
exemplification of the present invention.
                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
            AAW31385 standard, Peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112059/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succlnimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disciosure; Page 244; 733pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-NOV-2000
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                                                                                   1 SRXHXHSMEXR 11
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1 srahqhsmetr 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DP,
                                                                                                                                                                                                                       31 AA;
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                                                                                                                                                Conservative
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                            Score 43, DB 22
Pred. No. 0.026;
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                                                                                                                                             Mismatches
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neurotransmitter.
                                                                                                                                                                          22; Length 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to aibumin prevents length of in vivo activity
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RESULT 1
AAB10356
ID AAB1
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                                                                                                                                                                                                                     cc ligand polypeptide corresponding to amino acid residues 22 to 53 of the sequence represented in AAW31383 and is used in an assay to monitor cligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. A central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a syndrome, in the rapputic agent for dementla, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper and polyphagla, ct hyperlipidaemia, hypercholesterolaemia, hyperalyogridsemia, furner syndrome, neurosis, asthma, rheumatold arthritis, spinal injury, translent brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebeliar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or calpopalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                        Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; ilgand binding; pharmaceuticai; modulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a peptide fragment from a novel rat this and polypeptide corresponding to amino acid residues 22 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand peptide for G protein-coupied receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-363672/
N-PSDB; AAV02422.
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                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 179; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-1996;
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                                12
                                                                                                        1 SRXHXHSMEXR 11
                                                                            Similarity 72.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukusumi S,
Y, Kitada C;
                                                                                                                                                                                                                   3
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                      91.5%;
72.7%;
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                                                                                                                                     Score 43; DB
Pred. No. 0.02
0; Mismatches
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                                                                                                                                                     DB 18;
0.026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hosoya
                                                                                                                                                                   Length 32;
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                                                                                                                                     0,
                                                                                                                                     Gaps
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AAB10356

AAB10356 standard; peptide; 32 AA

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                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the 6 protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, yout and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                                            Rat; corticotrophin releasing hanalgesic; hyperaldosteronism; Addison's disease; adrenal glan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
WD200135984-A1
                       Rattus
                                                                                                Rat CRH
                                                                                                                       24-AUG-2001
                                                                                                                                                  AAG62525
                                                                                                                                                                         AAG62525 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                     srahqhsmetr 11
                                                                                                                                                                                                                                                              SRXHXHSMEXR 11
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                                                                                               releasing
                                                                                                                                                                                                                                                                                       Similarity 72.3
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                    32
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                                                                                                                       (first
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                                                                                             protein related peptide SEQ
                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                  91.58;
72.78;
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                                             gland
                                                                                                                                                                                                                                                                                     Score 43; DB
Pred. No. 0.02
0; Mismatches
                                                                                                                                                                         32
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                                                                     hormone; CRH; G protein receptor ligand;
                                                          hypercortisoisemia; hypoadrenocorticism;
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                                             hyperfunction; obesity.
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                                                                                                                                                                                                                                                                                                  DB 21;
0.026;
                                                                                               ID NO:
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PHIXAXR PRESENTANT
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Best Local
                                                 I8-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
 Fujli R,
Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyssic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercroticolated, secondary or chronic hypoadrenocorticism, Addison's disease (Including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenai gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                 G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pltuitary; central nervous system; pancreas; pro
                                                                                                                                                                   Rat
                                                                                                       26-DEC-1996;
                                                                                                                           10-JUL-1997
                                                                                                                                               W09724436-A2
                                                                                                                                                                                       therapeutic agent.
                                                                                                                                                                                                                               Rat type G
                                                                                                                                                                                                                                                     06-APR-1998
                                                                                                                                                                                                                                                                          AAW31386;
                                                                                                                                                                                                                                                                                             AAW31386
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of G proteln receptor ligand or peptide corticotropin releasing hormone secretion -
                              (TAKE ) TAKEDA
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26-SEP-2000;
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srahqhsmetr 11
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Fukusuml S,
Y, Kitada C;
                                                                                                                                                                                                                                proteln-coupled
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                                                                                                                                                                                                                                                                                                                                                                                                                                         32
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 69;
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2000JP-0297073
                                                                                                                                                                                                                                                   (first entry)
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                                                 96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                               CHEM IND
                                                                                                       96WD-JP03821
                                                                                                                                                                                                                                                                                            Peptlde;
                                                                                                                                                                                                                                                                                                                                                                                                91.5%;
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         Habata
                               LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinuma
                                                                                                                                                                                                                               receptor ligand fragment
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Pred. No.
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          Hlnuma
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0.026;
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          Hosoya
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AAB10357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                               Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig
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                                                                                                                                                                                                               06-JUL-2000.
                                                                                                                                                                                                                                                                                   Rattua sp.
                                                                                                                                                                                                                                                                                                                    veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB10357 atandard; peptide; 33 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
Physiologically-active polypeptide recognized as ligand
                                                                   Matsumoto H,
                                                                                                                                         25-DEC-1998;
                                                                                                                                                                                                                                                WD200038704-AL
                                                                                                                                                                                                                                                                                                                                                                                                          Rat oxytocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB10357;
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on in the central nervous system, pancreas and pituitary gland
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as drugs
medicine
                                                                                                                protein coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
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Disclosure; Page 58; 72pp; Japanese

This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expuision of placenta, uterine recovery failure, caesarean secretion, atoppage of srtificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This promoter. aequence represents a rat peptide which acta as an oxytocin aecretion

Sequence u u 8

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Query Match
Best Local Similarity
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Ş
                 Conservative
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Search completed: September 13, Job time: 501 sec 2002, 09:18:36

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156
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Database :

A\_Geneseq\_032802:\*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Rat prolactin-rele	AAY87504	21	31	94.2	147	11
Human oxytocin sec	AAB10362	21	31	94.2	147	10
Rat oxytocin secre	AAB10355	21	31	94.2	147	· vo
Murine pituitary-d	AAW95174	20	31	94.2	147	00
Murine pituitary-d	AAW95173	20	31	94.2	147	7
Human 19P2 ligand.	AAW87615	20	31	94.2	147	5
Rat 19P2 iigand.	AAW87614	20	31	94.2	147	u
∍ liga	AAW97235	20	31	94.2	147	4
Rat type ligand po	AAW97233	20	31	94.2	147	Ç.
Rat type G protein	AAW31384	18	31	94.2	147	2
Human type G prote	AAW31391	18	31	94 2	147	
Description	ID	BB	Query Match Length DB	Query Match	Score	Result

2 2 X 2

WPI; 1997-363672/33. N-PSDB; AAV02428.

147 94.2 83 22 AAA65123 147 94.2 83 22 AAA6523 147 94.2 87 18 AAW3139 147 94.2 87 20 AAW9722 147 94.2 87 21 AA81032 147 94.2 87 22 AAG6233 146 93.6 31 18 AAW3137 146 93.6 31 20 AAW9701 146 93.6 31 21 AAW9538 146 93.6 31 21 AAW9538 146 93.6 31 21 AAW9538	3332766557432	) <i>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</i>
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## ALIGNMENTS

RESULT	II.T 1	
AAW3	AAW31391	
b	31391	standard; Peptide; 31 AA.
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ಗ	AAW31391;	
X		
	06-APR-1998	'(first entry)
×		•
Œ	Human type G prote	Human type G protein-coupled receptor ligand fragment 1.
×	,	
X	G protein-coupled a	G protein-coupled receptor; ligand binding; pharmaceutical;
X	modulator; pituita:	modulator; pituitary; central nervous system; pancreas; prophylactic;
××	therapeutic agent.	
×		
S	Homo sapiens.	
×		
PN	W09724436-A2.	
9	`10-JUL-1997.	
×		
ΡF	26-DEC-1996; 96W	96WO-JP03821.
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		96JP-0246573.
PR		95JP-0343371.
	15-MAR-1996; 96JI	96JP-0059419.
		96JP-0211805.
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PA	(TAKE ) TAKEDA CHEM IND LTD	IND LTD.
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PΙ	Fujii R, Fukusumi	S, Habata Y, Hinuma S, Hosoya M;
ΡI	Kawamata Y, Kitada C;	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a peptide fragment from a novel human type cligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AAM31390 and is used in an assay to monitor ligand binding to the 6 protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesteroiaemia, hyperglyceridaemia, hypercholesteroiaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyper- syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebeiiar degeneration, oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                    G protein-coupled receptor;
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                                                 Kawamata
                                                                                        (TAKE ) TAKEDA
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f, Kitada C;
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of the G
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WP1; 1999-105614/09

Fujii R,

Hinuma

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Matsumoto H;

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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                   30-DEC-1998.
                                                                                                                                                                                                                 22-JUN-1998;
                                                                                                                                                             23-JUN-1997;
                                                                                                            (TAKE ) TAKEDA CHEM IND LTD.
                                                          Fujii R,
         WPI, 1999-105614/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hdard; peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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CC|||||||
/pdinpawycgrgirpvgrf 31
                                                                                Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pcco, 28
                                                                                                                                                                                                                                          98WO-JP02765.
                                                                                                                                                                                         97JP-0165437
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                                                                                               Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147; DB 20;
Pred. No. 2.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                        Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XX The present sequence represents a human type ligand fragment. It can be present sequence represents a human type ligand fragment. It is seen to the course of the invention. The specification describes a great for modulating prolactin secretion which compled receptors defor a sent for modulating prolactin secretion can be unequised for great for promoting prolactin secretion can be unequised for protein. The agents for promoting prolacting the greating or preventing hypometabolism. They can by used for promoting protein secretion as an aphrot reating or preventing to result in a domestic mammal and as used for the agents for considering prolactin secretion can be used for the autoinmune disease, inhibiting prolactin secretion can memoribe a succious parts for prolacting prolacting promome, and a succious succious and infertility, indome, argonz-del castilo syndrome, argonz-del castilo syndrome or preventing concessively. Chiarity from the promome, argonz-del casting or preventing concessively the syndrome, and as contracting or preventing the inhibitory agents can also be used for tracting or preventing the process of the inhibitory agents and process of tracting or preventing the process of the inhibitory agents and process of tracting or preventing considering placents for the inhibitory agents and process of tracting or preventing the process of the inhibitory agents and process of the process of the inhibitory agents and process of the process of
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                                                                                                                                                                                                                                                                                                                                                      AAW87614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW87614;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19P2 ligand; G protein coupled receptor; pituitary; 19P2 ligand; G protein coupled rat; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP887417-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                      by cleavage producing a 19p2 pituitary G protein receptor ligand by cleavage producing a 19p2 pituitary G preventing and treating dementia, of a fusion protein, useful for preventing and treate breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                    Moriya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                        Claim 5; page 34; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98EP-0111725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-0172118-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score 147; ps 20;
pred. No. 2 3e-17;
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guenaga M,

Tanaka

Mismatches

Length 31; Indels

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Gaps

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seq74-fused-to-seq73.rag use of G protein-coupled receptor ligands - for modulating protection or placental function, e.g. for treating menopausal secretion or placental function, e.g. for abnormal pregnancy syndrome, tumours, autoimmune disease or abnormal pregnancy

Page 4

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28-APR-1997,
                                                      27-APR-1998;
                                                                                            05-NOV-1998.
                                                                                                                      Pitultary-derived ilgand polypeptide; G-protein coupled orphan receptor; strange, screen; therappartic binding; central nervous system; pancreas; creutzfeld-Jakob disease; parkinson's disease; senile dementia; ilgand; muzine; secretion; diabetes; cancer; rheumatold arthritis; growth hormone; gene therapy, transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC Protein-coupled receptor ligand 1992L. A method suitable for the ligand in high-level production of the human pituitary G the ligand in high-level production of 1992L comprises expressing and silf fibroblast sas a recombinant fusion protein e.g. with core been modified to include an N-terminal cysteins residue. The crown that has been protected in the treatment and prevention by cyanylation followed by the general of the treatment and prevention of various diseases protectin secretion-stimulating and can be completely expected by the general of call are brovescular demental, and dementia associated to the crown by cyanylation followed by with general of call-takeb's), endocrine of various diseases including to comprise the same protection of various diseases. Pick's disease, Hunthigton's disease, and diseases, pick's disease, Hunthigton's disease, Pakinson's compounds, the condition of various disease including the protection of the condition of various disease of diseases of the condition of various disease of diseases of the condition of various disease of the condition of various disease of the condition of various disease, including the condition of various disease of the consciousness it is also useful for prevention and treatment of the protactin of th
                                                                                                                                                                                                                                                                                  Murine pituitary-derived iigand mature polypeptide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW95173;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95173 standard; Peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRE 31
1 srthrhsmeirtpdinpawyasrgirpvgrE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tecal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 83.9
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 35; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast cancer, renal fallure and autoimmune disease
97JP-0109974
                                     98WO-JP01923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.23
83.98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 147; DB 20: Length 31;
0; Mismatches 5; Indels
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RESULT
AAW95174
ADW95174
AC AAW9
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DT 10-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC This represents the matured murlne pitultary-derived ligand polypeptide CC sequence. The polypeptide is a ligand for the G-protein coupled orphan CC receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with CC a vector containing the ligand polypeptide. The ligand polypeptide encoding DNA are used to CC fragments, modulate function of the pitultary, central nervous system, CC produce a recombinant ligand polypeptide. The ligand polypeptide, and its CC modulate binding of the polypeptide to screen for agents that CC modulate binding of the polypeptide to the receptor; to quantify the CC amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, CC Parkinson's or Huntington's diseases: Creutzfeld-Jakob disease; poisoning the heavy metals or drugs; dlabetes; schizophrenia; disorders of growth CC hormone secretion; cancer; rheumatoid arthritis, epilepsy and many CC others, also to improve post-operative nutritional status and as conversed or its mutein are used to study the function of the polypeptide encoding CC DNA or its mutein are used to study the function of the polypeptide. CC expressing genes, as models of disease, for drug screening and as source of call lines. The ligand polypeptide DNA is used as a source of probes and to develop transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor, GPR10; UHR-1; modulator; pituitary: central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
                                                              27-APR-1998;
                                                                                                                          05-NOV-1998
                                                                                                                                                                                                                                                    Mus sp
                                                                                                                                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine pltuitary-derived ligand polypeptide antigenic epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW95174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95174 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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for treating disorders of central
pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (flrst entry)
                                                                                                                                                                                                                                                                                                                transgenic
                                                              98WO-JP01923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 31
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20;
2.3e-17;
hes 5;
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                                                                                                                                                                                                                                                                                                                                             vasopressor,
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1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31

Matches Query Match Best Local

Similarity

94.2%;

Conservative

0

Score 147; DB 20; Pred. No. 2.3e-17; 0; Mismatches 5;

Length 31; Indels

0:

Gaps

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diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatold arthritis, epllepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. Sequences AAM95174 to AAW95178 represent antigenic epiotpes which can be used for the preparation of anti-ligand polypeptide antibody.
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to scene for agents the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkingon's or Huntington's
Sequence
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for treating disorders of central nervous system, pituitary and
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                                                                                                                Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig
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25-DEC-1998;
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                                                                                 Rattus sp
                                                                                                     veterinary medicine;
                                                                                                                                                          Rat oxytocin secretion promoting peptide SEQ ID NO:
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                          Physiologically-active polypeptide recognized as ligand by protein-coupled receptor protein, for promoting secretion as drugs for diseases relating to oxytocin secretion and i
                                                                                                                                                                                                                                                                                                                             treatment; disease; pain; atonic bleeding; uterine recovery caesarean section; artificial fertilization; galactostasis;
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                                                                                                          Identifying modulators of body weight by a combination of a coor ceil-based assay to identify modulators of GPR10, followed vivo assay for the compounds effect on e.g. feeding behavior.
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14-OCT-1998;
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feeding behaviour; food intake;
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The invention relates to a method for identifying compounds useful for modulating body weight. The method comprises call-free and/or call-based assays that identify compounds which bind to and/or activate or inhibit the activity of GPRIO, a G protein-coupled receptor. These assays are then followed by an in vivo assay of the effect of the compound on feeding behaviour, body weight or metabolic rate in a mammal. Prolactingleasing peptide (PrRP; AAY87504) is a ligand of GPRIO. Binding of PrRI releasing peptide (PrRP; AAY87504) is a ligand of GPRIO.

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                                                                                         The Invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences ANY49290-302 represent peptide fragments of the 19P2 ligand.
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dylng diseases related
srahqhsmetrtpdinpawytgr91rpv9rf 31
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                                                                                                              26; Conservative
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o ligand abnormality
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                                                                                                                 Mismatches
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anaigesic;
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                                                                                                                                                                      Human
                                                                                                                                                                                                                          AAG62531;
                                                                                                                                                                                                                                                   AAG62531 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
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26-SEP-2000; 2000JP-0297073
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          17-NOV-2000; 2000WO-JP08119
                                      25-MAY-2001
                                                              WO200135984-A1
                                                                                       Homo sapiens
                                                                                                                 Addison's disease;
                                                                                                                               analgesic; hyperaldosteronism;
                                                                                                                                         Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
                                                                                                                                                                                                24 - AUG - 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corticotrophin releasing hormone; CRH; G protein receptor iigand; gesic; hyperaidosteronism; hypercortisolaemia; hypoadrenocorticism; son's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-355552/37.
                                                                                                                                                                                                                                                                                                                 srahqhsmetrtpdinpawytgrgirpvgrf 31
                                                                                                                                                                     CRH releasing protein related peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Page 69; 90pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                Similarity
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.3e-17;
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                                                                                                                             hypoadrenocorticism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corticotropin releasing hormone secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of G protein receptor ligand or peptide
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26-SEP-2000; 2000JP-0297073.
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pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s derived by analysis of the total score distribution.
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A. Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqP-emb1/AA1981.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqP-emb1/AA1982.DAT:*

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3: /SIDS1/gcgdata/hold-geneseq/geneseqP-emb1/AA1984.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneseqP-emb1/AA1985.DAT:*

5: /SIDS1/gcgdata/hold-geneseq/geneseqP-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/hold-geneseq/geneseqP-emb1/AA1987.DAT:*

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8.615 Million cell updates/sec
             Human type G prote
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modulator; pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                        26-DEC-1996;
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                                                                 Fujii R, Fukusumi S,
Kawamata Y, Kitada C;
                                                                                                           (TAKE ) TAKEDA CHEM IND LTD
                    WPI: 1997-363672/33.
N-PSDB: AAV02428.
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Bovine G protein-C
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Bovine pituitary-d
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Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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2; Page 184; 258pp; Engiish.
         peptide for G protein-coupled receptor - acts by modulating
on in the central nervous system, pancreas and pituitary giand
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This sequence represents a peptide fragment from a novel human type collegand polypeptide corresponding to amino acid residues 23 to 53 of the CC sequence represented in AAW31390 and is used in an assay to monitor compositions containing this ligand may be used as a pituitary monitor compositions containing this ligand may be used as a pituitary function composition. This ligand revous system modulator or a pancreatic function composition and could have specific applications as a private function composition of the could have specific applications as a private function composition of the could have specific applications as a private function composition of the could have specific applications as a private function composition of the consciousness, antiety syndrome, hyperkinetic compositions, disturbance of consciousness, antiety syndrome, schizophrenia, composition of the consciousness, antiety syndrome, schizophrenia, composition, hypercholesterolaemia, hyperglyceridaemia, composition, partiety, asthma, rheumatoid arthritis, spinal injury, composition, composition, atopic dermatitity, spinocerebellar degeneration, configuration of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.

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                                                             Query Match

Best Local Similarity 100.0

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                         AAW97235
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AAW97235;
        AAW97235 standard; peptide; 31
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06-MAY-1999 (first entry) type iigand polypeptide fragment.

Ry e ligand; modulation; prolactin secretion;

Xx 'coupled receptor; GPCR; hypoowarianism; genecyst cacogenesis;

Xx 'syndrome; eurhyroid; hypometabolism; lactation;

Xx 'monomatosis; brain tumour; emmeniopathy; autoimmune disease;

Xx 'MO9858963-Ajdrome; syndrome; argonz-dei castilo syndrome;

D 30-DEC-1998. nn; unthrifty fetus; abnormai saccharometabolism;

22-UDW-1n. oxytocia.

(TAKE ) TAREDA CHEN IND LTD. Fujli R, 23-JUN-1997; Hinuma s, 97JP-0165437. 98WO-JP02/ Kawamata Y, Matsumoto h

WPI; 1999-105614/09.

Use of G protein-coupled receptor ligands - for modulating prolactin serretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy

Claim 3; Page 159; 241pp; English.

The present sequence represents a human type ligand fragment. It colored is used in the course of the invention. The specification describes of ligand polypeptide or a salt, for a grotein which comprises a salt, for a grotein coupled receptor (GPCR) or treating or preventing hypovarianism, generating secretion can be used for coupled receptor (GPCR) or syndrome, enthyroid or hypometabolism. They can by used for promoting contributing prolactin secretion can be used for inhibiting prolactin secretion can be used for treating or preventing contributing prolactin secretion can be used for treating or preventing contributing prolactinoma, infertility, impotence, amenoriopathy, autoimmuna disease, contributions, chiari-trommel syndrome, amenoriopathy, autoimmuna disease, condulating placental function can be used for treating or preventing condulating placental function can be used so contraceptives. The agents for condulating placental function can be used as contraceptives. The agents for choriccarcinoma, hydatid moie, intuption moie, aboutton, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocla.

片 ş Query Match Best Local s Matches 31 ω Similarity Conservative 100.0%; Score 171; DB 20; 100.0%; Pred. No. 4.1e-19; tive 0; Mismatches 0; Indels Length 31; 0 Gaps

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AXX PER SECOND S AAW87615 RESULT 19P2 ligand; (prolactin rel therapy. Human 19p2 ligand. AAW87615 standard; Peptide; 31 AA. 29-MAR-1999 AAW87615; releasing G (first entry)

Protein coupled receptor; pituitary; asing peptide; human: dementia; breast cancer;

27-JUN-1997, ,8661-אטע-25 30-DEC-1998 EP887417-A2. Homo sapiens. 97JP-0172118, 98EP-0111725.

(TAKE ) TAKEDA CHEM IND LTD. Nishimura O, Suenaga ĭ Tanaka r;

WPI; 1999-047884/05.

Claim 5, Page 35, S6pp, English Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease by cieavage dementia,

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RESULT
AAH10362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ammonolysia. 1971 has prolactin secretion atimulating and (at CC high doses) prolactin secretion inhibiting properties. It can be used in the treatment and prevention of various diseases. It can be considered that the treatment and prevention of various diseases. It can be senile dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's consease, Pick's disease, Huntington's disease, Infectious diseases of the consecution of the properties or metabolic disease or consciousis (e.g. hypothyroidism, vitamin Bl2 deficiency, alcoholism, contextion by druga, metal and organic compounds), tumourlgenic contextication by druga, metal and organic compounds; tumourlgenic context of the consciousness and treatment of consciousness. It is also useful for prevention and treatment of consciousness. It is also useful for prevention and treatment of consciousness. It is also useful for prevention and treatment of consciousness associated with prolactin hypo and hypersecretion consciousness, infertility, impotence and autoimmune disease breat cancer, infertility, impotence and autoimmune disease. The laps polypeptide/amide is also useful as a test categority of the prolactin secretory function or as a disorders). The laps polypeptide/amide is also useful as a test cancer in mammalian farm animals.
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                                                                                                                                                                                                                                                                                                      Human; oxytocin secretion promoter; G protein coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failur caeaarean aection; artificial fertilization; galactostasia; goat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. human basic fibroblast growth factor (see AAV83796-97) that he been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation foilowed by
                                                                                                                                                                                                                                                                                                                                                                                  Human
                                               Matsumoto H,
                                                                                                                                                                                     06-JUL-2000
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                                                                                                                                                                                                                                                                                           veterinary medicine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                      New monoclonal antibodies, u
studying diaeases related to
                                                                                                                                                                                          21-MAY-1998;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; 19p2 ligand; diagnoaia; prolactin secretion;
pituitary; regulatory mechanism; central nervous system; pancreat
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                                                                                                                                                                                                                99WO-JP02650
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The invention provides a monoclonal antibody which has a apecific reaction with the part peptide of the C-terminal of 1992 ligand or derivative. The antibodies can be used in diagnosia or to treat or prevent diseases associated with abnormality in the pituitary funct regulatory mechanism (e.g. promotion of prolactin accretion), centi

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                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 31; Conservative (
                                                                                                                                   The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisoidemia, secondary or chronic hypodremocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                         Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
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26-SEP-2000; 2000JP-0297073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; corticotrophin releasing hormone;
analgesic; hyperaldosteronism; hypercort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CRH releasing
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hypoadrenocorticism;
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10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying
peptidase
                                                                                                                                                                                                                                                                      bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succilindidy) and maleimide groups) attached a less therapeutically active amino acid region (IV), which covalently
                                                                                                                                                                                         intracellular uptake and interference with physiological procamb90829 to AAB92441 represent peptides which can be used in exemplification of the present invention.
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blood component; modification; succinimidyl: maleimido group; amino;
hydroxyl; thloi; hormone; growth factor; neurotransmitter.
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100.
illarity 100.
Conservative
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990S-0159783.
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                            Score 171; DB 22;
Pred. No. 4.1e-19;
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in vivo activity
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RESULT
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                                                                                                                                                                                                                 This sequence represents a peptide fragment from a novel human type illigand polypeptide corresponding to amino acid residues 23 to 54 of the sequence represented in AAW31330 and is used in an assay to monitor illigand binding to the G protein-coupled receptor protein Paramaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function commodulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper and polyphagia, for hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperis syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, cransient brain ischaemia, epilepsy, amyiotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerabellar degeneration, consense and/or consolusatia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting
                                                                                                            Matches
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28-DEC-1995;
15-MAR-1996;
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                                                                  SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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)B; AAV02429.
                                                    srthrhsmeirtpdinpawyasrgirpvgrf 31
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                                                                                                                         Similarity
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                                                                                                                                                                                                          of the G protein-coupled receptor protein.
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                                                                                                            Conservative
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96JP-0059419.
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                                                                                                      100.0%; Pr
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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                                                                                                                        Score 171; DB 1
Pred. No. 4.2e-1
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                                                                                                            Mismatches
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em, pancreas and
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RESULT 1
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; plg;
                                                                                                                                                                                                                                                                                                        AAG62532 standard; peptIde;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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31; Conserv
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Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenel gland hyperfunction; obesity.

Human 24-AUG-2001 AAG62532;

CRH

protein

related

peptide SEQ

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(first entry)

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AAW31393
ID AAW:
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                         18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful as an analyssic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence describes a method of controlling the secretion of controlling the use of a G protein controlling the secretion of CRH and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 74; 90pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein receptor ligand or peptide for controlling corticotronin releasing hormone secretion .
                                                                                                                                             W09724436-A2
                                                                                                                                                                                                                                               Human type G protein-coupled receptor ligand fragment 3.
                                                                                                                                                                                                                                                                          06-APR-1998
                                                                                                                                                                                                                                                                                                                           AAW31393 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor ligand. This can be used to control the secretion of CRH and useful as an analyssic or for treating process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitada C,
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                            therapeutic
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26-SEP-2000; 2000JP-0297073;
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(TAKE ) TAKEDA
                                                                                          26-DEC-1996;
                                                                                                                   10-JUL-1997
                                                                                                                                                                                                        nodulator; pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nvention.
                                                                                                                                                                                                         protein-coupled receptor; ligand binding;
odulator; pituitary; central nervous system
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                             agent.
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                         96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
  CHEM IND
                                                                                          96WO-JP03821.
                                                                                                                                                                                                                                                                                                                           Peptide; 33
  LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 171; DB :
Pred. No. 4.2e-
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                                                                                                                                                                                                         system;
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                                                                                                                                                                                                        pancreas; prophylactic;
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CC Injury polypeptide corresponding to amino acid residues 23 to 55 of the CC ligand polypeptide corresponding to amino acid residues 23 to 55 of the CC sequence represented in AAW31330 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypergrolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC capable of altering the binding activity of the ligand affecting CC capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujii R,
Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligand peptide for G protein-coupied receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-363672/33.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hosoya M;
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Ouery Match
Best Local Similarity
Matches 31; Conserv \_ 1 SRTHRHSMEIRTPDINPAMYASRGIRPVGRF 31 srthrhsmeirtpdinpawyasrgirpvgrf 31 100.0%; llarity 100.0%; Conservative ( 0 Score 171; DB 18; Pred. No. 4.4e-19; Mismatches 0 Length Indels 33 9 Gaps 0

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AAB10364 RESULT AAB10364; AAB10364 24-NOV-2000 12 standard; (first peptide; entry) u u

Human; oxytocin secretion promoter; G protein coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; miik production. (O.

Human oxytocin secretion promoting peptide SEQ ID NO:

34

Homo sapiens.

WO200038704-AJ

06-JUL-2000

22-DEC-1999; 99WO-JP07199

25-DEC-1998;

98JP-0369585

(TAKE ) TAKEDA CHEM IND LTD

Matsumoto Ξ Kitada C, Hinuma

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RESULT JAG6 2533 ID AAG6 2533 ID AAG6 2533 ID AAG6 2533 ID AAG6 XX AAG6 XX Huma KW Bnall KW Bnall KW Bnall KW Addid XX Home XX Home XX Home XX Home XX Home 25-3 XX IS-1 PR 26-1 XX IS-1 PR 26
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Best Local
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The present sequence describes a method of controlling the secretion controlling the use of a G prote conticotrophin releasing hormone (CRH), involving the use of a G prote receptor ligand. This can be used to control the secretion of CRH and useful as an analyssic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism,
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26-SEP-2000;
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                                                                                                                                                                                                                   Use of G protein receptor iigand or peptide for controlling conticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analgesic; hyperaldosteronism; h;
Addison's disease; adrenal gland
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                                                                                                                                                                      Disclosure;
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                                                                                                                                                                   Page 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000JP-0297073
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Pred. No. 4.4e-19;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g hormone; CRH; G protein receptor ligand;
hypercortisolaemia; hypoadrenocorticism;
nd hyperfunction; obesity.
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                                                          G protein
CRH and is
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This sequence represents a novel human type ligand polypeptide encoded CC by pHOB7 which is used in an assay to monitor ligand binding to the GC protein-coupled receptor protein. Pharmaceutical compositions CC containing this ligand may be used as a pituitary function modulator. This CC central nervous system modulator or a pancreatic function modulator. This CC capent for dementia, depression, hyperkinetic syndrome, disturbance of CC consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone CC secretory disease, hyper- and polyphagia, hypercholesterolaemia, the hyperlipidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, cc amylotrophic lateral scierosis, acute myocardial infarction, cc spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthms, epilepsy, infertility and/or oligogalactis. Assays
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Best Local
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09724436-A2
                                                                                                                                                                                                                                           Claim 3; Page 183; 258pp; English.
                                                                                                                                                                                                                                                                     Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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N-PSDB; AAV02427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-1997
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modulator; pituitary; central nervous system; pancreas; pro
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Y, Kitada C
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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Pred. No. 4.4e-1
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Best Local S
Matches 31
The present sequence represents a human type ligand polypeptide. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a 6 protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, enthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodistac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autolimune disease, prolactinoma, infertility, impotence, amenorihea, gaiactourhea, accomegaly, Chiari-Frommel syndrome, Argonz-de Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome car dyszoospermia. The inhibitory agents can also be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; plituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dygzoospermia; contraceptive; placental function; chorlocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocla; prolactin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein coupled receptor protein.
                                                                                                                                                                                                                                               Disclosure; Page 158; 24lpp; English.
                                                                                                                                                                                                                                                                              Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-105614/09.
N-PSDB; AAX15526.
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                                                                                                                             contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
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1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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Search completed: Job time: 499 sec

September 13,

2002, 09:18:34

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23

srthrhsmeirtpdinpawyasrgirpvgrf

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
AC. NO! AAW31394
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DM protein - protein search, using sw model

9 September 13, 2002, 09:18:34; Search tlme 399.68 Seconds (without alignments) 6.114 Million cell updates/sec

Title: Perfect score: US-09-446-543A-73

**TPDIHPAWYXXRGIRPVGRFXX** 22

Scoring table: BLOSUM62

747574 seqs, 111073796 residues Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB scq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minlmum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_032802:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is darived by analysis of the total score distribution.

Regult Ho.	Score	Query Match	Length DB	Ħ	ID	Description
P	105	96.3	20	16	AAW31394	Human type G prote
Ŋ	105	96.3	20	20	AAW97236	Human type ligand
w	105	96.3	20	2	AAB10365	
4	105	96.3	20	21	AAY49294	1982 ligand peptid
Jun	105	96.3	20	22	AAG62534	Human CRH releasin
<u>@</u>	105	96.3	20	<u>ې</u>	AAB90992	Prolactin releasin
7	105	96.3	21	8	AAW31395	Human type G prote
00	105	96.3	21	21	AAB10366	Human oxytocin sec
9	105	96.3	21	22	AAG62535	Human CRH releasin
10	105	96.3	22	18	AAW31396	Human type G prote
11	105	96.3	22	21	AAB10367	Human oxytocin sec

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н	2	Prolactin releasin	ይ	CRY I	igand	2 llgand p	ytocin sec	oxytocin s		ine pituitary	ъ.	Bovine pituitary-d	Bovine G protein-c	ype G	Numan CRH releasin	Human oxytocin sec	Human typc Iigand	O	CRH reies	500	type	relea	oxytoca	e G pro	reieas	ctin	ᄗ	ligai	OXYEO	19P2	type is	type G pro	Human CRH releasin	1/-

## ALIGNMENTS

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CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the CS sequence represented in ANW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperipidaemia, hypercholesteroleemia, hypergripycridaemia, compositions, neurosis, asthma, rhemmatoid arthritis, spinal injury, CC Turner's syndrome, neurosis, asthma, rhemmatoid arthritis, spinal injury, CC acute myocardial infarction, infertility, spinocerebeilar degeneration, CC oligopalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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Matches 18
                                                                                                                                                                                                                                        Rat type ligand; modulation; prolactin secretion; gonecyst cacogenesis; gonecyst-cacogenesis; protein-coupled receptor, GPCR, hypoporarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinome; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; turuption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
             Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                          Human type ligand polypeptide fragment.
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                                                                                                                                                                                                      HOMO
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                                           (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 185;
             Hinuma
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2.5e-11;
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Best Local
        Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, and in veterinary as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                            ₩PI;
                                                                                                                                                                                                                                                                                                                                                Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; plg;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein-coupled receptor ligands - for modulating prescretion or placental function, e.g. for treating menopausal
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                                                                                                                                                                                                                                                                        WO200038704-AL
                                                                                                                                                                                                                                                                                                                                                                                                                  Human oxytocin secretion promoting peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB10365 standard;
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                                                                                                                                        (TAKE ) TAKEDA
                                                                                                                                                                         25-DEC-1998;
                                                                                                                                                                                                         22-DEC-1999;
                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    veterinary medicine;
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2.6e-11;
hes 2;
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Best Local S
Mstches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel oxytocin secretion-regulating sgent which contains a ligand peptide or its sait for the G protein-coupled receptor protein. It is useful in the form of drugs for amediorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, terrine recovery failure, csessresn section, stoppage of artificial fertilization or gaiactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central mervous regulatory mechanism, and pancrestic function regulatory mechanism. The antibody-based immunosassy can slso be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                  Disclosure; Page 26; 73pp; Japanese.
                                                                                                                                                             studying
                                                                                                                                                                                                                              Matsumoto H,
                                                                                                                                                                                                                                                                                                          20-MAY-1999;
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                                                                                                                                                            monoclonal antibodies, dying diseases related
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18; Conserv
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/ mechanism; centrai nervous system
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Pred. No. 2.6e-11;
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abnormality
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Best Local S
Matches 18
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                                                       Best Local
                                                                Ouery Match
                                                                                                                               The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or smellorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including horedom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrensi giand hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                 Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                 Sequence
                                                                                                                                                                                                                                             Claim 4; Page 75; 90pp; Japanese.
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26-SEP-2000; 2000JP-0297073
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Addison's disease: sdrenal gland hyperfunction; obesity.
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18; Conserv
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18; Conserv
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Pred. No. 2.6e-11;
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2.6e-11;
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                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) C comprising a therapeutically active amino acid region (III) and a CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to CC a less therapeutically active amino acid region (IV), which covalently CC bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. CC (1) are useful for modifying therapeutic peptides e.g. hormones, growth CC factors and neurotransmitters, to protect them from peptidase activity CC in vivo for the treatment of various disorders. Endogenous therapeutic CC administration due to rapid degradation by peptidases in the body. CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (haif CC infe) and specificity as bonding to large molecules decreases (CC intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the creative contracellular interference with physiological processes.
                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conser
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10-SEP-1999;
15-OCT-1999;
AAW31395;
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                          AAW31395 standard;
                                                                                                                                                                                                                                       Sequence
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hydroxyl; thiol; hormone; growth factor; neurotransmitter
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99US-0153406.
99US-0159783.
                           Peptide; 21
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2.6e-11;
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                                                                                                                                                                                                                             CC This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 54 of the CC sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic construence, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, figure, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, cransient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebeilar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or cligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                   RESULT
                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
   AAB10366 standard;
                                                                                                                                                                                                                            Sequence
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N-PSDB; AAV02432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09724436-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human type G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulator; pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor; ligand binding; pharmaceutical;
odulator; pituitary; central nervous system; pancreas; prophylactic;
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                                                                                                               1 TPDINPAWYXXRGIRPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukusumi S, '
                                                                                                                                             96.3%;
nilarity 90.0%;
Conservative
                                                                                                                                                                                                                             21
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95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-JP03821
peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Habata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H
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                                                                                                                                               0
                                                                                                                                             Score 105; DB 18;
Pred. No. 2.8e-11;
0; Mismatches 2
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                                                                                                                                                                             DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hosoya M;
                                                                                                                                                                           Length 21;
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AAB10366

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RESULT
AAG62535
                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                           This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, protein-coupled receptor protein, for promoting secretion and in veterinary and drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; cassarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                              Human
                                                                                                                  24-AUG-2001
                                                                                                                                        AAG62535;
                                                                                                                                                            AAG62535
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                   Addison's disease;
                                                             analgesic;
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200038704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                             ø
                                                                                           CRH releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oxytocin
                                                           corticotrophin releasing hormone; CRH; G protein receptor sic; hyperaidosteronism; hypercortisolaemia; hypoadrenocori
                                                                                                                                                                                                                                                            18;
                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                         Conservative
                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0369585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-JP07199
                                                                                                                                                           peptide;
                                                  adrenai gland
                                                                                           protein related peptide SEQ
                                                                                                                entry)
                                                                                                                                                                                                                                                                    96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoting peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinuma
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                                                                                                                                                                                                                                                                   Score 105; DB 21;
Pred. No. 2.8e-11;
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                                                                                                                                                                                                                                                          Migmatches
                                                   hyperfunction;
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                                                 ia; hypoadrenocorticism;
obesity.
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                                                                                                                                                                                                                                                                             Length
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RESULT 10
AAW31396
ID AAW313
Matches
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Best Local
                                                                      18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysis or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaidosteronism, hypercortisolaemia, secondary or chronic hypeadrencorticism, Addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                      Fujii R,
                                                                                                                                                                                                                                                      G protein-coupied receptor; iigand binding; pharmaceuticai;
modulator; pituitary; centrai nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                      06-APR-1998
                                                                                                                                                                                                                                                                                                                                                                       AAW31396 standard; Peptide;
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                                                                                                                                                                10-JUL-1997
                                                                                                                                                                                       WO9724436-A2
                                                                                                                                                                                                                                                                                           Human type G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corticotropin releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-1999;
26-SEP-2000;
                                             (TAKE ) TAKEDA
                                                                                                                                                                                                                                          therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND
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                                                                                                                                     26-DEC-1996;
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TPDINPAWYXXRGIRPVGRF 20
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G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
          ×
      Fukusumi S, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein receptor ligand
                                                                                                                                                                                                                                                    pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
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                                                                                                                                                                                                                                        agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-0327900
2000JP-0297073
                                                                                                                                                                                                                                                                                           protein-coupled.receptor ligand fragment
                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                      96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                              CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90pp; Japanese.
                                                                                                                                                                                                                                                    centrai nervous system;
                      Habata
                                              LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105; DB 22;
Pred, No. 2.8e-11;
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                      Hinuma
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                     Hosoya
                                                                                                                                                                                                                                                   pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of CRH and 1s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 11
AAB10367
ID AAB103
XX AAB103
XX Human
AX Human
XX Homo &
XX VOLCE
IN WO2000
XX WO2000
XX WO2000
XX WO2000
XX Homo &
XX WO2000
XX YOLCE
IN WO2001
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XX Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represented in ARMINION and is used in an assay to monitor colligion binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function composition. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic cyndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, cynyperprolactinaemia, hypercholesterolaemia, hypercylocaridaemia, cynypercylocaridaemia, cynypercylocaridaemia, cynypercylocaridaemia, cynypercylocaridaemia, hypercylocaridaemia, hypercylocaridaemia, hypercylocaridaemia, hypercylocaridaemia, cynypercylocaridaemia, cynypercylocaridaemi
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Best Locai s
Matches 18
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N-PSDB;
   Physiciogically-active polypeptide recognized as ligand protein-coupled receptor protein, for promoting secretic
                                                                                                                                                             Matsumoto
                                                                                                                                                                                                                                                                                          25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                    22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200038704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; oxytocin secretion promoter; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human oxytocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB10367,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB10367 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligand
                                                                                                                                                                                                                       (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                2000-452298/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPDINPAWYXXRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1997-363672/33
DB; AAV02433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aitering
of the G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                             Kitada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%;
                                                                                                                                                             Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoting peptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production.
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Pred. No. 2.9e
0; Mismatches
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ding; uterine recovery failure; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
.9e-11;
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   s ligand by secretion
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   of G
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oxytocin.
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RESULT 1
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Best Local
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medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytoch secretion e.g. weak pains and atonic bleeding, before and after expuision of piacenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                            Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                  Kitada C,
                                                                                                                                                                                                                            18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
                                                                                                                                                                                                                                                             17-NOV-2000; 2000WO-JP08119
                                                                                                                                                                                                                                                                                                      WO200135984-Ai.
                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                                                 Addison's
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                                                                                                                                                             2001-355552/37.
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                                                                                                                                                                                                                                                                                                                                               corticotrophin releasing hormone; CRH; G protein receptor ligand; sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; n's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diseases relating to oxytocin secretion and
                                                                                                                                                                                                                                                                                                                                                                                          releasing
                                                                                                                                                                                   Matsumoto H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 64;
                                                                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
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Pred. No. 2.
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.9e-11;
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The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G proteir receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or smellorating diseases associated with CRH secretion such as hyperaidosteronism, hypercortisolaemia, secondary or chronic hypoadrencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the

protein H and is

Disclosure;

Page 75; 90pp; Japanese

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CC This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the CC sequence represented in AAW31390 and is used in an assay to monitor CC digand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, thypergrolactinaemia, diabetes, cancer, pancreatitis, renai disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC translent brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC capable of altering the binding activity of the ligand affecting CC activation of the grotein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         Fujii R,
Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary, central nervous aystem; pancreas; pro
                                                                                                                                                                                                                                                                                             Ciaim
                                                                                                                                                                                                                                                                                                                                     Ligand
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                                                                                                                                                                                                                                                                                                                       function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-1996;
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                                                                                                                                                                                                                                                                                          2; Page 184; 258pp; Engiish.
                                                                                                                                                                                                                                                                                                                 peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi S, ,
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Hosoya M;
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RESULT 14
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          The present sequence represents a human type ligand fragment. It
CC is used in the course of the invention. The specification describes
CC an agent for modulating prolactin secretion which comprises a
CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
CC protein. The agents for promoting prolactin secretion can be used for
CC treating or preventing hypocovarianism, genecyst cacogenesis, menopausai
CC syndrome, euchyroid or hypometabolism. They can by used for promoting
CC inhibiting prolactin secretion can be used for treating or preventing
CC inhibiting prolactin secretion can be used for treating or preventing
CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
CC prolactionma, infertility, impotence, amenorrhea, galactorrhea,
CC prolactions, infertility impotence, amenorrhea galactorrhea,
CC prolactions, infertility syndrome, Argonz-del Castilo syndrome,
CC prolactions, infertility syndrome, Argonz-del Castilo syndrome,
CC prolactions of the syndrome of the syndrome of the agents for
CC comegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
CC comegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
CC controlactions, hydrome, lymphoma, Sheehan syndrome or dyszoospermia.
CC controlactions, hydrome, hydrome, about on mole, about on mole, about of treating or preventing
CC chorres agents and about a horrary includes the syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                        Use of G protein-coupled receptor ligands - for modulating presecretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-105614/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1997;
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12 tpdinpawyasrglrpv9rf 31
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90.0%;
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Pred. No. 4.3e-11;
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lipidmetabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                 for modulating prolactin
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oxytocia

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RESULT 15
AAW87615
 Thia is the amino acid sequence of the human pituitary G commercial high-level production of 1992L comprises expressing CC the ligand in host ceils as a recombinant fusion protein e.g. with CC human basic fibroblast growth factor (see AAV83796-97) that has CC been modified to include an N-terminal cysteine residue. The CC high doses protactin secretion setimulating and (at CC high doses) protactin secretion-inhibiting properties. It can be CC used in the treatment and prevention of various diseases including: CC with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's CC disease, Pick's disease, Huntington's disease), infectious diseases (e.g. Creutzfeidt-Jakob's), endocrine or metabolic disease or cc diseases (e.g. bypothyroidism, vitamin B12 deficiency, alcoholism, CC intoxication by druga, metal and organic compounds), tumourigenic CC subarachnoidal heamorrhage, and other types of dementia, derpession, CC hyperactive child syndrome (microencephalopathy) and disturbance of CC consciousess. It is also useful for prevention and treatment of CC disease associated with prolactin hypo and hypersecretion consciousness. It is also useful for prevention and treatment of CC disease consciousness. It is also useful for prevention and treatment of CC disease associated with prolactin hypo and hypersecretion consciousness. It is also useful for prevention and treatment of CC disease associated with prolactin hypo and hypersecretion consciousness. It is also useful for prevention and treatment of CC disease associated with prolactin hypo and hypersecretion disease in the consciousness of the consciousness. It is also useful for hyporal action hypersecretion consciousness is considered with prolactin hypo and hypersecretion consciousness.
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing a 1972 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breaat cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19P2 ligand; G protein coupled receptor; pituitary; prolactin releasing peptide; human; dementia; breast cancer;
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and seminal vesicle
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Pred. No. 4.3e-11;
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dementia,
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Search completed: September 13, 2002, 09:18:34 Job time: 499 sec
                                                                                                                             Query Match
Best Local Sim
Matches 18;
                                                                                                                                                                                                                           osteoporosis, menopausai syndrome and renal failure (hyposecretion disorders). The 1992 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                                                                                                                                                  Sequence
                                                                                                                            Local Similarity 90.0
                                                                 12 tpdinpawyasrgirpvgrf 31
                                                                                   1 TPD1NPAWYXXRGIRPVGRF 20
                                                                                                                                                                                                   31 AA;
                                                                                                                                         96.3%;
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                                                                                                                                         Score 105; DB 20;
Pred. No. 4.3e-11;
                                                                                                                               Mismatches
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 09:18:34; Search time 399.68 Seconds (without allgoments) 6:114 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73 109

Scoring table: TPDINPAWYXXRGIRPVGRFXX 22

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 1008
Listing first 45 summaries

Database : A\_Geneseq\_032802:\* 1: /SIDS1/qcqda+>/

1: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID  1 105 96.3 20 18 AAW31394 Human type G prote 2 105 96.3 20 20 AAW97236 Human type ligand 3 105 96.3 20 21 AAS10365 Human oxytocin sec 4 105 96.3 20 21 AAX49294 19P2 ligand peptid 5 105 96.3 20 22 AAX62534 Human CRH releasin 6 105 96.3 20 22 AAS90992 Prolactin releasin 6 105 96.3 20 18 AAW31396 Human CRH releasin
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Peptide PrRP20 fra	AAB46954	2.2	20	95.4	104	Ü
in relea	AAB90996	22	20	95.4	104	4
Prolactin releasin	AAB90994	22	20	95.4	104	w
eı	AAG62527	22	20	95.4	104	i.
н	AAG62519	22	20	95.4	104	H
2 ligand	AAY49302	21	20	95.4	104	o
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ytocki secr	AAB10358	21	20	95.4	104	8
oxytocin s	AAB10350	21	20	95.4	104	7
Pituitary-	AAW95175	20	20	95.4	104	6
ine pituitary	AAW95191	20	20	95.4	104	ŭ
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ype G	AAW31387	18	20	95.4	104	ĭ
CRH relea	AAG62530	22	87		105	ŏ
OXYTO	AAB10361	21	87		105	9
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CRH rele	AAG62533	22	ω u		105	8
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CRH rele	AAG62532	22	υ C3		105	ដ
OXY LOC	AAB10363	21	32		105	2
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n CRH re	AAG62531	22	<u>3</u> 2		105	6
ligand per	AAY49291	21	31	٥.	.105	7
oxyto	AAB10362	21	31	96.3	105	6
19P2	AAW87615	20	31	96.3	105	5
type ligand	AAW97235	20	Ω L	96.3	105	4
type G pro	AAW31391	18	3	96.3	105	ū
Human CRH releasin	AAG62536	22	22	96.3	105	2
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### ALIGNMENTS

ž	X	X	X	×	B	X	3	×	ಕ್ಷ	X	Ħ	AAW31394	RESULT
	therapeutic agent.	modulator; pituitary; central nervous system; pancreas; p	6 protein-coupled receptor; llgand bindlng; pharmaceutica		Human type G protein-coupled receptor llgand fragment 4.		06-APR-1998 (first entry)		AAW31394;		AAW31394 standard; Peptide; 20 AA.	1394	CO 1

utical; as; prophylactic;

Homo sapiens

W09724436-A2

10-JUL-1997

26-DEC-1996; 96WO-JP03821.

18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996; 96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805.

(TAKE ) TAKEDA CHEM IND LTD.

Fujii R, Fukusumi S, Kawamata Y, Kitada C; Habata Y, Hinuma Ś Hosoya M;

WPI; 1997-363672/33. N-PSDB; AAV02431.

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function

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central

nervous

system, pancreas and pituitary giand

Ligand peptide for G protein-coupled receptor - acts by modulating

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RESULT
AAW9723
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Matches 18
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                                                                                                                                                                                                                                                                                                           Rat type ligand; modulation; prolactin secretion; gonecyst cacogenesis; gonetein-coupled receptor; GPCR; hypowarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autolemune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommei syndrome; Argonz-del Castilo syndrome; forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to mainto acid residues 34 to 53 of the sequence represented in AAR31390 and is used in an assay to monitor ligand binding to the 6 protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic appropriate the formal prophylactic or therapeutic agent for dementia, depression, hyperkinetic appropriate the formal prophylactic or therapeutic agent for dementia, depression, hyperkinetic appropriate the formal prophylactic or therapeutic agent for dementia, depression, hyperkinetic appropriate the formal prophylactic or therapeutic agent for dementia, depression, hyperkinetic appropriate the formal prophylactic or therapeutic agent for dementia depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human type ligand polypeptide fragment.
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                Fujii
                                                                                              23-JUN-1997;
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                                                                                                                                                                                                                                                                                              abnormal lipidmetabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes a nagent for modulating prolactin secretion which comprises a company of the invention. The specification describes can agent for modulating prolactin secretion which comprises a company of the agents for promoting prolactin secretion can be used for treating or preventing hypovarianism, genecyst cacogenesis, menopausai syndrome, euchyroid or hypometabolism. They can by used for promoting conhibiting prolactin secretion can be used for treating or preventing conhibiting prolactin secretion can be used for treating or preventing conhibiting prolactin secretion can be used for treating or preventing confusion, infertility, impotence, amenorrhea, gainctorrhea, caromegaly, Chiari-Frommei syndrome, Argonz-del Castilo syndrome, can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing conducating placental function can be used for treating or preventing conducation and hydatid mole, irruption mole, abortion, unthrifty fetus, abortion, abortion, unthrifty fetus, abortion is acceptable.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Physiologically-active polypeptide recognized as ligarized protein-coupled receptor protein, for promoting secrets as drugs for diseases relating to oxytocin secretion medicine
                                                                                                                                                                                  25-DEC-1998;
                                                                                                                                                                                                                   22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                             Ruman; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bieeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ruman oxytocin secretion promoting peptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 166; 24lpp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein-coupled receptor ilgands - for modulating projectin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                  veterinary medicine;
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OM protein - protein search, using sw model
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Copyright (c) 1993 - 2000 Compugen Ltd.
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September 13, 2002, 09:18:36; Search time 399.68 Seconds (without alignments) 3.057 Million cell updates/sec

Sequence:	Perfect score:	Title:
1 SRXHXNSMEXR 11	47	US-09-446-543A-74

Run on:

quence:	T SKORANSMEAR II	;
oring table:	BLOSUM62	

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Searched: 747574 seqs, 111073796 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

Regult	Score	% Query Match	% Query Match Length	DB	ID	Description
۲	43	91.5	31	18	AAW31384	
ಏ	43	91.5	31	20	AAW97233	
u	43	91.5	31	20	AAW87614	Rat 19P2 ligand.
4	43	91.5	31	20	AAW95173	_
5	43	91.5	31	20	AAW95174	Murine pitultary-d
6	43	91.5	31	21	AAB10355	Rat oxytocin secre
7	43	91.5	31	21	AAY87504	Rat prolactin-rele
<b>&amp;</b>	43	91.5	31	21	AAY49292	19P2 11gand peptld
9	43	91.5	31	22	AAG62524	Rat CRH releasing
10	43	91.5	31	22	AAB90993	Prolactin releasin
11	43	91,5	32	18	AAW31385	Rat type G protein

# UI	44	ı.	2	41	40	39	38	37	36	36	34	E C	2	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	
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89.4	89.4	89.4		89.4		89.4	89.4	89.4	89.4	89.4	•	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4		89.4	89.4	•	•				•	•	•	۲	91.5	-	
32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	3	30	29	29	15	15	83	83	68	83	82	33	E C	i U	2	32	
18	18	22	22	22	22	22	21	21	21	21	21	20	20	20	20	20	18	18	21	20	18	20	18	22	21	20	18	20	22	21	18	22	21	
AAW31372	AAW31392	AAB73370	AAB90995	AAB90991	AAG62531	AAG62516	AAY49298	AAY49291	AAY49290	AAB10362	AAB10347	AAW95188	AAW87615	AAW87613	AAW97218	AAW97235	AAW31371	AAW31391	AAY49299	AAW95184	AAW31369	AAW97229	AAW31399	MAG62523	AAB10354	AAW97225	AAW31383	AAW95172	AAG62526	AAB10357	AAW31386	AAG62525	AAB10356	<
Ö	Human type G prote	pt	Prolactin releasin	Prolactin releasin	Human CRH releasin	ĸ	11gand	ligand	ligand per	Human oxytocin sec	oxytocin s	Bovine pituitary-d	Human 19P2 ligand.	19P2 11gan	Bovine pitultary-d	Numan type ligand		Human type G prote	19P2 ilgand peptld	Bovine pituitary-d			Synthetic ligand l	Rat CRH releasing	Rat oxytocin secre	Rat type ligand po	Rat type G protein	Murine pituitary-d	Rat CRH releasing	ũ	Rat type G protein	re1	Rat oxytocin secre	

# ALIGNMENTS

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WPI; 1997-363672/33. N-PSDB; AAVO2421.	<pre>Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M; Kawamata Y, Kitada C;</pre>	(TAKE ) TAKEDA CNEM IND LTD.			28-DEC-1995; 95JP-0343371.		26-DEC-1996; 96WO-JP03821.		10-JUL-1997.	109 244 30 - 22 2		Rat sp.		therapeutic agent.	modulator; pitultary; central nervous system; pancreas; prophylactic;	G protein-compled recentor: ligand binding: pharmacentical.	Rat type G protein-coupled receptor ligand fragment 1.	An one thing (track mines)	De auto-1000 / frest patrici	AAW31384;	AAW31384 standard; Peptide; 31 AA.	1384

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Clalm 5; Page 34; 56pp; English

CHEM IND LTD 97JP-0172118 98EP-0111725

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Suenaga

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Tanaka

by cleavage dementla,

This sequence represents a peptide fragment from a novel rat type illgand polypeptide corresponding to amino acid residues 22 to 52 of the aequence represented in AMM31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pitultary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic appropriation or therapeutic agent for dementia, depression, hyperkinetic Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland 2 Page 179; 258pp; English.

syndrome, disturbance of consciousness, anxiety syndrome, achizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hyperchoiesterolaemia, hypergrotactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperproductinaemia, diabetes, cancer, pancreatitis, renal disease, transient brain ischaemia, epilepsy, amylotrophic lateral aclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, tranma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.

Sequence 31

8 Ş Query Match Best Local S Matches 8 \_ ۳ ພ SRXHXHSMEXR 11 srahqhsmetr 11 8; Conserv 91.5%, Allarity 72.7%, Conservative Score 43; DB Pred. No. 0.02 0; Mlsmatches Indels 0, Gaps

AAW97233 standard; peptide; 31 ζ

AAW97233;

06-MAY-1999 (firat entry)

Rat type ligand polypeptide fragment.

RESULT
AAW97233
ID
XX AAW9
XX AAW9
XX AAW9
XX AAW9
XX Rat
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KW G pr
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X G protein-coupled receptor; GPCR, hypocvarianism; gonecyst cacogenesis; menopausal ayndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; lmpotence; amenorrhea; galactorrhea; acromegaly; Chlari-Frommel syndrome; Argonz-del Castilo syndrome; acromegaly; Chlari-Frommel syndrome, Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyazoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; aportion; unthrifty fetus; abnormal saccharometabolism; hydrometabolism; Rat type ligand; abnormal lipidmetabolism; modulation; prolactin secretion; oxytocia

Rattus

W09858962-AL

30-DEC-1998.

22-JUN-1998; 98WO-JP02765

23-JUN-1997, 97JP-0165437

(TAKE ) TAKEDA CHEM IND LTD.

Fujll R, Hlnuma Ś Kawamata Y, Matsumoto Ξ

DB 18; 0.026; Length 31, 9 RESULT
ANW87614
ID ANW87614
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ID ANW87614
ID ANW8 AC ANW8
ID Rat
XX 19P2
KW 1POI
KW Thei
XX PN EP88
XX EP88
XX Thei
XX Thei CC is used in the course of the invention. The specification describes CC an agent for modulating prolactin secretion which comprises a CC ligand polypeptide or a sait, for a g protein-coupled receptor (GPCR) CC protein. The agents for promoting prolactin secretion can be used for creating or preventing hypocovarianism, gonecyst cacogenesis, menopausal CC syndrome, euthyrold or hypometabolism. They can by used for promoting CC lactation in a domestic mammal and as an aphrodisiac. The agents for CC inhibiting prolactin secretion can be used for treating or preventing CC prolactinoma, infertility, impotence, amenorate, autoimmune disease, CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, CC The inhibitory agents can also be used for treating or preventing CC modulating placental function can be used for treating or preventing CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrift forms. 밁 Ş Query Match Best Local Matches Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease WPI; 1999-047884/05 Morlya T, 25-JUN-1998; 30-DEC-1998 Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy (TAKE ) TAKEDA 27-JUN-1997; EP887417-A2 Rattus sp. therapy. 1992 ligand; G protein coupled receptor; pituitary; prolactin releasing peptide; rat; dementia; breast Rat 19P2 ligand 29-MAR-1999 AAW87614; AAW87614 standard; Peptide; 31 Sequence Claim 3, WPI; 1999-105614/09 1 SRXHXHSMEXR 11 w arahqhsmetr 11 8 Slmllarity Page 153; 24lpp; English Nishimura 31 Conservative (firat entry) ξ

91.5%; 72.7%;

Score 43; DB 20 Pred. No. 0.026; Mismatches

20;

Length 31; Indels

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Perfect score:
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156
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747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Com
                                                                                             SRXHXHSMEXRTPDINPAWYXXRGIRPVGRFXX 33
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: 747574

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22. \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1990.DAT: \* A\_Geneseq\_032802:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.

No.	Score	Query Match Length	Length	BG	ID	Description
1	147	94.2	31	18	AAW31391	Human type G prote
2	147	94.2	31	18	AAW31384	•
w	147	94.2	31	20	AAW97233	Rat type ligand po
4	147	94.2	31	20	AAW97235	Human type ligand
5	147	94.2	31	20	AAW87614	Rat 19P2 ligand.
o	147	94.2	31	20	AAW87615	Human 19P2 llgand
7	147	94.2	31	20	AAw95173	Murine pituitary-d
œ	147	94.2	31	20	AAW95174	Murine pituitary-d
9	147	94.2	31	21	AAB10355	Rat oxytocin secre
10	147	94.2	31	21	AAB10362	Human oxytocin sec
11	147	94.2	31	21	AAY87504	Rat prolactin-rele

	19P2 ligand peptid		AAY49290	21	31		146	U
	ø		AAB10347	21	31		146	4
	pitul		AAW95188	20	31		146	ū
	19P2 ligan		AAW87613	20	31		146	2
	pituitary-		AAW97218	20	31		146	41
	Bovine G protein-c		AAW31371	18	31		146	0
	CRH relea		AAG62530	22	87		147	39
	Human oxytocin sec		AAB10361	21	87		147	38
	Human type ligand		N	20	87		147	37
	à		AAW31390	18	87		147	36
			AAG62523	22	83		147	35
			AAB10354	21	.83		147	34
			AAW97225	20	83		147	33
	·O		AAW31383	18	83		147	32
	Murine pitultary-d		AAW95172	20	82		147	31
	Human CRH releasin		AAG62533	22	33		147	30
	Rat CRH releasing		AAG62526	22	3		147	29
	en oxyt		AAB10364	21	<b>ω</b>		147	28
•	oxytoci		AAB10357	21	33		147	27
	ype G prote1		AAW31386	18	ω W		147	26
			AAW31393	18	3		147	25
			AAG62532	22	32		147	24
	Rat CRH releasing		AAG62525	22	32		147	23
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	oxytoci		AAB10356	21	32		147	21
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	æ		AAW31392	18	32		147	19 '
			9099	22	31	-	147	18
	Prolactin releasin		99	22	31		147	17
			AAB90991	22	31		147	16
	an CRH		AAG62531	22	1		147	15
	CRH releasin		252	22	31		147	14
	19P2 ligand peptid		AAY49292	21	31	94.2	147	13
	2 ligand pepti		4929	21	31		147	12
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### ALIGNMENTS

멸	žž	ž 5	RESULT AAW313	
, 06-APR-1998 (first entry)	AAW31391:	AAW31391 standard; Peptide;	RESULT 1 AAW31391	
3		ide;		
		31		
		31 AA.		

Human type G protein-coupled receptor ligand fragment 1.

G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; protherapeutic agent. pancreas; prophylactic;

Homo sapiens

W09724436-A2

26-DEC-1996; 96WO-JP03821

10-JUL-1997.

18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996; 96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805.

(TAKE ) TAKEDA CHEM IND LTD.

Fujii R, Fu Kawamata Y, Fukusumi S, Y, Kitada C; Habata к Hinuma Ś Hosoya M;

WPI; 1997-363672/33. N-PSDB; AAV02428.

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Kawamata
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Y, Kitada C;
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This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to annotate residues 23 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperlipidaemia, hyperchoiesterolaemia, hyperchoiesterolaemia, hyperphagia, CC hyperlipidaemia, diabetes, cancer, pancreatitis, renai disease, CC Turner's syndrome, neurosis, asthma, rheumatold arthritis, spinal injury, cacute myocardiai infarction, infertility, spinocerebellar degeneration, CC done fracture, trauma, atopic dermatitis, osteoporosis and/or capable of altering the binding activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ciaim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page
the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258pp;
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밁
                                          Matches
                                                    Query Match
Best Local
                                       Local Similarity
nes 26; Conserv
           1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
srthrhsmeirtpdinpawyasrgirpvgrf 31
                                         Conservative
                                                   94.2%;
                                         0
                                                   Score 147; DB 18;
Pred. No. 2.3e-17;
                                         Mismatches
                                         ផ
                                                          Length
                                         Indels
                                                             31;
                                        0
                                        Gaps
```

Sequence

3

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06-APR-1998
                                                                               AAW31384;
                                                                                                                      AAW31384 standard; Peptide;
Rat type G protein-coupled receptor ligand fragment 1.
                                                                                                                                                             N
                                      (first entry)
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G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
therapeutic agent.
                                   central nervous system; pancreas; prophylactic;
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0 RESULT 밁 Š Matches Rat type ligand polypeptide fragment. w

Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland

Claim 2; Page 179; 258pp; English.

cc modulator. This ligand could have specific applications as a probability or therapeutic agent for dementia, depression, hyperkinetic cyrophylactic agent for dementia, depression, hyperkinetic cyrophylactic agent for consciousness, anxiety syndrome, schizophrenia, cyrowth hormone secretory disease, hyper- and polyphagia, cyroperipidaemia, hypercholesterolaemia, hyperglyceridaemia disease, cyroperipidaemia, hypercholesterolaemia, hyperglyceridaemia injury, cyroperipidaemia, hypercholesterolaemia, hyperglyceridaemia, spinal injury, cyropersyndrome, neurosis, astima, rheumatoid arthritis, spinal injury, cyroperipidaemia ischaemia, epilepsy, amylotrophic lateral sclerosis, cyroperipidaemia, epilepsy, amylotrophic lateral degeneration, compounds which are colloqualactia. Assays can also be developed to screen compounds which are compounds of attering the binding activity of the ligand affecting constitution of the G protein-coupied receptor protein. ligand polypeptide corresponding to amino acid residues 22 to 52 of the sequence represented in AAW31383 and is used in an assay to monitor ligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function This sequence represents a peptide fragment from a novel rat ligand polypeptide corresponding to amino acid residues 22 to Pharmaceutical

Sequence 3

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Query Match
8est Local Similarity
Conservative
                                     94.2%;
83.9%;
                              Score 147; DB
Pred. No. 2.3e
0; Mismatches
                               0
                                     DB 18;
2.3e-17;
                                            Length
                               Indels
                               0
                              Gaps
                               0
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AAW97233;
 06-MAY-1999
                                          AAW97233
                                         standard; peptide;
(first entry)
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Rat type ilgand; modulation; prolactin secretion; gonecyst cacogenesis; grotein-coupled receptor; GPCR; hypovazianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommes i syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthiffy fetus; abnormai saccharometabolism; abnormal lipidmetabolism; oxytocia.

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Fujli R,
                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                        30-DEC-1998
                                                                                                                                  W09858962-A1
                                                                               22-JUN-1998;
 Hinuma S,
                                                    97JP-0165437
                                                                               98WO-JP02765
  Kawamata Y,
  Matsumoto H;
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4AW31391
A-genesey-032802
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Title: Perfect score: Sequence: OM protein - protein search, using sw model Scoring table: US-09-446-543A-61 171 BLOSUM62 Gapop 10.0 , Gapext 0.5 September 13, 2002, 09:10:15; 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. ; Search time 399.68 Seconds
(without alignments)
8.615 Million cell updates/sec

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

747574

747574 seqs, 111073796 residues

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A\_Geneseq\_032802:\* 1: /SIDS1/gcgdata/ /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11	10	9	00	7	6	UI	4	w	N	<b>-</b>	Result
171	171	171	171	171	171	171	171	171	171	171	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match 1
ω ω	32	32	32	31	31	31	31	31	31	31	Length DB
18	2	21	18	22	22	2	2	20	8	18	:
AAW31393	AAG62532	AAB10363	AAW31392	AAB90991	AAG62531	AAY49291	AAB10362	AAW87615	AAW97235	AAW31391	ID
Human type G prote	Human CRH releasin	Human oxytocin sec	Human type G prote	Prolactin releasin	Human CRH releasin	19P2 ligand peptid	Human oxytocin sec	Human 19P2 ligand.	_	Human type G prote	Description

X II IX R R

Fujii R, Fukusumi S, Kawamata Y, Kitada C;

наbata Y,

Hinuma Ś

нозоуа м;

WPI; 1997-363672/33. N-PSDB; AAV02428.

30 21 AAW9721 31 20 AAW9721 31 21 AAY4929 31 21 AAY4929 31 21 AAY4929 31 21 AAY4929 31 21 AAW9518 32 18 AAW9117 32 20 AAW9518 32 21 AAG6251 32 21 AAW9117 32 21 AAW9137 32 18 AAW9137 32 18 AAW9137 32 18 AAW9139 33 21 AAAW9518 36 21 AAW9722 37 AAY4929 38 21 AAW9722 38 22 AAG6251 39 22 AAW9722 39 20 AAW9722 39 21 AAB1035 39 22 AAG6251 39 22 AAG6251	15 15 16	
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### ALIGNMENTS

RESULT AAW31391 ID AAW	LT 1 1391 AAW31391 standard; Peptide; 31 AA.
ÃC	AAW31391;
9 X	06-APR-1998 (first entry)
×	
É	Human type G protein-coupled receptor ligand fragment 1.
Z X	G protein-coupled receptor: ligand binding: pharmaceutical:
£	modulator; pituitary; central nervous system; pancreas; prophylactic;
××	therapeutic agent.
, ·	Homo sapiens.
P	WO9724436-A2.
×	
èĕ	10-JUL-1997.
ਚ > ਚ >	26-DEC-1996:
×	
PR	18-SEP-1996;
PR	28-DEC-1995;
PR	15-MAR-1996;
PR	12-AUG-1996;
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PA	(TAKE ) TAKEDA CHEM IND LTD.

function in the centr

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cc sequence represented in AAW31390 and is used in an assay to monitor cc ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function cc modulator. This ligand could have specific applications as a proposition correction cc modulator. This ligand could have specific applications as a proposition containing this ligand may be used as a pituitary function cc modulator. This ligand could have specific applications as a proposition could have specific applications as a proposition of the prophylactic or therapeutic agent for dementia, depression, hyperkinetic cc trauma, growth hormone secretory disease, hyper- and polyphagia, cc hyperipidaemia, hypercholesterolaemia, hypergriveridaemia, collegand, consciptional injury, cc hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, cc hyperprolactinaemia, neurosis, asthma, rheumatoid arthritis, spinal injury, cacute myocardial infarction, infertility, spinocarebellar degeneration, cc oligogalactia, Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cc activation of the G protein-coupled receptor protein.
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AAW97235
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Matches 31
                                                                                                                                                                                                                                              G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; ammenorihea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole: abnormal lipidmarkaria.
               Fujii R,
                                               (TAKE ) TAKEDA
                                                                                                                22-JUN-1998;
                                                                                                                                                                               W09858962-A1
                                                                                23-JUN-1997;
                                                                                                                                                30-DEC-1998
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                            abnormal lipidmetábolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW97235 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
               Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
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Pred. No. 4.1e-19;
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             Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment from
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101

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English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human type ligand fragment. It

CL is used in the course of the invention. The specification describes

CL an agent for modulating prolactin secretion which comprises a

CL ligand polypeptide or a salt, for a G protein coupled receptor (GPCR)

CL protein. The agents for promoting prolactin secretion can be used for

CL treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal

CL syndrome, euthyroid or hypometabolism. They can by used for promoting

CL inhibiting prolactin secretion can be used for treating or preventing

CL inhibiting prolactin secretion can be used for treating or preventing

CL prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CL prolacting and produced syndrome, Argonz del Castilo syndrome,

CL concegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,

CL prolacting placental function can be used for treating or preventing

CL modulating placental function can be used for treating or preventing

CL choornel syndrome, hydatid mole, irruption mole, abortion, unthrifty fetus,

CL choornel agents for the syndrome or dyszoospernia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 31;
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Best Local
                                   Producing a 1992 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                                                                   WPI; 1999-047884/05.
                                                                                                                                                                                                                            Moriya
                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                       27-JDN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP887417-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 19P2 ligand.
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Title:
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1: /cgn2_6/ptodata/2,
2: /ggn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Match
     Minimum Match 08
Maximum Match 1008
Listing first 45 aummaries
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Gapop 10.0 , Gapext 0.5
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109
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:*
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US-09-105-678A-46
US-09-127-6971-64
US-09-121-208-46
US-09-121-208-47
US-09-121-208-48
US-09-121-208-48
US-09-121-208-49
US-09-121-208-49
US-09-105-678A-49
US-09-105-678A-49
US-09-105-678A-49
US-09-105-678A-49
US-09-105-678A-49
US-09-105-678A-49
US-09-105-678A-49
US-09-105-678A-49
US-08-776-971-69
US-08-776-971-138
US-08-776-971-138
US-09-105-678A-34
US-08-776-971-138
US-09-105-678A-34
US-08-776-971-50
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(without alignments)
3.933 Million cell updates/sec
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Sequence
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6 46, Appl
6 46, Appl
6 47, Appl
6 47, Appl
6 48, Appl
6 48, Appl
6 48, Appl
6 49, Appl
6 41, Appl
6 42, Appl
6 43, Appl
6 44, Appl
6 44, Appl
6 45, Appl
6 45, Appl
6 46, Appl
6 47, Appl
6 48, Appl
6 48, Appl
6 49, Appl
6 49, Appl
6 49, Appl
6 49, Appl
7 49, Appl
7 49, Appl
8 49, Appl
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Query Match Best Local S Matches 18

Similarity

96.38;

Score 105; DB 3; Pred. No. 1.8e-11; 0; Mismatches 2

Length 20 Indela

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Gapa

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18;

Conservative

US-09-105-678A-46  US-09-105-678A-46  Sequence 46, Application US/09105678A  Patent No. 6103882  GENERAL INFORMATION: APPLICANT: Suenaga, Masato APPLICANT: MOCIYA, Takeo APPLICANT: Tanaka, Yoko APPLICANT: Tanaka, Yoko APPLICANT: N18hlmura, Osamu TITLE OF INFUNTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52 CORRESSONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street CITY: Boston STRIE: WA COUNTRY: USA ZIT: 02109 COMPUTER READABLE FORM: KEDIUM TYEE: FLORY COMPUTER LBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: DETENTION Release \$1.0, Version \$1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A FILING DATE: 27-JUN-1998 PRIOR APPLICATION UNDERE: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: ARBISTRATION TON SEED 11 NO. 46: SEQUENCE CHARACTERISTICS: LENGTH: 20 mmlno acids TYPE: maino acids TYPE: Deptide US-09-105-678A-46	28 104 95.4 20 4 US-08-776-971-98 Sequenc   39 104 95.4 20 4 US-09-421-208-34 Sequenc   30 104 95.4 21 3 US-09-121-208-34 Sequenc   31 104 95.4 21 3 US-09-105-678A-40 Sequenc   32 104 95.4 21 3 US-09-105-678A-41 Sequenc   33 104 95.4 21 4 US-08-776-971-9 Sequenc   34 104 95.4 21 4 US-08-776-971-51 Sequenc   35 104 95.4 21 4 US-09-421-208-35 Sequenc   36 104 95.4 21 4 US-09-421-208-35 Sequenc   37 104 95.4 21 4 US-09-105-678A-36 Sequenc   38 104 95.4 21 3 US-09-105-678A-36 Sequenc   39 104 95.4 22 3 US-09-105-678A-42 Sequenc   40 104 95.4 22 4 US-08-776-971-50 Sequenc   41 104 95.4 22 4 US-08-776-971-52 Sequenc   42 104 95.4 22 4 US-08-776-971-52 Sequenc   43 104 95.4 22 4 US-08-776-971-52 Sequenc   44 104 95.4 21 3 US-09-105-678A-7 Sequenc   45 104 95.4 31 3 US-09-105-678A-8 Sequenc   56 Sequenc   57 Sequenc   57 Sequenc   58 Sequenc   58 Sequenc   59 Sequenc   59 Sequenc   50
	Sequence 98, Appl Sequence 34, Appl Sequence 35, Appl Sequence 35, Appl Sequence 9, Appli Sequence 35, Appl Sequence 35, Appl Sequence 36, Appl Sequence 41, Appl Sequence 10, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 36, Appl Sequence 37, Appli Sequence 38, Appli Sequence 31, Appli Sequence 31, Appli

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TPDINPAWYXXRGIRPVGRF

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                                                                                                                                                                              ; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-776-971-64
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; Sequence 64, Applicati
; Patent No. 6228984
; GENERAL INFORMATION:
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                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47.
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTN: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIDR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
TPDINPAWYASRGIRPVGRF 20
                       TPDINPAWYXXRGIRPVGRF 20
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COUNTRY: U
                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUKUSUMI, Shoji
Kitada, Chieko
OF INVENTION: POLIPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08776971B
                                                                               Conservative
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Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinuma, Shuji
Habata, Yugo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                96.3%; Score 105; DB 4; Length 20; 90.0%; Pred. No. 1.Be-II;
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US-09-105-678A-47; Sequence 47, App. , Patent No. 6103
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PI
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE DIKE, BRONSTEIN, METHOD
                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECONMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208 FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Massto
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Ogamu
TITLE OF INVENTION: METNOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-TUN-1998
APPLICATION NUMBER: TP 172118/1997
FILING DATE: 27-TUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -42I-208-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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   STREET:
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Boston
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                    130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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                                 BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                     PRODUCING A 19P2 LIGAND
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US-08-776-971-65
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GENERAL INFORMATION:
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TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIF: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CONIIN, David G. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TPDINPAWYXXRGIRPVGRF 20
                                                          COMPUTER: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06 Feb-1997
                                                                                                                                                                                                                                                                                                    HOSOYA, MASAKI
FUJII, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
APPLICATION NUMBER: PCT/JP96/03821 P1LING DATE: 28-DEC-1996
                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                        STREET: 130 Water Street
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Pred. No. 1.9e-11;
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US-09-42I-208-47
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                                                                                                                                                                                                                                                                                                                 COUNTRY:
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: MOLECULE TYPE: protein
: FRAGMENT TYPE: Internal
: SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-65
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
ANDER
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Ose
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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NAME: Conlin, David G.
REGISTRATION NUMBER: 2
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FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996
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90.0%;
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                                          48466-342
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Pred. No. 1.9e-11;
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US-09-105-678A-48
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                                                              Matches
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Best Local Similarity
                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: CONLIN. DAVId G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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1NFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: M
                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: 11near
                                                                                                                                                                                              TYPE: amino acid
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TYPE: amino acid
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                    1 TPD1NPAWYXXRGIRPVGRF 20
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TPDINPAWYASRG1RPVGRF 20
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Pred. No. 1
                                                                        Score 105; DB 3
Pred. No. 2e-11;
                                                            Mismatches
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                                                                                      DB 3;
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
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GENERAL INFORMATION:
                                                                                              Query Match
Best Local Similarity
                                                                             Matches
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ 1D NO: 66:
SEQUENCE CHARACTERISTICS:
                  1 TPD1NPAWYXXRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 8/246573
FILING DALE: 18-SEP-1996
ATIORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM 1YPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
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DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
TPDINPAWYASRG1RPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DALE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                 LENGTH: 22 amino acids
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                                                                             Conservative
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Hosoya, Masaki
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                                                                         96.3%; Score 105; DB 4
90.0%; Pred. No. 2e-11;
live 0; Mismatches
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RESULT 9 US-09-421-208-48

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RESULT 10
US-09-105-678A-9
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Best Local :
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INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                          APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CONIII, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tanaka, LONG APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
THE THE PROPERTIES A 19P2 LIGAND
                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                ADUM:
STREET: 1.
STREET: 1.
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                   Match 96.3%;
Local Similarity 90.0%;
ses 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
QPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYXXRGIRPVGRF 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                  USA
                                                                 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 amino acids
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Pred. No. 2e-11;
O; Mismatches
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APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REFERENCE/DOCKET NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                  APPLICATION NUMBER: US/09/
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SUEDBAYS, Takeo
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, YOKO
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
TITLE OF INVENTION: 52
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION: 617-523-3400
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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MOLECULE TYPE: peptide
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LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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                                                   REGISTRATION NUMBER:
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                                                                                                                                                                                 US/09/105,678A
                                                                                                                            JP 172118/1997
                                               27,026
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Pred. No. 3e-11;
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Patent No. 6228984
GENERAL INFORMATION:
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Best Local Similarity 90.0
Matches 18; Conservative
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SEQUENCE CHARACTERISTICS:
                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM COMPETIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 11-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORREY/AGENT IMPORMATION:
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TOPOLOGY: linear
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                 NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                          LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fikusumi, Shoji
Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/087769718
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Habata, Yugo
Kawamata, Yuji
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Fujii, Ryo
Fukusumi, Shoji
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Pred. No. 3e-11;
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; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-08-776-971-61
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                                                                                                      Query Match
Best Local Similarity 90.0
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GENERAL INFORMATION:
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Best Local 9
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 7-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tanaka, YOKO
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRE
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CITY: Boston
STATE: MA
COUNTRY: USA
1 TPDINPAWYXXRGIRPVGRF 20
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12 TPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
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Moriya, Takeo
Tanaka, Yoko
Nishimura, Osamu
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                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                          96.3%;
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                                                                                                                      Score 105; D8 4
Pred. No. 3e-11;
0; Mismatches
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Pred. No. 3e-11;
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RESULT

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; MOLECULE TYPE: peptide
US-09-421-208-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATE 27-JUN TELLING DATE: 27-JUN TELLING DATE: 27-JUN TELLING TORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27.026
REFERENCE_DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
"FIREHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
ETLING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
APPLICATION DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, App. No. 62585/
                                                                                                                                                                                                           Sequence 44, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.3%;
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                                                                                                 APPLICANT: Suenaga, Nasato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, YOko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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NEDIUM TYPE: Fioppy disk
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APPLICANT: MOTIYa, Takeo
APPLICANT: Tanaka, YOko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 1992 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                    CORRESPONDENCE ADDRESS:
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                                                    STREET:
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COUNTRY:
                                                                     ADDRESSEE:
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                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP I30 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
I30 Water Street
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Pred. No. 3e-11;
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Search completed: September 13, 2002, 09:20:57 Job time: 622 sec
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Best Local Similarity
Matches 18; Conserv
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ETILING DATE: 26-UN-1998
PRIOR APPLICATION DATA: JP 172:
APPLICATION NUMBER: JP 172:
ETLING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON111, DAY1d G.
REGISTRATION NUMBER: 27.02
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                          12 TPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                           I TPDINPAWYXXRGIRPVGRF 20
                                                                                                                                                                 Conservative
                                                                                                                                                                            96.3%; Score IO5;
90.0%; Pred. No. 3.
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                                                                                                                                                                                                 Length 32;
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13

**4**)

Title: Perfect score: Run Total number of hits satisfying chosen parameters: Scarched: Scoring table: OM protein protein search, using sw model BLOSUM62 Gapop 10.0 , 203130 segs, 96089334 residues September 13, 2002, 09:23:57; US-09-446-543A-73 Copyr1ght TPDINPAWYXXRG1RPVGRFXX 22 GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd Gapext 0.5 ; Search time 172.41 Seconds
(without alignments)
i2.261 Million cell updates/sec 203138

Minimum Maximum seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

P1R\_71:\*
1: p1r1:\*
2: p1r2:\*
3: p1r3:\*
4: p1r4:\* pir1: \* pir3: \* pir4: \*

Database

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMAR1ES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	Ф	7	6	S		ω	2	-		Result
41	41	41	41	41	41	41	41.5	42	42	42.5	43	43	43	43	43	43	43	43	43	43	43.5	44	44	45	46	49	49.5	104		Score
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C83160	T00708	в69009	G82844	T40084	T35426	H70744	T35901	T35841	T45619	T49717	T30197	OYURGA	A87448	AG0502	AH3166	
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#### ALIGNMENTS

R;Yamada, M.; Dzawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 201, 53-56, 2001
A;Title: Isolation and characterization of the rat projectin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Accession: JC7607 망 Ş A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite rejease from rat anterior release, and stimulation of ACTH secretion from the pituitary. proiactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 A;Gene: PrRP A;1ntrons: 33/1 A; Molecule type: DNA A; Residues: i-83 < YAM> C; Genetics: Query Match 95.4
Best Local Similarity 90.0
Matches 18; Conservative 95.4% 90.0% 0 Score 104; DB 2; Pred. No. 5.le-10; 0; Mismatches 2 Longth 83; indels 0 Gaps 0

RESULT N

Conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PAD C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 \*sequence\_revision 15-Sep-2000 \*text\_change 3i-Dec-2000 C;Accession: F83376
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Rature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID;20437337

A;Status: preiiminary A;Molecule type: DNA A;Residues: 1-664 <STO> A;Crossireferences: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN A;Experimental source: strain PAO1

PA2151

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A;Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F
as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frobr
J.D.; Junquelra, M.L.; Kamper, E.L.; Kltajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, F.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri, D.,
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva JJ., W.A.; da Silvai,
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva JJ., W.A.; da Silvai,
A;Reference number: A59328
C.Genetics: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 **LEMA_UPER_1 **C. C. Accession: #82852
R. anonymous, The Xylelia fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
A.Title: The genome sequence of the plant pathogen Xylelia fastidiosa.
A; Reference number: A82515; MUID:20365717
A; Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule type: DNA
A:Residus: 1-790 <DEH>
A:Cross-references: EMBL:AL132959
A:Experimental source: cultivar Co
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A; Residues: 1-333 <SIM>
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A; Status: preliminary
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A; Introns: 39/1; (
A; Note: F15G16.60
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A;Accession: T47959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F15G15.60 - Arabidopsis thaliana C;Spccies: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change C;Accession: T47959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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9; Conserv
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Pred. No.
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Pred. No. 3.9;
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A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A; Reference number: A82950; MUID:20437337
A; Accession: G83400
                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PA1952 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F38E11.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Qct-1999
C:Accession: T21969
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-250 <STQ>
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A; Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1;
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A; Accession: T21969
A; Status: prelimina
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A;Experimental source: clone F38E11
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A; Residues: 1-767 <WIL>
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                                                                                                                                                                                            A; Experimental source:
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Matches 8
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Gene: PA1952
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Best Local :
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Best Local
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                                  2 PDINPAWYXXRGIRPVG
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PALNCAWEQLRALRPSG
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                                                                   Similarity
8; Conserv
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8; Conservative
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                                                                     Conservative
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                                                                                                                                                                                             Strain PAQ1
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75.0%;
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                                                                     <u>ب</u>
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Pred. No. 7.3;
2; Mismatches
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Pred. NO. 24;
1; Mismatches
                                                                                    Score 44;
Pred. No.
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7.3;
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Larbig,
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Nature 406,
A;Title: Con
                    probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa (;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Scp-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: C83292 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig , Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein PH1420 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: F71015
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida DNA Res. 5, 55-76, 1998
A;Title: Complete #equence and gene organization of the genome of a hyper-th A; Reference number: A71000; MUID:98344137
                                                                                                                                                                                    RESULT
C83292
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745623
hypothetical protein Fl3G24.180 - Arabidopsis thailana
hypothetical protein Fl3G24.180 - Arabidopsis thailana
C;Species: Arabidopsis thailana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45623
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A; Residues: 1-1501 <BEV>
A; Cross references: EMBL: AL133421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; submitted to the Protein Sequence Database, Oecember 1999
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C;Superfamily:
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F71015
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A; Residues: 1-284 <KAW>
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Best Local Similarity
Matches 10; Conserv
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F13G24.180
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      Complete
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      genome
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      sequence
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Pred. No. 85;
5; Mismatches
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Pred. No. 13;
    of Pseudomonas aeruginosa
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    PAO1,
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    an
                                                            P.; Hickey,
A.; Larbig,
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Kushida,
opportunistic
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C:Accession: G75608
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                            A;Description: The sequence of C. A;Reference number: 221157
A;Accession: T32376
A;Status: preliminary: translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-232 <WHI>
A; Cross-references: GB: AECO01862;
A: Cross-references: GB: AECO01862;
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G75608
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A; Residues: 1-220 <STO>
A; Cross-references: GB:AE004709;
A; Experimental source: strain PAC
C; Genetics:
          A; Map position: (A; Introns: 31/3;
                                                             A; Experimental source: strain C; Genetics:
                                                                             A;Cross-references: EMBL:AF025462; PIDN:AAB71002.1; GSP0B:GN00021; A;Experimental source: strain Bristol N2; clone K10F12
                                                                                                               A; Molecule type: DNA
A; Residues: 1-309 < WOH>
                                                                                                                                                                                                  submitted to the EMBL Oata Library, September 1997 A; Description: The sequence of C. elegans cosmid K10F12.
                                                                                                                                                                                                                                   C; Accession: T32376
R; Wohldmann, P.; Beck, C.
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C;Species: Oeinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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C;Superfamily: plaice glutathione transferase
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A;Accession: C83292
A:Status: preliminary
                                             A; Gene: CESP:K10F12.4
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3; 123/2;
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, L.; Utterback,
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196/3; 239/1

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A:Status: prellminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-376 <SMT>
A:Cross references: EMBL:L03791; NID:9156642; PIDN:AAA28273.1; PID:g156643
A:Cross references: EMBL:L03791; NID:9156642; PIDN:AAA28273.1; PID:g156643
C:Superfamily: vertebrate rhodopsin
C:Kcywords: chromoprotein; G protein-coupled receptor; lipoprotein; photore
F:318/Binding site: retinal (Lys) (covalent) #status predicted
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A:Residues: 1-376 <SMI>
A:Residues: 1-376 <SMI>
A:Cross-references: EMBL:L03792; NlD:gl56644; PIDN:AAA28274.1; PID:gl56645
A;Cross-references: EMBL:L03792; NlD:gl56644; PIDN:AAA28274.1; PID:gl56645
C:Superfamily: vertebrate rhodopsin
C:Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photorer; 318/Binding site: retinal (Lys) (covalent) #status predicted
                                       RESULT
G64720
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A;Title: Opsins from the lateral eyes and ocell1 of the horseshoe A;Reference number: A48197; MUID:93317641
A;Accession: B48197
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C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
C;Accession: B48197
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C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
C;Accession: A48197
R;Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.
Proc. Natl. Acad. Scl. U.S.A. 90, 6150-6154, 1993
probable amino acid transport protein yaaJ, sodium-dependent -
C;Species: Escherichla coli
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R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; F
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohamorrhagic Escherichia coli ol57:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable Inner membrane transport protein ECs0007 [imported] - Escherichia coli C:Species: Escherichia coli C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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F;178-194/Domain: transmembrane *status predicted <TM4>
F;178-194/Domain: transmembrane *status predicted <TM5>
F;208-224/Domain: transmembrane *status predicted <TM5>
F;303-319/Domain: transmembrane *status predicted <TM7>
F;349-365/Domain: transmembrane *status predicted <TM8>
F;391-407/Domain: transmembrane *status predicted <TM8>
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C; Superfamily:
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A;Title: The complete genome sequence of Escherichia A:Reference number: A64720; MUID:97426617
A;Accession: G64720
                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA000007; PIDN:BAB33430.1; PID:g13359463; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-476 <HAY>
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                                                                                                Score 43; DB
Pred. No. 32;
2; Mismatches
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Maximum Minimum

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1: sp_arches:*
2: sp_bacterls:
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
6: sp_mamma
7: sp_mhc:*
6: sp_mamma
7: sp_pha*
10: sp_p;
11: sp_r
12: sp_r
13: sp_1
14: sf
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sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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sp_rodent:*
sp_vlrus:*
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Q12804
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O95367 homo sapien Q12804 homo sapien Q22h19 zymomonas m Q9del2 gallus gall sus gall Q9hnp4 halobacteri Q9d882 mus musculu Q9d882 mus musculu Q9dae5 mus musculu Q9dae5 mus musculu Q9dae5 mus musculu Q9x0w5 thermotoga Q9jn22 a9robacteri Q9ull6 drosophila Q9w1t8 dro
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 Q12804;
Q12804;
01-MOV-1996
01-NOV-1996
01-DEC-2001
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SEQUENCE FROM M.A.

REDLINE-99093483; PubMed-9874765;

H$16h J.O., Zhou S., Chen L., Young D.B., Hayward S.D.;

H$16h J.O., Zhou S., Chen L., Young D.B., Hayward S.D.;

"CIR, a corepressor linking the DMA binding factor CBF1 to
deacetylase complex.";

deacetylase complex.";

Proc. Natl. Acad. Sci. U.S.A. 96:23-28(1999).

EMBL; AF098297; AAD05243.1; -.

SEQUENCE 450 AA; 52328 MW; 96AA8BF69CB73357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCBI_TaxID=9606;
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7; Conserv
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Q9A0B5
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Q9aus0 oryza sativ
Q94h07 oryza sativ
Q94yz0 pylaiella 1
Q940W8 neisseria m
Q9jti0 neisseria m
Q9jtz5 mus musculu
Q41320 secale cere
Q9q3u4 cymbidium m
Q9p826 candida alb
Q9p826 candida alb
Q9p829 oryza sativ
Q20938 caenorhabdi
Q960f3 drosophila
Q9f788 uncultured
Q62157 mus musculu
Q9v2c9 drosophila
Q9ny8 drosophila
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Q9a0b5 streptococc
Q05268 baclllus su
Q23359 caenorhabd1
Q9asa8 oryza satlv
Q9cyq7 mus musculu
Q9xa23 streptomyce
Q9c230 neurospora
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Neognathae; Galliformes; Phasianidae;

Phasianinae;

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Q9DE12;
01-MAR-2001 (TrEMBLrel. 16, Cr.
01-MAR-2001 (TrEMBLrel. 16, La.
01-DEC-2001 (TrEMBLrel. 19, La.
DNA-DEPENDENT PROTEIN KINASE C.
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09RH19;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ

EMBL; AF088997; AAF18273.1; ...

InterPro; IPR003317; Cyto_ox_2.

Pfam; PF02322; Cyto_ox_2; 1.

SEQUENCE 340 AA; 37206 MW; 3D7038A3F72EC31
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Bacterla;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
CYTOCHROME OXIDASE D SUBUNIT B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chal K.x., Li L., Chao J., Chao L.;
"Recepin: a novel human liver cDNA encoding a
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ
EMBL; U03644; AAA17853.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LIVER;
Chal K.X., Li L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPIN.
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Lee J.S., K
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PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 451 AA; 52942 MW; 157F04804DA0817E CRC64;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutherla; Primates;
    Eukaryota;
                                            DNA-PKCS
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                        gallus (Chicken).
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E CATALYTIC SUBUNIT.
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"Identification of four highly conserved re Immunogenetics 51:965-973(2000).
EMBL: AB016240; EAA36956.1; ..
InterPro; IPR003151; FAT.
InterPro; IPR003152; FATC.
InterPro; IPR00403; P13_PI4_kinase.
InterPro; IPR00403; P13_PI4_kinase.
Pfam; PF02250; FAT; 1.
Pfam; PF02250; FAT; 1.
Pfam; PF02260; FATC; 1.
Pfam; PF04264; PI3_PI4_kinase; 1.
SMART: SMO0145; PI3_K; 1.
PROSITE; PS00915; PI3_4_KINASE_1; UNKNOWN_1
PROSITE; PS0090; PI3_4_KINASE_3; 1.
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01-MAR-2001
01-MAR-2001
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MG W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukia H.D., Lasky S.R., Belljan N.S., Thorsson V., Sbrogne J.,
Shukia H.D., Lasky S.R., Belljan N.S., Thorsson V., Sbrogne J.,
Shukia H.D., Lasky S.R., Belljan N.S., Thorsson V., Sbrogne J.,
Swartzell S., Weit D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Halobacteriales; Halobacterium.
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TISSUE-LYMPHOCYTE;
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ŚEQUENCE FROM N.A.

ŚTRAIN-C57BL/6J; TISSUE-TESTIS;

ŚTRAIN-C57BL/6J; TISSUE-TESTIS;

MEDLINE-21085660; PubMed-11217851;

Kawal J., Shinagawa A., Shlbata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Klyosawa H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Klyosawa H., Kasukawa T., Salto Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto
                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata:
Mammaila; Eutheria; Rodentia;
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STRAIN-C57BL/6J: TISSUE-SMALL INTESTINE;
NEDLINE-21085660; PubMed-11217851;
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Mammaiia; Eutheria; I
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Sciurognathi; Murldae;
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Best Local
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Science 282:754-759(1998).
EMBL: AE001289; AAC67745.1;
InterPro; IPR001736; PLD.
Pfam; PF00614; PLDc; 2.
SMART; SM00155; PLDc; 2.
Endonuciease; Complete proteome.
SEQUENCE 383 AA; 43383 MM; 481
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CT154
Chlamydla trachomatis.
Bacteria; Chlamydlales: C
NCBI_TaxID=813;
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EMBL; AK005900; BAB24307 1; -.
MGD; MGI:1914185; 1700023B02R1k.
SEQUENCE 286 AA; 32818 MW; 068003C5E894827B
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Mltcheil W.P., Olinger L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Fiether C., Fijita M., Gariboldi M.,
RA Sakai K., Dkido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Dkido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustinclih S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Ringwaid M., Radriguez I., Sakamoto N.,
RA Gustincich S., Ringwaid M., Radriguez I., Sakamoto N.,
RA Gustincich S., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
RA Hayaahizaki Y.,
RA Hayaahizaki Y.,
RA Haselsha H., Sato G., Babayaka I., --
DR EMBL, AK006260; Babayaka I., --
DR EMBL, AK006260; Babayaka I., --
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STRAIN-MSB8 / DSM 3109;

MEDLINE-99287316; PubMed-10360571;

Nelson K.E. Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillipa C.A., Richardson D.,

Haldelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White D.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacterla froi
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01-NDV-1999
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Mua musculus (Mouse).
Mua musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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NCBI_TaxID=2336;
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MEDLINE=21085660; PubMed=11217851;
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MGI:1914185; 1700023B02R1k.
xPro; IPR000345; CytC_heme_bind.
ITE; PS00190; CYTCCHOME_C; UNKNOWN_1.
ENCE 450 AA; 51852 MW; F32F11BE6D6A4EAC
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09JN22;
01-DCT-2000
01-DCT-2000
01-DEC-2001
                                             Q9UIL6 PRELIMINARY; PRT; 756 AA. Q9UIL6; Q9W5AB; Q9W5AB; Q1-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation EG:BACR42II7.8 PROTEIN (CG14625 PROTEIN). EG:BACR42II7.8 DR CG14625 PROTEIN). Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Octopine-type Ti plasmid sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL, AF242881; AAF77134.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The conjugal transfer system of Agrobacterium tumefacions type "I plasmids is closely related to the transfer system plasmid and distantly related to "I plasmid vir genes."; J. Bacteriol. 178:4248-4257(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-96312368; PubMed-8763954;
Alt-Morbe J., Stryker J.L., Fuqua C.,
Winana S.C.,
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6; Conserv
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                      Metazoa;
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Pred. No. 66;
1; Mismatches
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                                                                                                                                                                                                               Best Local
Matches
                                                                                                                                                                                                                                   Query Match
Best Local
09V731
09V731;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                             Papagiannakis G., Spanos L., Bolshakov V., Siden-Kiamos 1., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AE003420; AAF45592.1; ALT_INIT. EMBL; AL121806; CAB65885.1; FlyBase; Flygn004058; EG:BACR42117.8. InterPro, IPR000873; AMP-bind. PRDSITE; PS00455; AMP-BINDING; UNKNDWN_1.
                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-DREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Ephydroldea; Drosophiiidae; Drosophlia.
                                                                                                                                        373
                                                                                                                                                            SRXHXHSMEXR 11
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  (TrEMBLrel. 13, Created)
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A Abril J.F., Abdyani A., An H.J., Andrews Pfankoch C., Baidyan D.,
RA Bailew R.M., Basu A., Baxondale J., Bayraktaroglu L., Beasley E.M.,
RA Belsev R.M., Basu A., Baxondale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broksteln P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Broksteln P., Brottler P.,
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RA Borkova D., Botchan M.R., Bouck J., Broksteln P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Broksteln P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Brerizz G.,
RA Glodek A., Gong F., Gorreil J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorreil J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harils N.L., Harvey D., Hellman T.J., Hernandez J.R., Houck J.,
RA Harils N.L., Larvey D., Hellman T.J., Hernandez J.R., Houck J.,
RA Harils N.L., Larvey D., Hellman T.J., Kennison J.A., Ketchum K.A.,
RA Klamnel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Lai Z.,
RA Klamnel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Lai Z.,
RA Klamnel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.L.,
RA McLion D.R., Welson K.A., Nixon K., Muzny D.M., Nelson D.L.,
RA McLion D.R., Welson K.A., Nixon K., Muzny D.M., Nelson D.L.,
RA McLion D.R., Welson K.A., Nixon K., Muzny D.M., Nelson D.L.,
RA McLion D.R., Welson K.A., Nixon K., Muzny D.M., Nelson D.L.,
RA Wang Z.-Y., Wassarman D.A., Welson K.D., Scheeier F., Shen H.,
RA Wang S.M., Woodage T., Wonier R., Venter E., Wang A.H., Wang X.,
Ra Hell M., Kellman G.S., Pan S., Pland M., Elang S., Zho X., 
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;

Ephydroldea; Drosophilidae; Drosophila.
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01-OCT-2001 (Tremblrel 18,
CG12869 PROTEIN.
CG12869.
                                                                               Pfam; PF00135; COe
PRDSITE; PS00941;
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InterPro; IPR002018; Carboxylesterase_B.
InterPro; IPR000379; Est_lip_thioest_actsite
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AB027AB311B6311D
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Admins Lob Colliner S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA Mannarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S.A., Sabburner M., Henderson S.N.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Balley R.M., Dayle C., Baxter E.G., Helt G., Nelson C.R., Millos G.L.G.,
RA Abril J.F., Aqhayani A., An H.-J., Andrews Pfennkoch C., Baldwin D.N.,
Beason K.V., Bence P.V., Serman B.P., Bhandari D., Botshavy S.N.,
RA Bockow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokela D., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H. Codieu E. Concer A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokela S., Dunkov B.C., Dunn P.,
RA Dourbin K.J., Brayley B., Dahlke C., Mays A.D., Dietz S.M.,
RA Golser C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Genn P., Harris S., Flaischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helmann T.J., Hernandez J.R., Houck J.,
RA Harris M.L., Blavey D., Helmann T.J., Hernandez J.R., Houck J.,
RA Harris M.L., Blavey D., Helmann T.J., Hernandez J.R., Houck J.,
RA Harris M.L., Blavey D., Welmann T.J., Hernandez J.R., Ketchum K.A.,
RA Harris M.L., Blavey D., Helmann T.J., Hernandez J.R., Ketchum K.A.,
RA Harris M.L., Blavey D., Helmann T.J., Hernandez J.R., Ketchum K.A.,
RA Harris M.L., Blaves J., Land T.J., Wel M., H., Ling Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLood M.P., Pacleb J.M.,
RA Mount S.M., Woodson K.A., Mazon K., Muzay D.M., Nelson D.L.,
RA Kimmel B.E., Kodira C.P., Welson M., Skupski M.P., Smi
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Eukaryota; Metazoa; Arthropoda; Tarcheata; Hexapoda; Inserta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroldea; Drosophilidae; Drosophila.
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       Conservative
                                                                                        domain.
AA; 96
                                                                                        96704 MW;
66.0%; Score 31; DB 5; 50.0%; Pred. No. 1.5e+02; tive 1; Mismatches 4
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Best Local :
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae;
Carabidae Conjunctae; Blackburnia.
NCBI_TexID=155387;
                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF337627; AAK28869.1; -.
Interpro; IPR000970; wnt1.
Pfam; PF00110; wnt; 2.
SMART; SM00097; WNT1; 1.
NDN_TER 1 1 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrei. 01-JUN-2001 (TrEMBLrei. 01-OCT-2001 (TrEMBLrei.
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147 AA;
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Search completed: September 13, 2002, 09:29:28 Job time: 1073 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: Scptember 13, 2002, 09:30:49; Search time 80.21 Seconds (without alignments) 5.310 Million cell updates/sec

US-09-446-543A-74 47 1 SRXHXHSMEXR 11

Title: Perfect score: Sequence:

scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DD seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

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PEPTIDE
PEPTIDE
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Homo sapiens (Human).
Homo sapiens (Human).
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Homo sapiens (Human).
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Projectin-releasing peptide precursor (PrRP) (Projectin-releasing hormone) (Contains: Projectin-releasing peptide PrRP31; Projectin-releasing peptide PrRP31; Projectin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujli R., Fukusumi S., Ho
Seklguchi M., Kitada C.,
Sumino Y., Fujino M.;
"Tissue distribution of p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98268781; PubMed-9607765; Hinuma S., Habata Y., Fujil R., Kawamata Y., Ho Kitada C., Masuo Y., Asano T., Matsumoto H., St Kitada C., Masuo Y., Asano T., Matsumoto H., St Kurokawa T., Nishimura D., Dnda H., Fujino M.; "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10498338;
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                    SRTHRHSMEIR 33
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                                                                                          Similarity
8; Conserv
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PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

ANIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
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T., Nishimura
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0.0082;
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0.014;
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Sekiguchi M.,
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ra D., Dnda F
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                                                                                                                                   P23482;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1997 (Rel. 35, Last sequence updared)
16-OCT-2001 (Rel. 40, Last annotation updared)
16-OCT-2001 (Rel. 40, Last annotation updared)
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PEPTIDE
PEPTIDE
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SEQUENCE
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Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kurokawa T., Nishimura D., Dnda H., Fujino M.,
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PRDT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM
STRAIR-K12;
                                                                                                                            Hydrogenase-4
HYFB DR B2482.
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Memmalia; Eutheria;
                                               Escherichia.
NCBI_TaxID=562;
                                                                                     Bacteria; Proteobacteria;
                                                                                                          Escherichia
                                                                                                                                                                                                                                       HYFB_ECDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimule expression directly to secrete PRL.

-1- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALANUS.
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NCBI_TaxID-9913;
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8; Conserv
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72.78;
               CHARACTERIZATION
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0; Mismatches
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PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP
08AC35A13B0FA908 CRC64;
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Sekiguchi M.,
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EMBL; AE000335; AAC75535.1; --
EMBL; D90876; BAA16360.1; --
EMBL; D90877; BAA16370.1; --
PIR; D49749; D49749.
ECOGene: EC11282; hyfb.
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Pfam; PFO
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Yamamoto Y., Alba N., Baba T., Nayashl K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori N., Nakade S., Nakamura Y., Nashimoto N.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.
Oshima N., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Giasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick N.A., Goeden M.A., Rose D.J.,
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"Construction of a contiguous 874-kb sequence of the Escherichia Ki2 genome corresponding to 50.0-68.8 mln on the linkage map an
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"A molecular a
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SIMILARITY: TO POLYPEPTIDE 5 OF OF CHLOROPLASTS OR MITOCHONDRIA.
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PF00361; oxidored_q1; 1.
Preductase; Transmembrane; In
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30-MAY-2000 (Rel. 39, Created 30-MAY-2000 (Rel. 39, Last se 16-OCT-2001 (Rel. 40, Last an NypothetLoal 53.3 kDa proteir RV3480C OR MT3584 OR MTCY13EJ Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Narr Cordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davles R., Deviin K., Feltweil T., Gentles S., Namlin N., Nolroy Nornsby T., Jagels K., Krogh A., Klean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rejandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Hycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Aliand D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Aliand D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwlnn M.L., Naft D., Nickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg (

Beicher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula)
   Hypotheticai protein;
CONFLICT 427 42
SEQUENCE 497 AA; 5:
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
-i- SIMILARITY: BELONGS TO THE UPP0089 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[2]
                                                                                                  EMBL; 295390; CAB08703.1; -
EMBL; AE007161; AAK47943.1;
TIGR; MT3584; -.
                                                                                                                                                       entities requires a license agreement (See http://www.lsb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                  InterPro; IPR004255; UP
Pfam; PF03007; UPF0089;
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                                                                                                                                                                                                                                                                                                                                                Whoie genome comparison of Mycobacterium tuberculosis clinical and
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. 39, Last sequence update)
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. 3 kDa protein Rv3480c.
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modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.lsb-
or send an email to license@isb-sib.ch).
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01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 49.2 kDa protein IMP4-MSKI intergenic region
YNL074C OR N2359 OR YMKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. MOL. Biol. 218:557-568(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-217 FROM M.A. MEDLINE=91202535; PubMed=2016746; Gatti D., Tzagoloff A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequencing a cosmid clone or reveals 12 new open reading of six ORFs.";
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MEDLINE-96267764: PubMed-8701611;
Poehlmann R., Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
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271350; CAA95948.1; -.

X57360; -; NOT_AMMOTATED_CDS.

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STRAIN-K12 / MG165
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STRAIN-K12 / MG1655;
MEDLINE=97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna M.T., Burland Riley M., Coilado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis M.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for cor entities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                 Ramaiingam R., Prasad R., Shivapr. "Molecular cloning and sequencing Mcra protein in Escherichia coli."
J. Blosci. 17:217-232(1992).
                                                                                                                                                                                                                                                                                                                                     Hiom K.J., Sedgwick S.G.; "Cloning and structural characterization Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
5-methylcytosine-specific restriction enzyme
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Van der Wilk F., Dullemans A.M., Verbeek M.,
"Isolation and characterization of APSE-1, a
the secondary endosymbiont of acyrthosiphon p
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Viruses; dsDNA viruse
"The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 173:7368-7373(1991).
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM M.A.
MEDLINE=92041637; PubMed=1938927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
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15-DEC-1998 (Rel. 37, I
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ECOGENE; EC10573; mCTA.
InterPro; IPR002711; HNH.
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PfBm; PF01844; HNH; 1.
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"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).

-I- FUNCTION: RESTRICTION OF 5-METHYL AND THE SPECIFIC DNA SEQUENCE C(ME)CGG.
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Homo sapiens (Human).

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                                                                   "A human homologue of the Drosophila sex determination factransformer-2 has conserved splicing regulatory functions. Proc. Natl. Acad. Sci. U.S.A. 93:9004-9009(1996).
-I- FUNCTION: MAY INTERACT WITH SPECIFIC PRE-MRNAS AND AFE SPLICING PATTERNS.
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Ritagawa M., Makino K., Mosuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto N., Nishio Y., Saito N.
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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MEDLINE-96392356; PubMed-8799144;
Dauwaider B., Amaya-Manzanares F., Mattox W.;
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16-OCT-2001 (Rel. 4
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Heat shock factor F
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol
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RA VOS P. HONEIGELI J. Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Van der Schueren J., Frymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Walter S., Berndt A., Petters S., Van Staveren M., Dirkse W.,
RA Hoizer E., Brandt A., Petters S., Van Staveren M., Dirkse W.,
RA Hoizer E., Brandt A., Petters S., Van Staveren M., Dirkse W.,
RA Hoizer E., Brandt A., Petters S., Van Staveren M., Dirkse W.,
RA Hoizer E., Brandt A., Petters S., Van Staveren M., Dirkse W.,
RA Hoizer E., Brandt A., Petters S., Van Staveren M., Dirkse W.,
RA Hoizer S., Hempel S., Reldpausch M., Landerth S., Van den Duele H.,
RA Hoizer S., Hempel S., Reldpausch M., Landerth S., Van den Duele H.,
RA Hoizer S., Hempel S., Reldpausch M., Landerth S., Van den Duele H.,
RA Chark L., Dogett J., Hall S., Ray M., Lennard N., Wellay K.,
RA Chark L., Dogett J., Hall S., Ray M., Lennard N., Wellay K.,
RA Charle S., de Haan N., Maarse A.C., Schmefer M., Muelier A., Reyes R.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argitiou A., Vitala D., Ligori R., Piravandi E.,
RA Gibbons T., Waller R., Schmidt W., Lecharry A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casauberta E.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Teann D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Teann D., Jesse T.,
RA Schohn M., Murray J., Sheet P., Cordes M., Habstrash K.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Minx P., Bentley D., Fluton B., Miller N., Scott K., Johnson D.,
RA Altreille P., Couthey L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Altreille P., Couthey L., Charley B., Malter N., Greco T., Kemp K.,
RA Altreille P., Couthey L., Charley B., Berkley C., Layman D.,
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Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douke Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermain Hilbert H., Duesterhoft A., Noores T., Jones J.D.G., Eneva T., Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C., Delseny M., Voet M., Voickaert G., Mewes H.-W., Klosterman S., Schueller C., Chalwatzis N.;

*Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thallana.*;
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                                                                                                                                                                                                                                                                                           Nature 402:769-777(1999).
-!- FUNCTION: DNA-BINDING PROMOTER ELEMENTS (HSE)
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TDR000232;
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                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@lsb-sib.ch).
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OI-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ketol-acid reductoisomerase (EC 1.1.1.86) (Ac
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PRINTS; PR00056; HSFDOMAIN.
PRODOm; PD001788; HSF_DNA_bind;
SMART; SM00415; HSF; 1.
PROSITE; PS00434; HSF_DOMAIN; 1.
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MEDLINE-97080504; PubMed-8921849;
Gusberti L., Cantoni R., de Rossi
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                                                      the European Bioinformatics Institute. The second of the second use by non-profit institutions as iong
                                                                                                           -i- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
-i- PATHMAY: VALINE AND ISOLEUCINE BIOSYXTHESIS; SECOND STEP.
-i- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
                                                                                                                                                                              Gusberti L., "Cloning and
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or send an emali to license@isb-sib.ch).
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MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garrier T., Churcher C., Harris |

RA Gordon S.V., Elgimeler K., Gas S., Barry C.E. III, Tekala F.,

RA Dadcock K., Basham D., Brown D., Chililngworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Sceger K., Skelton S., Squares S., Squares R.,

RA Rutter S., Sceger K., Skelton S., Squares S., Squares R.,

RA Suiston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

"U complete genome sequence.";

"L Nature 393:537-544(1998)."
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MCT-2001 (Rel. 40, Last annotation update)
Keto1-acid reductoisomerase (EC i.l.1.86) (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxyiacii reductoisomerase).
ILVC OR RY3001C OR MT3081 OR MTV012.15C.
Mycobacterium tuberculosis.
Bactoria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pfam; PF01450; I1vC; 1.

Oxidoreductase: Branched-chain amino acid biosynthesis;

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SEQUENCE 333 AA; 36058 MW; 336AC0BD51563DE2 CRC64
                                                                                                                                                                                                                              laboratory strains.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP
- (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
-!- PATHWAY: VALINE AND ISOLEUCINE BIOSYNTHESIS; SECOND STEP.
-!- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
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Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Saizbe
Belcher A., Utterback T., Weldman J., Khouri H., Gili J., Miku
                 EMBL; AL021287; CAA16086.
EMBL; AE007128; AAK47410.
TIGR; MT3081; -
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Parkhill J., Wren B.W., Mungail K., Ketiey J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd:
Jageis K., Karlyshev A.V., Mouie S., Palien M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keto1-acid reducto1somerase (EC 1.1.1.86) (Acetohydroxy-acid 1someroreductase) (Alpha-keto-beta-hydroxylacil reducto1somerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _CAMJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000506; Acetohydrxac_isomrdctse. Pfam; PF01450; IivC; 1. Oxidoreductase; Branched-chain amino acid bio
                                                                                                               EMBL; AL139075; CAB75268.1; -.
Interpro: IPR000506; Acetohydrx
Pfam; PF01450; 11vC; 1.
Oxidoreductase; Branched-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PHN5;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campyiobacter jejuni
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ILVC OR CJ0632.
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Pred. No. 22;
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InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003659; PSI.
InterPro; IPR001627; Sema.
Pfam; PF000477; Ig; 1.
Pfam; PF01403; Sema; 1.
                                  DISULFID
CARBOHYD
CARBOHYD
                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- SUBCELLULAR LOCATION: Secreted (By similarity).
-I- DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE OLFACTORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC VESTCLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND SONITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES OUTSIDE THE NERVOUS SYSTEM. RATER BIRTH, MESENCHYMAL LEVELS DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC SETS OF NEURONS IN THE CNS. IN THE MATURE CNS, IT IS DETECTABLE IN MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORTEX, CEREBRELLAR PORKINJE CELLS, AS WELL AS A SUBSET OF CRANTAL AND SETNAL MOTONEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM3A_RAT
Q63548;
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial criticies requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaugen J.;

"Anatomy of rat semaphorin III/collapsin-1 mank expression and
relationship to developing nerve tracts during neuroembryogenesis.";

J. Comp. Neurol. 375:378-392(1996).

J. Comp. Neurol. 375:378-392(1996).

J. COMP. Neurol. 375:378-392(1996).

THE FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THEIR
TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS TO
ENGAGE IN THE FORMATION OF SPECIFIC NERVE TRACTS. BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Semaphorin 3A precursor (Semaphorin III) (Sema III)
                                                                                                                                                                                                             SMART; SM00409; IG; SMART; SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WISTAR;
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Mammalia; Eutherla;
                                                                                       DOMAIN
                                                                                                                                                                                            Signal; Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                           protein;
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Rodentia;
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                                                                                                                                                                                            domain; Multigene
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            IG-LIKE C2-TYPE DOMAIN.
ARG/LYS-RICH (BASIC).
BY SIMILARITY.
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N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
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                                                                                                                                         SEMAPHORIN 3A.
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                                                                                                                                                                                            family;
. .) (POTENTIAL)
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01-0CT-1996
01-0CT-1996
                                                                                                                                         SGD; SOOK
                                                                                                                                                                 EMBL;
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallaworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreilie P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Pelus Rifken L., Railes L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R., Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSN5 OR YDR335W OR D9651.5.
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SRLNNHQMEMR
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                                                 Similarity 54.9
6; Conservative
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(MAR-1996)
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1224 AA; 142117
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A; Residues: 1-83 <YAM>
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## ALIGNMENTS

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prolactin-releasing peptide - rat C;Species: Rattus norvegicua (Norway rat) C;Date: 30-Jun-2001 #sequence_revialon 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7607 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishi1, S.; Shlbuaawa, N.; Hashlda, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 A;Contents: Spleen A;Accession: JC7607
                                                                                                                                                          R;Chao, L.
aubmitted to the EMBL Data Library,
a:Reference number: G06292
A;Cross-references: EMBL:U03644; NID:g476104; PIDN:AAA17853.1; PID:g476105 C;Genetics: A;Gene: recepin
                                                                                                                                                                                                                                             C;Speclea: Homo aapiena (man)
C;Date: 21-Dec-1996 *sequence_revlaion
C;Accession: G01227
                                                                        A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-451 <CHA>
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C;Comment: This peptide induces arachidonic acid metabolite release
release, and atimulation of ACTH secretion from the pitultary.
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nilarity 72.7%;
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0; Mlsmatches
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Hydrogenase-4 component B (BC 1.-.-.,

G; Species: Escherichia coli

C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997

C; Accession: A65024; D49749

C; Accession: A65024; D49749

m : Shao, Y.
                                                                                                                                                  A;Molecule type: DMA
A;Molecule type: CHAY>
A;Residues: 1-672 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36767.1; PID:gl3362814; GSPDB:GH00154
                                                                                                                                                                                                                                                DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                 hydrogenase 4 membrane subunit [imported] - Escherichia coli (strain O157:H C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: H91046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross references: GB:AE000335; GB:U00096; MID:91788821; A;Experimental source: strain K-12, substrain MGl655 R;Andrews, S.C.; Harrison, P.M.; Guest, J.R. J. Gen. Microbiol. 137, 361-367, 1991 A;Title: A molecular analysis of the 53.3 minute region of A;Reference number: A49749; MUID:91202105 A;Accession: D49749
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R; Dlattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pern A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia A; Reference number: A64720; MUID: 97426617
A; Accession: A65024
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C; Superfamily:
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A; Status: preliminary
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C; Keywords: oxi
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A; Residues: 1-34 <AND>
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A; Residues: 1-672 <BLAT>
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Yasunaga, T.; Kuhara, S.;
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Shiba, T.; Hat
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M.; Shinagawa, H.
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A; Experimental:
C; Genetics:
A; Gene: Rv3480c
hypothetical protein Vng2006c [imported] - Halobacterium sp. MRC-1 (;Species: Halobacterium sp. HRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: D84351 C;Access
                                                                                                                                                                                      RESULT
D84351
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A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Altle: Deciphering the biology of Mycobacterium tuberculosis from the complet A; Reference number: A70500; MUID:98295987
A;Accession: E70558
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DMA
A;Residues: 1-497 < COL>
A;Residues: 1-497 < COL>
A;Residues: 1-497 < COL>
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-5091
C;Accession: D85991
R;Perna, M.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.
R;Perna, M.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.
Liler, L.; Grotbeck, E.J.; Davis, M.W.; Lim, A.; Dimalanta, E.; Potamousls, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv3480c - Mycobact C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision C;Accession: E70568
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A;Experimental source: strain H37Rv
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A;Experimental source: strain O157:H7, substrain EDL933
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A; Residues: 1-672 <STO>
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6; Conserv
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5; Conserv
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/Cobacterium tuberculosis
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Pred. No.
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Pred.
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23;
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Potamousis, K.;
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Holroyd,
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M.; Shukla, H.D.;

Lasky

D.W.; Maddocks, D.G.;

Jab1c

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A; Reference number: S27287
A; Accession: S27290
A; Molecule type: DNA
                                                                                                                                                                                                                        N;Aiternate names: protein N2359; protein YNL074c C;Speckes: Saccharomyces cerevisiae C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 C;Accession: S53906; S77290; S63006; S63935 R;Poehlmann, R.; Phllippsen, P. submitted to the EMBL Data Library, April 1995 submitted to the EMBL Data Library, April 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Leithauser, B.; Keller, R.; Cruz, R.; Danson, M.J.; Hough, Jung, K.N.; Alam, M.; Freitas, T.

Proc. Nati. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Danieis, C.J.; Dennis, P.P.; Omer, A.D.;
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID: 20504483
A; Accession: D84351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch Science 282, 754-759, 1998
8;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia A;Reference number: A71570; MUID:99000809
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecuie type: DNA
A;Residues: 1-196 <5T0>
A;Cross-references: GB:AE004437; NID:gl0581437; PIDN:AAG20176.1; GSPDB:GN00138
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                                                                                                R; Tzagoloff,
                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-452 <POE>
                                                                                                                                                                                  A; Reference number: S53896
A; Accession: S53906
                                                                                                                                                                                                                                                                                                                                                          YMKi protein -
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A; Experimental source: serotype 1
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                                                                                                                    A;Cross-references: EMBL:X86470; NID:g791101; PID:g791112
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Best Local S
Matches 6
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Best Local Similarity 54.5%;
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6; Conserv
                                                                                                                                                                                                                                                                                                                                                          yeast (Saccharomyces cerevisiae)
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54.5%;
                                                                           Library, January 1991
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D, strain UW-3/Cx
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Pred. No. 17;
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           5-methylcytosine-specific restriction enzyme A (EC C;Species: Escherichia coii C;Date: 21-Apr-1992 tesquence_revision 21-Apr-1992 C;Accession: A41424; S48131; D64861
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A41424
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11

21-Apr-1992 #text\_change

04-Mar-2000

3.1.21.-) - Escherichia coii

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ATP-dependent DNA heilcase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: G72279
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G72279
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A;CroSs-references: EMBL:X57360
R;Poehlmann, R.: Philippsen, P.
submitted to the Protein Sequence
A;Reference number: S62997
A;Accession: S63006
                                                                                                                                                                                  A;Gene: TM1238
C;Superfamily: helicase
                                                                                                                                                                                                                                                                                                                                               Nature 399, 323-329, 1999
A;Title: Evidonce for lateral gene transfer between A;Reference number: A72200; MUID:99287316
A;Accession: G72279
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                                                                                                                                                                                                                                          A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36313.1; PID:g498
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                  A; Molecuie type: DNA
A; Residues: 1-648 < ARN>
                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: SGD:S0005018; MIPS:YNL074c A;Map position: 14L
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A;Accession: S63935
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370 RSHSNSLE 377
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6; Conserv
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                                                                               Conservative
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62.5%;
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54.58;
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ced. No. 40;
Mismatches
                                                                               M1smatches
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to the EMBL Data Library, Aprii
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heat shock transcription factor MSF1 - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 01-Aug-1995 #sequence_revision 24-Mar-1999 #text_change 16-Jun-2000
C;Accession: F71447; S52641; S62227; S38B73
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P; Wedler, H.; Wedler, E.; Wambutt, R.; Wettzenegger, T.; Pohl, T.M.; Terryn, H.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulydomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ang
C.; Chalwatzis, H.
A;Title: Analysis of I. 9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-495 <BEV>
A;Cross references: GB:297344; HID:92245126; PIDH:CABIO555.I; PID:92245134
R;Huebcl, A.; Schoeffl, F.
Plant Mol. Biol. 26, 353-362, 1994
A;Rotession: S52641
A;Accession: S52641; MUID:95036006
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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A;Reference number: A4124; MUID:92041637
A;Recession: A41244
A;Status: preliminary
A;Molecule type: DHA
A;Residues: 1-277 <rtf(b)
A;Cross-references: GB:M76667; HID:9146793; PIDN:AAA68481.1; PID:9146794
A;Cross-references: GB:M71232, 1992
A;Title: Molecular cloning and sequencing of mcrA locus and identification
A;Cress-reference number: A58131
A;Status: preliminary
A;Cross-references: EMEL:219104; HID:941984; PIDN:CAA79520.1; PID:941985
A;Cross-references: EMEL:219104; HID:941984; PIDN:CAA79520.1; PID:941985
A;Cross-references: EMEL:219104; HID:941984; PIDN:CAA79520.1; PID:941985
A;Residues: 1-277 <rt>A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;A;Cross-references: GB:AE000215; GB:U00096; NID:91787405; PIDN:AAC74243.1;
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-277 <rt>A;Cross-references: GB:AE000215; GB:U00096; NID:91787405; PIDN:AAC74243.1;
A;Status: nucleic strain K-12, substrain MG1655
A;Gene: mcrA; mc; rglA
A;Map position: 25 min
C;Superfamily: Escherichia coli 5-methylcytosine-specific restriction enzyn
C;Reywords: endonuclease; hydrolase; restriction modification system
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Bacteriol. 173, 7368-7373, 1991
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Burland, V
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     thioredoxin reductase homolog yumC - Bacillus subtilis
c;Species: Bacillus subtilis
c;Species: Bacillus subtilis
c;Date: 10-Sep-1999 **sequence_revision 10-Sep-1999 **text_change 16-Jun-2000
C;Accession: B70015
C;Accession: B7
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A; Residues: 1-215, 'M', 217-284, 'D', 286-335, 'T', 337-389, 'Y', 391-469,474-4
A; Cross references: EMBL:X76167
A; Accession: $62227
A; Molecule type: mRNA
A; Residues: 31-215, 'M', 217-284, 'D', 286-335, 'T', 337-389, 'Y', 391-469,474-8; Huebel, A.: Schoeffl, F.
submitted to the EMBL Data Library, November 1993
A; Description: Arabidopsis heat shock factor: isolation and characteriz A; Reference number: $38873
A; Accession: $38873
A; Accession: $38873
A; Molecule type: DNA
A; Residues: 1-215, 'M', 217-284, 'D', 286-335, 'T', 337-389, 'Y', 391-461, 474-4
A; Cross references: EMBL:X76167; NID:g429154; PIDH:CAA53761.1; PID:9429
                                                                                                                                                                                                                                                                             A; Experimental :
C; Genetics:
A; Gene: BH3408
C; Superfamily:
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A; Map position: 4COP9-4G3845
A; Introns: 111/3
C; Function: <TFC>
C; Function: transcription factor that binds to heat shock promoter elements
A; Description: transcription factor that binds to heat shock promoter elements
C; Superfamily: tomato heat shock transcription factor HSP8; HSF DNA-binding dom
C; Keywords: DNA binding; heat shock; leucine zipper; nucleus; stress-induced pr
F; 53-148/Domain: HSF DNA-binding domain homology <HSF>
F; 18I-202/Region: leucine zipper
                                                                                                                                                                                                                                                                                                                                                    A; Nolecule type: DHA
A; Nolecule type: DHA
A; Residues: 1-330 <STO>
A; Cross-references: GB: AP001518; GB: BA000004; NID: g10175792;
A; Cross-reartal source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84075
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
C;Date: 01-Bec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
C;Date: 01-Dec-200
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Cross-references: EMBL:X76167
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           2 RXHXHSME 9
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EMBL:X76167; NID:g429154; PIDH:CAA53761.1; PID:9429155
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71;
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A;Gene: llvC
C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hd
C;Keywords: intramolecular transferase; isoleucine-valine biosynthesis; laomerase; oxidd
F;18-200/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ketol-acid reductoisomerase (EC 1.1.1.86) - Mycobacterium avium N;Alternate names: acecohydroxy acid isomeroreductase C;Specles: Mycobacterium avium avium C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: JC5166
                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residucs: 1-333 <GUS>
A;Cross-references: GB:L49392; NID:g1196506; PIDN:AAB38428.1; PID:g1196509
                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Gusbertl, L.; Cantoni, R.; De Rossl, E.; Branzoni, M.; Rlccardi, G. Gene 177, 83-85, 1996
A;Title: Cloning and sequencing of the ilvBNC gene cluster from Mycobacterium avium. A;Reference number: JC5164; MUID:97080504
A;Accession: JC5166
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A;Gene: yum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-332 <KUN>
Search completed: September 13, 2002, 09:24:06 Job time: 781 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15201.1; PID:g2635708
A;Experimental source; strain 168
                                                                                                                                           Query Match
Best Local Similarity 45.3
Thomas 5; Conservative
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Bost Local Similarity 62.5
Matches 5; Conservative
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45.5%;
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62.5%;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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Match
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47
      September 13, 2002, 09:20:59; Search time 136.62 Seconds (without alignments)
I.967 Million cell updates/s
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-09-105-678A-37
US-09-172-353-4
US-08-776-971-47
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US-09-421-208-39
US-09-421-208-39
US-09-421-208-39
US-09-421-208-39
US-09-776-971-124
US-08-776-971-124
US-08-776-971-124
US-08-776-971-137
US-08-776-971-39
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US-08-776-971-39
US-08-776-971-39
US-08-776-971-39
US-09-105-678A-39
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-3
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8, Appli
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38, Appli
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39, Appli
39, Appli
49, Appli
49, Appli
45, Appli
124, Appli
127, Appli
129, Appli
29, Appli
31, App
                 Query Match
Best Local Similarity
Matches 8; Conserv
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	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	
	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	
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ALIGNMENTS	US-08-776-971-I35	US-08-776-971-59	US-08-776-971-II3	US-09-42I-208-45	US-09-421-208-33	US-08-776-971-63	US-08-776-971-7	US-09-105-678A-45	US-09-105-678A-33	US-09-421-208-44	US-09-42I-208-32	US-08-776-971-62	US-08-776-97I-6	US-09-105-678A-44	US-09-105-678A-32	US-09-421-208-43	US-09-421-208-3I	US-09-421-208-9	
	Sequence 135, App	Sequence 59, Appi	Sequence 113, App	Sequence 45, Appl	Sequence 33, Appl	53	Sequence 7, Appli	Sequence 45, Appl	ü	Sequence 44, Appl	Sequence 32, Appi	Sequence 62, Appl	Sequence 6, Appl1	Sequence 44, Appl	Sequence 32, Appl	•	Sequence 31, Appl	Sequence 9, Appli	

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPUTES:
SOFTWARE: PALENTIN Release #I.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
17-10N DATA: 27-JUN-1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANGENESS:
TYPE: amino acid
STRANGENESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-09-105-678A-8
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DI
STREET: 130 W
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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Score 43; [

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Length 31; Indeis

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US-09-105-678A-37
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                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                               Sequence 4, Application US/09172353 Patent No. 6197530
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Best Local :
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           APPLICANT: Stricker-Kongra, Albin
APPLICANT: Gu, Wei
TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILE REFERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/172,353
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172:
FILING DATE: 27-JUN-1997
ATFORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
   SOFTWARE:
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APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: F1OPPY disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09 FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
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b. 6103882
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Similarity 72.7%;
B; Conscrumt:
FastSEQ for Windows Version 3.0
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130 Water Street
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ER: 48466-342
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Pred. No. 0.012;
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US-08-776-971-47
Sequence 47, Application US/08776971B; Patent No. 6228984
; GENERAL INFORMATION:
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Best Local S
Matches 8
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LENGTH:
                                                                                                                                                       TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DF 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-NGC-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/ACENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
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nes 8; Conserv
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                                                                                                                                                                                                        REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible OPERATING SYSTEM: DOS
                                                          TOPOLOGY:
                                                                                                                                                                                            TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Hosoya, Masaki
                                                            linear
   SEQ ID
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Pred. No. 0.012;
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     47:
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RESULT 6
US-09-42I-208-37
; Sequence 37, Application US/0942I208
; Patent No. 6258561
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-8
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US-09-421-208-8
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Matches
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                                                                                                                                                               Matches
                                                                                                                                                                             Query Match
Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CONTIN, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                     I SRAHQHSMETR 1I
                                                                                                                                  I SRXHXHSMEXR I1
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                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHOD OF PRODUCING A 19P2 LIGAND
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                                                                                                                                                                                                                                                                                                                                                                                                                           27,026
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Pred. No. 0.01
0; Mismatches
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0.012;
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Best Local S
Matches B
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                                                                                              STREET:
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US-09-105-678A-38

; Sequence 38, Application US/09105678A

; Patent No. 6103882

; Patent No. 6103882
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                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Suenaga, Magato
APPLICANT: Suenaga, Magato
APPLICANT: Tanaka, Yoko
APPLICANT: Hishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE: ADDRESS:
STATE: MA
COUNTRY: USA
ZIP: 02109
COMDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Vishimura, Osamu
TITLE OF INVENTION: METHOD OF PI
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 173
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIÎN, DAVIG G.
REGISTRATION NUMBER: 27.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 02109
                                                                                                  CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                      ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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B; Conserv
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I30 Water Street
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72.7%;
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Pred. No. 0.
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; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-105-678A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 32 amlno acids
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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                                                                                                                                             COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette
                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & COSHMAN, LLP
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                 APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
                                                     APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NOMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukusumi, Shoji
Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
IR OF SEQUENCES: 140
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Hosoya, Masaki
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JP 8/211805
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                                                               PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 09/105,678

PRILING DATE: 26-JUN-1998

PRILING DATE: 27-JUN-1997

PRILING DATE: 27-JUN-1997

PRICARTION NUMBER: JP 172118/1997

ATTORNEY/AGENT INFORMATION:

NAME: CON11n, David G.

REFERENCE/DOCKET NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tanaka, Yoko
APPLICANT: NISHIMURA, OSAMU
APPLICANT: NISHIMURA, OSAMU
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
ENGTH:
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TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                   02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3, Application US/09421208 6258561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-AUG-1996
NUMBER: JP 8/246573
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130 Water Street
                                                        617-523-6440
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32 amino aclds
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Pred. No.
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; STRANDEDNESS:
; TOPOLOGY: 11n
; MOLECULE TYPE:
US-09-421-208-38
RESULT 11
US-08-776-971-49
; Sequence 49, Application US/08776971B
                                                                                                                       Query Match
Best Local Similarity
Thes 8; Conserve
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; MOLECULE TYPE:
US-09-105-678A-39
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US-09-I05-678A-39
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Best Local Similarity 72.7
Matches 8; Conservative
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECONMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
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                                                                                                                                                                                                                                                     STRANDEDNESS:
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72.7%;
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72.78;
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Pred. No. 0.012;
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Pred. No. 0.013;
0; Mismatches
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TOPOLOGY: Linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID
US-08-776-971-49
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                                                                                                  US-09-421-208-39
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                                                                                                                       RESULT
Sequence 39, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Massato
APPLICANT: Moriys, Takeo
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Best Local Similarity
Matches 8; Conserv
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GENERAL INFORMATION:
APPLICANT: Ninu
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TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617-523-3440
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-DEC-1996
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MAG-1996
APPLICATION NUMBER: JP 8/216573
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, Dav1d G.
REGISTRATION NUMBER: 27,026
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APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                           SRXHXNSMEXR 11
                                                                                                                                                                                SRAHQNSMETR 11
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Kitada, Chieko
OF INVENTIN: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                                                                                                                                                                                                                               Conservative
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Kawamata, Yuji
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Pred. No. 0.013;
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RESULT 13
US-08-776-971-45
; Sequence 45, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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TELEPHONE: 617-523-4400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 39:
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
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APPLICANT: Nishimura, O:
TITLE OF INVENTION: METI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/421,208 FILING DATE:
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                                                                                                              HOSOYA, MASKI
FUJII, RYO
FUKUSUMI, Shoji
KITEGA, Chieko
TITLE OF INVENTION: POLVPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                              APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRXHXHSMEXR 11
                                                                     CITY: Boston
STATE: MA
                                                                                                         STREET: I30 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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Pred. No. 0.013;
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RESULT 14
US-08-776-971-124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 124, Applicat Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-NG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 18-DEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-DEP-1996
ATTORNEY/ACENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
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hes 8; Conserv
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OPERATING SYSTEM: DOS
SOETWARE: FRASESEQ FOR WINDOWS VERSION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
STREET: 130 Water Street
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                  FUKUSUMI, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 617-523-3400
      CURRENT
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
ENT APPLICATION DATA:
                                                                                                                                COUNTRY: USA
ZIP: 02109
                                                                                                                                                                       STATE: MA
                                                                                                                                                                                           CITY: Boston
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Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fujii, Ryo
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Pred. No. 0.032;
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                                                                                                                                                                                                                                    ROBERTS & CUSHMAN, LLP
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Best Local Similarity 74..
""" tohes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 137, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: D1skette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION CANTA:
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                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: I30 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                   Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 17-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                         CITY: Boston
STATE: MA
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Hosoya, Masaki
Fujii, Ryo
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72.78;
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0; Mismatches
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 137
SEQUENCE CHARACTERISTICS:
                                                                                         22 SRAHQHSMETR 32
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FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                         SRXHXHSMEXR 11
                                                                                                                                                                                                                                                                                                                                            LENGTH: 83 amino acids
TYPE: amino acid
STRANDEDNESS: 91n91e
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APPLICATION NUMBER: JP 8/211805
FILING DATE: I2-AUG-1996
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APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
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72.78;
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Pred. No. 0.032;
0; Mismatches
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Result
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Maximum DB seq length: 200000000
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Maximum Match 100%
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Perfect score:
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 Pred. No. is the number of reaults predicted by chance to have a acore greater than or equal to the score of the result being printed, and is derived by analysia of the total score distribution.
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fung1:*

4: sp_human:*

5: sp_invertebrate

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7: sp_mhc:*

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10: sp_plant:*

11: sp_virus:*

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Match
September 13, 2002, 09:09:25; Search time 25.73 Seconds (without alignmenta) 221.875 Million cell updates/sec
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sp_unclassified:*
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           Q9%624 carassius a
Q918/6 rhodospiril
Q911/4 pseudomonas
Q910/2 pseudomonas
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Q910/2 pseudomonas
Q910/2 pseudomonas
Q910/2 pseudomonas
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Q931/7 streptomyce
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Q948/2 mus musculu
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# ALIGNMENTS

222	RESULT Q9L8J6 ID Q	В	Qy	Men	ŞQ	DR	R	R.	₽	7	꾸	Z	×	ጸ	8	గ్గ	S	DE	ğ	DŢ	ď	AC	Đ	Q9W624	RESILT
01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	LT 2 J6 Q918J6 PRELIMINARY; PRT; 692 AA.	50 HNVDNRSPEIDPFWYVGRGVRP1GRF 75	×	Query Match 62.8%; Score 98; DB 13; Length 117; Best Local Similarity 53.8%; Pred. No. 3e-08; Matches 14; Conservative 8; Mismatches 4; Indels 0; Gaps	SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;	EMBL: AB020024: BAA76662.1;	Submitted (NOV-1998) to the EMBL/GenBank/DD8J databases.	"Carassius RFamide (C-RF amide).":	Satake H., Minakata H., Fulimoto M.:	TISSUE-BRAIN;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=7957;			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Carassius auratus (Goldfish).		(TrEMBLrel. 19, Last	12,	1999 (TrEMBLrel.	Q9W624;	Q9W624 PRELIMINARY; PRT; 117 AA.		T.T. 1
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Cheng Y.S., Branther C.A., Tsapin A., Collins M.L.P.;
Role of the N protein in assembly of the photochemical
center and intracytoplasmic membrane in Rhodospirillum
J. Bacteriol. 182:1200-1207(2000).
EMBL; AF202319; AAF37352.1; -.
InterPro; IPR003672; CobN-Mg_chelatase.
Pfam; PF02514; cobN-Mg_chelatase.
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ŚTRAINATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Nickey M.J., Brinkman F.S.L., Nufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.N., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:959-964(2000).
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01-MAR-2001 (TrEMBLre1. 16,
01-OCT-2001 (TrEMBLre1. 18,
01-OCT-2001 (PROTEIN PA2151.
                                                                                                                                                                                                                                                                                                                                          EMBL; AE004642; AAG05539.1;
InterPro; IPR004589; Actinin_act_blnd.
InterPro; IPR004661; Alpha_amylase.
Pfam; PF00128; Blpha-amylase; 1.
PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
Nypothetical proteon: Complete proteome.
SEQUENCE 664 AA; 76329 MW; 8F59FEED54C30BAD CRC64;
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Bacteria; Proteobacteria;
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Pred. No. 12;
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Best Local S
Matches 11
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X MEDLING-20437337; PubMed-10984043;

X MEDLING-20437337; PubMed-10984043;

A Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener A. Nickey M.J., 8rinkman F.S.L., Nufnagle W.O., Kowalik D.J., Lagro A. Nickey M.J., 8rinkman F.S.L., Nufnagle W.O., Kowalik D.J., Lagro A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. A. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Reizer J., Saier M.N., Hancock R.E.W., Lory S., Olson M.V.;

**TCOmplete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.*;

Topportunistic pathogen.*;

Nature 406:959-964 (2000).

REMBL; AE004709; AAG06209.1; -.

REMBL; AE004046; GST_C.

RINGEPTO; IPR004046; GST_C.
Query Match
Best Local Similarity
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Q91022;
01-MAR-2001 (TrEMBLre1
01-MAR-2001 (TrEMBLre1
01-DEC-2001 (TrEMBLre1
pROBABLE GLUTATHIONE S
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                                                                                          Nypothetical proteins sequence 790 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Strebphyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales: Brassicaceae; Arabidopsis.
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01-OCT-2000 (TYEMBLEEL 15, La
01-DEC-2001 (TYEMBLEEL 19, La
HYPOTHETICAL 87.4 KDA PROTEIN.
F15G16.60.
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SEQUENCE: 2
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Bacteria; Proteobacteria;
                                                                                                                                      EU Arabidopsis sequencing p
Submitted (JAN-2000) to the
EMBL; AL132959; CAB71097.1;
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Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
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20 AA; 24716 MW;
                                                                                                 87376 MW;
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                                                                                                                                                                 ncing project;
to the EMBL/GenBank/DDBJ
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Best Local Similarity 33.
Matches 11; Conservative
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01-DEC-2001 (TremBLrel. 1
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                                                                                                                                  Kawashlma T., Amano N., Kolke H., Makino S.-1., Higuchi S., Kawashlma Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Karunoshlba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.; "Archaeal adaptation to higher temperatures revealed by genore of Thermoplasma volcanium."; Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
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Hypothetical protein; Complete Proteome.
SEQUENCE 128 AA; 13481 MW; 4FF5B364C38396F6 CRC64;
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Bacterla; Cyanobacterla; Chroococcales;
NCBI_TaxID=1148;
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01-FEB-1997 (TrEMBLrel. 02, Cr
01-FEB-1997 (TrEMBLrel. 02, La
01-JUN-2000 (TrEMBLrel. 14, La
HYPOTHETICAL 13.5 KDA PROTEIN.
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MEDLINE-20570466; PubMed-11121031;
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STRAIN-GSS1 / DSM
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MEDLINE=97061201; PubMed-8905231;
                                                                 InterPro; IPR001451; Hexapep_transf
Pfam; PF00132; hexapep; 4.
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SEOUENCE 1271 AA; 141905 MW; 752
                                                                                                                                  Kormanec J., Bistakova J., Novakova R., Homerova D., Rei "Cloning and characterization of a new polyketide gene (Streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Kalto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kelschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fietcher C., Fujita M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Alyons P., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashivaru Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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"Functional annotation of a full Nature 409:685-690(2001).
EMBL: AK008242: BAB25553.1: -.
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SEQUENCE 277 AA; 31797 NW; 4
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Hayashizaki Y.;
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STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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Mammaila; Eutheria; Primates;
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A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
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A Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Rochiwa H.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bersh G.,
Balake J., Boffelli D., Bojunga N., Carnincl P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carnincl P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carnincl P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamilya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE=21085660; PubMed=11217851;
Kawal J., Shinagawa A., Shibata K.
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Sciurognathi; Muridae; Murinae; Mus
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AX MEDLINE=20365717; PubMed=10910347;

RA SImpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptlsta C.S.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptlsta C.S.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptlsta C.S.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptlsta C.S.,

RA Barros M.H., Bonaccorsl E.D., Bordln S., Bove J.M., Briones M.R.S.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,

RA Coutinho L.L., Cristofanı M., Dlas Neto E., Docena C., El-Dorry H.,

RA Facincani A.P., Perreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraya J.S., Franco M.C., Frohme M., Furlan L.R.,

RA Fraya J.S., Franco G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajlma J.P.,

RA Krieger J.E., Kuramae E.E., Lalyret F., Lambais M.R., Leite L.C.C.,

RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,

Machado M.A., Madeira A.M.B.H., Madeira H.M.F., Marino C.L.,

RA Menck C.F.M., Miracca E.C., Mlyaki C.Y., Monteiro-Viltorello C.B.,

RA Menck C.F.M., Miracca E.C., Mlyaki C.Y., Monteiro-Viltorello C.B.,

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RA Menck C.F.M., Miracca E.G., Mlyaki C.Y., Monteiro-Viltorello C.B.,

RA Menck C.F.M., Martlns E.A.L., Martlns E.A.,

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Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
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"1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9PH76;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYDROXYBENZOATE OCTAPRENYLTRANSFERASE.
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Bacteria, Proteobacteria;
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Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silva A.P., Terenzi M.F., Truffi D., Tsal S.M., Tsuhako M.H.,
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A Rature 406:151-159(2000).
BY EMBL, ABO03860, ARRS2BB1.1; -.
DR Ffam; PP01040; UbiA; 1.
DR Pfam; PP01040; UbiA; 1.
DR Pfam; PS00943; UBIA; UNKNOWN_1.
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Best Local
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045431;
                                                                                                                          "Genome sequence of the nematode C.elegans: Investigating blology.":
Science 282.2012-2018(1998).
EMBL; Z81074; CAB03039.1; -.
InterPro; IPR004098; Prp18.
InterPro; IPR003648; SFM.
Pfam; PF02840; Prp18; 1.
SMART; SM00500; SFM; 1.
                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLre1.
01-JAN-1999 (TrEMBLre1.
01-DEC-2001 (TrEMBLre1.
F32B6.3 PROTEIN.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Basham V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 333 AA;
                                                                                                                                                                                                                                                                                Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 LDPYWKLARGDRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 INPAWYXXRGIRPVG
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                          N
                         RXHXHSMEXRTPDINPAW
RKRLHQLELAQPDLNEGW
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7; Conserv
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                                                                                                                 40152 MW;
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38.9%;
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Caenorhabditls.
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Pred. No.
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Pred
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                                                                                                                 8EFCE683812BB401 CRC64;
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25;
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September

13, 2002,

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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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PRRP_BOVIN
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UNR_RAT
NER3_BOVIN
PLSC_HELPY
Y587_PASMU
NER3_HUMAN
UVRA_METTH
OPS1_LIMPO
CYCR_CHVI
YAAJ_ECOL1
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Compugen Ltd
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P81264 bos taurus
Q92935 homo sapien
P18395 rattus norv
O97859 bos taurus
Q25903 helicobacte
Q90n56 pasteurella
Q9uq49 homo sapien
Q90q49 homo sapien
Q90q49 homo sapien
Q95361 limulus pol
Q9247 chromatium
P30143 escherichia
P31795 radiation m
P32770 saccharomyc
P03357 akr murine
P1327 radiation m
P32771 sar murine
P11227 radiation m
Q9fbm3 streptomyce
Q66911 aquifex aeo
P11528 arbacia pun
Q9fbm3 streptomyce
Q66912 quifex aeo
P11528 arbacia pun
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                                                            PEPTIDE
MOD_RES
SEQUENCE
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# ALIGNMENTS

RESULT	.a 1
PRRP	RAT PRRP_RAT STANDARD; PRT; 83 AA.
38	
	30-MAY-2000 (Rel. 39, Liest sequence update)
	01-MAR-2002 (Rel. 41, Last annotation update)
D D	Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
8	releasing peptide PrRP20).
ρZ	Pattus porvegique (Rat)
88	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
88	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
×	1_TaxID=10116;
R	(1)
3 2	SEQUENCE FROM N.A.
RX	MEDLINE=98268781; PubMed=9607765;
5 ₹	osoya M.
Z :	Kurokawa T. Mighimura O. Onda H. Fulino M.:
3	"A prolactin-releasing peptide in the brain.";
2 2	Nature 393:272-276(1998).
₽;	TISSUE SPECIFICITY.
RX	PubMed=10498338;
7 ₹	
3 3	DERTYCHIE M., ALGUA C., AUTONOWA I., NIBHIMUIA O., OHUA M.,
곱 3	"Tissue distribution of prolactin-releasing peptide (PrRP) and its
급	receptor."
7	ui. Pept. 83:1-10(1999).
36	-i- FUNCTION: Stimulates projectin (PRL) rejease and regulates the
88	lactorophs directly to secrete PRL.
H I	-i- TISSUE SPECIFICITY: Widely expressed, with highest levels in
38	medulla oblongata and hypothalamus.
i i	This SWISS-PROT entry is copyright. It is produced through a collaboration
R	een the Swiss Institute of Bioinformatics and the EMBL outstatic
8 8	the European Bioinformatics Institute. There are no restrictions on its
36	use by non-profit institutions as long as its content is in no way modified and this attemport is not removed desired by and for commercial
នន	entities requires a license agreement (See http://www.isb-sib.ch/announce/
8	•
200	7777
X X	EMBU; ABUID4ID; BANZ9UZO.I; ". Hormone: Amidation: Signal: Cleavage on pair of basic residues.
-	BY SIMILARITY.
13	

PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-53 PROVIDE AMIDE GROUP).
D0C75A264EEE4F29 CRC64;

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RESULT 2
PRRP_HUMAN
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Best Loc
Matches
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P81277;
30-MAY-2000
                                                                                                PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Projactin-releasing peptide precursor (PrRP) (Projactin-releasing hormone) (Contains: Projactin-releasing peptide PrRP31; Projactin-releasing peptide PrRP31; Projactin-releasing peptide PrRP31; Projactin-releasing peptide PrRP31; Projactin-releasing peptide PrRP30].
                                                                                                                                                                                                                                                                                                                                                                   Fujli R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
Sumino Y., Fujino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinuma S., Habata Y., Fujii R., Kawamata Y., Ho
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   MIM;
                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Dynon-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98268781;
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                                                                                                                                                                             EMBL; AB015419; BAA29027.1;
                                                                                                                                                                                                                                                                                                                                                  receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10498338;
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                                                                                                                                 PEPTIDE
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23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                   μ.
                                                                                                                                                                                                                                                                                           IT Pept. 83:1-10(1999).

FUNCTION: Stimulates projectin (PRL) release and regulates expression of projectin through its receptor GPR10. May still the projection of projectin through a secret pRL.

lactotrophs directly to secrete PRL.
                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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                                                                                                                     Signal.
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f
                                                    94.2%;
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Pred. No. 1.3e-16:
0; Mismatches 5
                                                    Score 147;
Pred. No. 1.
                                                                                              BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP).

229A2F3F50CF981B CRC64;
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Kawamata Y., 1
T., Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                      DB 1;
1.3e-16;
5;
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                                                                                                                                                                                                                                                                                                                                                          peptide (PrRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hosoya M., Fu
Sekiguchi M.,
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                                                                                                                                                                                                                                                                                                                                                                                          Habata Y.,
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                                                              Length 87
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EXLI_HUMAN
ID EXLI_H
AC 092935
DT 15-JUI
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DE EXOSTC
GN EXTL1
OS HOmo :
OC Eukar)
OC Mamma:
OX NCBI_'
RN (1]
RP SEQUE
RX MEDLI
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Best Local S
Matches 26
                                                                                                                                                            EXL1_HUMAN
Q92935;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hormone;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rei. 39, Created)
30-MAY-2000 (Rei. 39, Last sequence update)
01-MAR-2002 (Rei. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOVIN
                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammaiia; Eutheria; Pi
                                                                                                                 15-JUL-1998 (Rei.
I6-OCT-2001 (Rei.
Exostosin-like i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRRP_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                releasing
    SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae;
                                            NCBI_TaxID-9606;
                                                                                                       EXTL1 OR EXTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB015417; BAA29025.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98268781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of prolactin through its receptor GPR10. Malactotrophs directly to secrete PRL.
TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
                                                                                                                                                                                                                                                                SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide PrRP20].
                                                                                      (Rel. 36, Creary,
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
(Rel 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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    PubMed-9037597
                                                            Chordata;
Primates;
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22
53
53
53
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Cetartiodactyla; Ruminantia; Pecora;
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3
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                 PROLACTIN-RELEASING PEPTIDE PRAMIDATION (G-54 PROVIDE AMIDE 08AC35A13B0FA908 CRC64;
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                                                            Craniata; Vo
Catarrhini;
                                                                                                                                                                                            PRT;
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No. 2.
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n its receptor GPR10. May sti
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                                                                          Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pair of basic
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                                                               Hominidae;
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ora; Bovoidea;
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                                                                                                                      protein)
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UNR_RAT
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OS RAT
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Best Local
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                                              UNR_RAT
P18395;
01-NOV-1990
01-NOV-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                             EMBL;
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EMBL;
EMBL;
EMBL;
EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wuyts W., Spieker N., Van Roy N., De Paepe A., De Boulle K., Willems P.J., Van Hui W., Versteeg R., Speleman F.; *Refined physical mapping and genomic structure of the EXTL1 ger Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M., "Identification and localization of the gene for EXTL, a of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                           SND
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                            Pfam; PF03016;
                                                                                                                                                                                                                                                                                                                                                     MIM; 601738;
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                                                                                                                                                          400
                                                                                                                                                                                12 TPDINPAWYXXRGIRPVGRF 31
                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reticulum (By similarity).
SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                            J. U67191; AAC51141.1;
AF083623; AAD02840;
AF083623; AAD02840;
AF083624; AAD02840;
AF083625; AAD02840;
AF083625; AAD02840;
AF083626; AAD02840;
AF083628; AAD02840;
AF083629; AAD02840;
AF083630; AAD02840;
AF083630; AAD02840;
AF083631; AAD02840;
AF083631; AAD02840;
AF083631; AAD02840;
AF083631; AAD02840;
AF133980; AAF73172;
AF153980; AAF73172;
                                                                                                                                                         SPQDFPFYYLQQGSRPEGRF 419
                                                                                                                                                                                                       Similarity 45.09; Conservative
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676 AA;
                                               (Rel.
(Rel.
(Rel.
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; Multigene i
10 30
                                                                                              STANDARD;
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74673
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                                                                                                                                                                                                                                                                                                                                 Exostosin.
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genes
                                               Last sequence up
                                                                       Created)
                                                                                                                                                                                                                                                                                                family; Transmembrane; Signal-anchor.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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in 1
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Pred. No. 11;
3; Mismatches
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                                                                                                                                                                                                                                                                                          (POTENTIAL)
 Craniata; Vertebrata; Euteleostomi;
                                                                                                PRT;
                                                                                                                                                                                                                                                                   B5E006A8762E5633 CRC64;
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                                                          update)
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                                               update)
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11;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                            NER3_BOVIN
097859;
01-MAR-2002
01-MAR-2002
01-MAR-2002
01-MAR-2002
Sialidase 3
                                                                                  Eukaryota; Metazoa
Mammalia; Eutheria
Bovidae; Bovinae;
NCBI_TaxID=9913;
                     Miyagi T.,
Sawada M.;
                                                                                                                                                                                                                           BOVIN 6
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SEQUENCE
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DOMAIN
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jeffers M., Paciucci R., Peilicer A.;

*Characterization of unr; a ggne closely linked to N-ra

*Characterization of unr; a ggne closely linked to N-ra

*Nucleic Acids Res. I8:4891-4899(1990).

-i- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Cytoplasmic.

-i- SUMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90370473; PubMed=2204029;
  associated
                                                        TISSUE-Brain;
                                                                                                                                          NEU3
                                                                                                                                                 01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Sialidase 3 (EC 3.2.1.18) (Membrane sialidase)
(N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR002059; Copfam; PF00313; CSD; 8.
SMART; SM00357; CSP; 5.
PR0SITE; PS00352; COLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S11210; S11210.
HSSP; P15277; 1MJC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52311; CAA36549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Testis;
                                           MEDLINE-99143165;
                                                               SEQUENCE FROM N.A.,
                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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             'Molecular
                                                                                                                                                                                                                                                                        583
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                                                                                                        Eutheria;
 cloning an
                                Wada
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                                                                                                                                                                                                                  STANDARD;
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                                         PubMed=9988745;
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and characterization of a page specific for gangliosides
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179
245
245
337
410
507
579
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579
                                                                                                        Chordata; Craniata; Vertebrata; Eute Cetartiodactyla; Ruminantia; Pecora;
                                 Iwamatsu
                                                                PARTIAL
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                                                                                                                                                                                                                                                                                                                          29.5%;
39.1%;
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                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                               SEQUENCE,
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Pred. No.
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                                                                AND CHARACTERIZATION
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                                Yoshikawa Y., Tokuyama
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            plasma
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                                                                                                                                                               (Ganglioside sialidase)
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             membrane
                                                                                                                    Euteleostomi;
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                                                                                                           Bovoidea;
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RESULT
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Matches 8
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-26695 / ATCC 700392;

STRAIN-26695 / PubMed-9252185;

MEDLINE-97394467; PubMed-9252185;

MEDLINE-9739467; PubMed-9252185;

MEDLINE-97394467; PubMed-9252185;

MEDLINE-97394467; PubMed-9252185;

MEDLINE-97394467; PubMed-9252185;

MEDLINE-9739467; PubMed-9739467;

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MEDLINE-9739467; PubMed-9739467;

MEDLINE-9739467; PubMed-9739467;

MEDLINE-9739467; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 27.....
-i- FUNCTION: Plays a role in modulate the lipid bilayer at the level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
ACT_SITE
                                                                                                                                                                                                                                                                                                        PLSC_HELPY STANDARD; PRT; 240 AA. 025903; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 1-acyl-sn-glycerol-3-phosphate acyltransferase acyltransferase) (1-AGPAT) (Lysophosphatldic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELPY
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                                                                                                                                                                                                                                                      PLSC OR HP1348.
Heilcobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                   Bacterla; Proteobacteria;
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CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(alpha-(2->6)-glycosidic linkages of terminal sialic resialpha-(2->6)-glycosidic linkages of terminal sialic resionidosaccharides, glycoproteins, glycolipids, colominic synthetic substrates.
Synthetic substrates.
SUBCELULAR LOCATION: Membrane-associated (By similarity rissue specificary: Expressed in brain.
SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RARPHSLMIYSDDLGATWHHGRLIKPM
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8; Conser
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Plays a role in modul
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FRIP MOTIF.

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POTENTIAL.

POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                   subdivision;
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 alpha-(2->6)-,
siallc residues in
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                                                                                                                                                                                                                                                                                                            2.3.1.51) (1-AGP acyltransferase)
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                                                                         Dougherty
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Matches
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TIGETPRO; IPRO02123; ACYILLA...

InterPro; IPRO02123; ACYILLA...

Pfam; PF01553; ACYILLA...

Pfam; PF01553; ACYILLA...

Phospholipid biosynthesis; Transferase; Acyilla.

Phospholipid biosynthesis; Transferase; Acyilla.

Phospholipid Acyilla.

Therefore membrane; Complete proteome.

Therefore membrane; Complete proteome.

Therefore membrane; Complete proteome.
                                                                                                                                                                                                                                                                            This SWI
between
                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPH
ACID BY INCORPORATING ACYL MOISTY AT THE 2 POSITION.
-i- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sen-glycerol 3-phosph
CoA + 1.2-diacyl-sn-glycerol 3-phosphate.
-i- SUBCELLULAR LOCATION: Inner membrane-associated (Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E. Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kel Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C. Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence
                              Match
                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Inner membrane-associated (Potential). SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                           ACYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                           SWISS-PROT entry 1s copyright. It 1s produced een the Swlss Institute of Bioinformatics and
              28.5%;
                Score
Pred.
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                                                                           22BD5D0EB190BBDD
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           DB
4.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen Helicobacter
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                                Length 240;
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MBL outstation –
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y587_PASMU
Q9CN56;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                            MEDLINE=21145866; PubMed=11248100; May B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., I May B.J., Zhang O., Li L.L., Paustian M.L., whittam T.S., I "Complete genomic sequence of Pasteurella multocida Pm70." Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                             Bacterla;
                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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9; Conser
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                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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RESULT
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Q9UQ49; Q9NQ
01-MAR-2002
                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                          Montí E., Bassi M.T., Papini N., Riboní Croci G., Preti A., Ballabio A., Tettamd "Identification and expression of NEU3, associated to the plasma membrane.";
Biochem. J. 349:343-351(2000)
                                                                          the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/acorsend an email to license@isb-slb,ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
51alidase 3 (EC 3.2.1.18) (Membrane sialida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE006094; AAK02671.1;
Hypothetical protein; Trans
SEQUENCE 288 AA: 33778 M
                       EMBL; Y18563
MIM; 604617;
                                    EMBL; Y18563: CAB96131.1; A
                                                                                                                                                    between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, expression, and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99335353; PubMed-10405317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (N-acetyl-alpha-neuraminidase 3).
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                                                                                                                                                                                         adrenal gland and thymus, followed by pancreas, liver, h
thymus. Weakly expressed in kidney, placenta, brain and
MISCELLANGOUS: Optimum ph 19 318.
SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                                                                                                                                  glycoconjugates.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)
alpha-(2->8)-glycosldic linkages of terminal siallc residues
oligosaccharides, glycoproteins, glycolipids, colominic acid
                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Highly expressed in skeletal muscle, testis, adrenal gland and thymus, followed by pancreas, liver, heart and
                                                                                                                                                                                                                                                                              synthetic substrates.
SUBCELLULAR LOCATION: Membrane-associated
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Plays a role in modulating the the lipid bilayer at the level of membrar
                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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8; Conservative
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             IPR002860;
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33778 MW; F4D;
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           BNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Commun.
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                                     ALT_INIT
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Pred. No. 9.7;
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Tettamanti G., Borsani G.;
f NEU3, a novel human sialidase
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sialidase)
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membrane-bound sialyl
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human ganglioside
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Best Local
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                                                                                                                                        "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
-1- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA (BY SIMILARITY).
-1- SUBGELLULAR LOCATION: Cytoplasmic (By Similarity).
-1- SUBGELLULAR LOCATION: Cytoplasmic (By Similarity).
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30-MAY-2000
30-MAY-2000
16-OCT-2001
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                                                                                                                                                                                                                                                                              Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubc Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothler B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar McDougall S., Shiner G., Goyal A., Piettrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Excinuclease ABC subunit A.
          EMBL; AE000828; AAB84949.1; InterPro; IPR003439; ABC_tr
                                            or send an
                                                                                            the European Bioinformatics Institute.
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8; Conserv
                                        and this statement is not remove requires a license agreement (San email to license@isb-sib.ch).
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                     *Opsins from the lateral eyes and ocelli of the horses'
Limulus polyphemus.";
Proc. Natl. Acad. Scl. U.S.A. 90:6150-6154(1993).
-I- FUNCTION: VISUAL PIGHENTS ARE THE LIGHT-ABSORBING N
MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSI
LINKED TO CIS-RETINAL.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: LATERAL EYE.
-I- FISSUE SPECIFICITY: LATERAL EYE.
-I- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR TH
BE PHOSPHORYLATED (BY SIMILARITY).
-I- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM
-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLE
-- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
16-OCT-2001 (Rel. 4
Lateral eye opsin.
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SOS response;
DNA-binding; z
NP_BIND 64
ZN_FING 74
SEQUENCE 962
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P35360;
01-JUN-1994
 TRANSMEM
DOMAIN
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                                                                                                            InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                          the European Bloinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Uentitles requires a license agreement (See htterities)
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MEOLINE-93317641; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Limulus polyphemus (
Eukaryota; Metazoa;
Limulldae; Limulus.
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                                                           PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; GPROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
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                                              Photoreceptor; Retinal protein; Transmembrane;
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ARE THE LIGHT-ABSORBING
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EMBL; L03782;
PIR; A48197; A
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P35361;
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DOMAIN
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DOMAIN
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Limulus polyphemus.";
Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).
-!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES TNAT MEDITATE VISION. TNEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
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Eukaryota; Metazoa;
Limulidae; Limulus.
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                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                    between
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MEDLINE=93317641; PubMed=8327495;
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SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: OCELLAR CELLS; MEDIAN OCELLI.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR
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29, Last sequence update)
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; Arthropoda; Chellcerata; Merostomata; Xiphosura;
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Pred. No. 18;
2; Mismatches
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                                                                                                           Gorson G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanti Qin H., Allen R., Knaff D.B.;

"Primary structure of genes encoding light-harvesting and reacenter proteins from Chromatium vinosum.";

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PHOXIDIZED PRIMARY ELECTRON DONOR.

-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
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PR1NTS; P
PROSITE;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
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Allochromatium.
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as iong as its content is in no way ifted and this statement is not removed. Usage by and for commercial
                                                                  ANCHOR (BY SIMILARITY).

PTW: BINDS FOUR HEME GROUPS PER MOLECULE.
SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHET
CYTOCHROME C SUBUNITS.
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EXTRACELLULAR.
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CYTOPLASMIC.
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EXTRACELLULAR.
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       SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
                                                                      Yura T., Mori H., Nagai H., Nagata T., Isono K., Mizobuchi K., Nakata A.:
"Systematic sequencing of the Escheric the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                             SEQUENCE FR
STRAIN-K12;
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Bacteria; Proteobacteria;
Escherichia.
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01-JUL-1993 (Rel.
16-OCT-2001 (Rel.
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SIGNAL
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InterPro; IPR000345; CytC_heme_bind.
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7; Conserv
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PS00190; CYTOCHROME_C;
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15-DEC-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Aspartyi protease: Endonuclease; Polyprotein.
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                     8, Appli
37, Appli
47, Appli
47, Appli
61, Appli
61, Appli
9, Appli
9, Appli
9, Appli
9, Appli
9, Appli
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13, Appli
14, Appli
14, Appli
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15, Appli
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16,
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US-09-105-678A-8
                 Query Match 94.3
Best Local Similarity 83.9
Matches 26; Conservative
                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 W
                                                                                                                                                                                      STRANDEDNESS
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                                                                                                                                                                                                                                    31 amino acids
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                                           94.28;
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Result

Database

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
146	146	146	146	146	146	146	146	146	146	146	146	146	146	146	146	147	147
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US-08-776-971-131		٠.	- 1	US-09-421-208-33		US-09-105-678A-33	US-09-421-208-32	90-	US-09-105-678A-32	US-09-421-208-31		US-08-776-971-97	US-08-776-971-5	US-09-105-678A-31	US-09-105-678A-7	US-08-776-971-138	US-08-776-971-135
Sequence 131, App	Sequence 122, App	Sequence 44, Appl	Sequence 1, Appl1	Sequence 33, Appl	Sequence 7, Appll	Sequence 33, Appl	Sequence 32, Appl	Sequence 6, Appl1	Sequence 32, Appl	Sequence 31, Appl	Sequence 7, Appl1	Sequence 97, Appl	Sequence 5, Appl1	Sequence 31, Appl	Sequence 7, Appli	Sequence 138, App	Sequence 135, App

## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: NIShlmura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAVID 6.

PEGITEMATION NUMBER: 37-026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09105678A Patent No. 6103882
                  REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 Water Street
617-523-3400
                                                  48466-342
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Score 147; DB Pred. No. 1.3e 0; Mismatches

DB 3; Length 31; 3e-17;

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US-09-105-678A-9
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                                                                                                                                                                                                              RESULT
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                                                                                                                                        Sequence 37, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yokeo
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 31;
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; MOLECULE TYPE:

US-09-105-678A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6103882
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ 1D NO: 37:
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
           APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: B
STATE:
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ZIP: 02109
                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                    STATE:
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6103882
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                                                                                                                                                                                                                                                                                                                      DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No. 1.3e-17;
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Gaps

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US-08-776-971-47
Sequence 47, Application US/08776971B; Patent No. 6228984; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3440
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS FILE REPERENCE: 0734/102001
CURRENT APPLICATION NUMBER: 05/09/172,353
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 31
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09172353
Patent No. 6197530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stricker-Kongra, Alain APPLICANT: Gu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                 TITLE OF INVENTION: POLYPROTEINS, NUMBER OF SEQUENCES: 140
                                                 CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                            APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
COUNTRY: USA
                             ClTY: Boston
                  STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                       Fujii, Ryo
                                                                                                                                                                                       Hosoya, Masaki
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Kawamata, Yuji
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Pred. No. 1.3e-17;
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Pred. No. 1.3e-17;
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                                                                                                                     THEIR PRODUCTION AND USE
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FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-776-971-47
                                                                                                                                                                                                                                                                                                                                                                                      US-08-776-971-61
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Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                 Sequence 61, Application Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONÎLD, DAVÎG G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPOTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTISE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,9718
                                                                                                                 FUKUSUMI, Shoji

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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TELEPHONE: 617-523-3400
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26; Conserv
                                                                                  CITY: Boston
STATE: MA
COMPUTER:
                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                      Application US/08776971B
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                                                                                                                                                                                                                                           Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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IBM compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09421208 Patent No. 6258561
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   PRIOR APPLICATION DATA:
                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                    STATE: MA
COUNTRY: US
ZIP: 02109
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APPLICATION NUMBER:
                                      FILING DATE:
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                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28 DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28 DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15 NAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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                                                                                                                                                                                                                                             Boston
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                                                                                                                                                                                                         USA
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US 09/105,678
                                                       US/09/421,208
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Pred. No. 1.3e-17;
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; MOLECULE TYPE:
US-09-421-208-8
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US-09-421-208-9
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GENERAL INFORMATION:
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: CON110, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3440
                                                                                   INFORMATION FOR SEQ ID NO:
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                                                                                                 REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                  FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coniin, David G.
REGISTRATION NUMBER: 27,0
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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LENGTH: 31 amino acids
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                   STRANDEDNESS:
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ropology:
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                               amino acid
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Moriya, Takeo
Tanaka, Yoko
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Pred. No. 1.3e-17:
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RESULT 11
US-09-421-208-43
; Sequence 43, Application US/09421208
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US-09-42I-208-37
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                                                                                                                                Query Match
Best Local Similarity 83.9
Conservative
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SOCTWARRE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
EILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
EILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
EILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 48466-342
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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Best Local
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Fioppy dlsk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 W
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                    LENGTH:
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26; Conservative
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Tanaka, Yoko
Nishimura, Osamu
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83.9%;
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                                                                                                                                           Score 147; DB 4;
pred. No. 1.3e-17;
0; Mismatches 5
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Pred. No. 1.3e-17;
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US-09-105-678A-38
; Sequence 38, Application US/09105678A
; Patent No. 6103882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09,
ETLING DATE: 25-UN-1998
APPLICATION NUMBER: JP 17:
ETLING DATE: 27-UN-1997
ATTORNEY/AGENT IHFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 31 amlno acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUHICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #I.0, Version #I.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
        COMPUTER READABLE FORM:
                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                             APPLICANT: NIShImura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUEHCES: 52
                                                                                                                                                             APPLICANT: Suemaga, Masa
APPLICANT: Moriya, Takec
APPLICANT: Tanaka, Yoko
APPLICANT: Nlshlmura, Os
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tanaka, Yoko
APPLICANT: Nlshimura, Osamu
                      STATE: MA
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Conlin, David G. REGISTRATION HUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109
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                                                                   CITY:
                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                26;
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Moriya, Takeo
Tanaka, Yoko
                                                                              E: DIKE, BROHSTEIN,
I30 Water Street
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                                    USA
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                                                                                                                                                                                            Takeo
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                                                                                                                                                                                                            Masato
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-1998
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48466-342
                                                                                                  ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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..3e-17;
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RESULT 13
US-09-105-678A-44
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 26
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                     MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                            APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                    APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                              STREET: L. Boston
                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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26; Conserv
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Pred. No. 1.
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..3e-17;
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US-08-776-971-48
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Best Local Similarity
                                                                                                     INFORMATION FOR SEQ ID NO: 48
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LENGTH: 32 amino acids
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
TOPOLOGY:
                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                      REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
                               STRANDEDNESS: single
                                                                                                                                                                                           NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                   TYPE: amino acid
                                                                                                                       TELEFAX: 617-523-6440
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Kawamata, Yuji
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Pred. No. 1.3e-17;
                                                                                                                                                                                              27,026
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COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM; DOS
SOFTWARE: FBatSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 28-DEC-1996
CLASSIFICATION NUMBER: UP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/25419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-ANG-1996
APPLICATION NUMBER: UP 8/21605
FILING DATE: 12-ANG-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 12-ANG-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELEFAX: 617-523-3400
TELEFAX: 617-523-3400
TELEFAX: 617-523-3400
TREFERM: 23 amino acids
STRANDEDNESS: single
TOPOLOGY: 11near

"COPTICE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 62: US-08-776-971-62
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GENERAL INFORMATION:
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Best Local Similarity 83.9
Conservative
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Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
MUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hogoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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83.9%;
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Pred. No. 1.3e-17;
0; Mismatches 5;
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                                Query Match 94.2
Best Local Similarity 83.9
Matches 26; Conservative
94.2%;
                                 0; Mismatches
                                         Score 147; DB 4;
Pred. No. 1.3e-17;
                                                Length 32;
                                 Inde1s
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                                 Gaps
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Search completed: September 13, 2002, 09:10:33 Job time: 138 sec

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Result
No.
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Maximum DB seq
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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# ALIGNMENTS

prolactin-releasing peptide - rat
C:Specles: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001
C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.: Ishizuka, T.: Hosoya,
Blochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene:
A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spieen
A;Accession: JC7607
A;Molecule type: DNA
A;Residues: 1-83 <YAM>
A;Cross-references: DDBD:AB040612; DDBJ:AB040613
C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.

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A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2151
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A;Gene: PrRP
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Similarity 83.9%;
26; Conservative
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A.; Larbly, K.; L
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-790 <DEH>
A;Cross-references: EMBL:AL132959
A;Cross-references: cultivar Coll
C;Genetics:
A;Map position: 3
A;Introns: 39/1; 678/2; 698/3; 773/:
                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F15G16.60 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change C;Accession: T47959 R;De Haan, M; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000 submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Pseudomon A;Reference number: A82950; MUID:20437337 A;Accession: C83292 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-220 <STO> A;Cross references: GB:AE004709; GB:AE004091; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa C;Specias: Pseudomonas aeruginosa C;Specias: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: C83292
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C;Superfamily: plaice glutathione transferase
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50; MUID:20437337
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                                                            hypothetical protein Rv3485c - Mycobacterium tuberculosis (strain H37RV) C/Species: Mycobacterium tuberculosis
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2:
C/Accession: B70569
                                                                                                                             RESULT
B70569
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamiin, N. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeiton, S.; Squares, Nature 393, 537-544, 1998
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C;Accession: S76955
R;Kanako, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asan o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unic
                                                                                                                                                                                                                                                                                                                                                                                                     R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
AC3169
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A; Cross-references: EMBL:D90917; GB:AB001339;
A; Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: $74322;
A; Accession: $76955
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Specles: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Atu5077 [imported] - Agrobacterium tumefaciens (strain C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                A;Gene: Atu5077
A;Genome: plasm:
                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                    A;Cross-references: GB:AE008687; PIDN:AAL45769.1; A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-118 <KUR>
                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: AC3169
                                                                                                                                                                                                                                                                                                                            A;Title: The Genome of the Natural A;Reference number: AB2577; PMID:11
                                                                                                                                                                                                                                                                                                                                                                  A; Authors: Yoo, H.; ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: AC3169
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                                  2 RXHXHSMEXRTPDI----NPAWYXXRGIRPVG 29
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KLHKHNAARRRPDIGARVQPATAPHRGLAGIG
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33.38;
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PMID:11743193
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                                                                     Score 46; DB Pred. No. 5; 4; Mismatches
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Pred. No.
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ada, T.; Watanabe, A.;
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I., Levy, R., Li,
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ida, M.; Ya
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17-Jul-1998 #text\_change 20-Jun-2000

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R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; i Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, 1 as-Neto, E.; Docena, C.; Ei-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitojima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi chado, M.A.; Madeira, A.M.B.N.: Madeira, H.M.F.; Marino, C.L.; Marques, N.V.; Martins, E.M.F.; Watsukuma, A.Y.; Wenck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Paimieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; de Silvei, A.Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Accession: H82852
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Ni Nature 406, 151-157, 2000
A;Title: The genome seguence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
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C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
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A;Residues: 1-333 <SIN>
A;Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1;
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C;Superfamily: ribitol dehydrogenase; short-chain alcohoi dehydrogenase
F;46-227/Domain: short-chain alcohol dehydrogenase homology <SADH>
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hypothetical protein F32B6.3 - Ca
C; Species: Caenorhabditis elegans
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A;Experimental source: strain H37Rv
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A; Residues: 1-314 <COL>
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8; Conservative
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7; Conserv
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Pred. No. 15;
2; Mismatches
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                                                 C; Superfamily: Rhodobacter capsulatus
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R;Jeffers, M.; Paclucci, R.; Pellicer, A.
Nucleic Acids Res. 18, 4891-4899, 1990
A;Title: Characterization of unr; a gene closely linked
A;Reference number: S11210; MUID:90370473
A;Accession: S11210
A; Residues: i 1236 <NAG>
A; Cross-references: EMBL: AB034704;
A; Experimental source: strain IL144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable unr protein - rat
C:Specles: Rattus norvegicus (Norway rat)
C:Date: 21-Nov-1993 #sequence_revision i0-Nov-1995 #text_change 05-Nov-1999
C:Accession: S11210
                                                   A;Status: preliminary; translated A;Molecuie type: DNA
                                                                                     A; Reference number: 225270
A; Accession: T50904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-798 <GEP>
A; Cross-references: EMBL: X52311;
C; Keywords: DNA binding
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A; Introns: 56/3; 105/1; 146/3; 185/1;
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                                                                                                                       submitted to the EMBL Data Li
A; Description: Determination
                                                                                                                                                          R;Nagashima,
                                                                                                                                                                         C; Accession: T50904
                                                                                                                                                                                         C;Date: 21-Jul-2000 #sequence_revision
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C;Species: Rubrivivax gelatinosus
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A; Residues: 1-348 <WIL>
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MBL Data Library, November 1999
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Pred. No.
                   PIDN: BAA94057.1
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magnesium-protoporphyrin Q-methyitransferase

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C:Accession: B75318

R:White, O.; Eisen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-157, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A:Reference number: A75250; MUID:20036896
A:Accession: B75318
RESULT
T48336
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R;Atlong, J.; Inoue, K.; Bauer, C.E.
Proc. Natl. Acad. Scl. U.S.A. 95, 14851-14856, 1998
A;Title: Tracking molecular evolution of photosynthesis by characterization of a large ference number: Z21036; MUID:99061957
A;Accession: T31462
A;Accession: T31462
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1992 (XID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ferripyochelln-binding protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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C;Species: Heliobacillus mobilis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
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A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-240 <WHI>
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity 34.6
Matches 9; Conservative
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T.; Zalewski,
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2002,

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A;Molecule type: DNA A;Residues: 1-637 <STO> A;Cross-references: GB:AE005673; NID:gl3424056; PIDN:AAK24472.1; GSPDB:GN00148 C;Genetics: A;Gene: CC2501
                                                                                                                                                                                                                                                              R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko , J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87559
                                                                                                                                                                                                                                                                                                                                                                                       sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus C;Specias: Caulobacter crescentus C;Decias: Caulobacter crescentus C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: D87559
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A; Introns: 63/1; 194/2;
A; Note: F15A17.180
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A;Residues: 1-501 <BEV>
A;Cross-references: EMBL:AL163002
A;Experimental source: cultivar Columbia; BAC clone F15A17
C;Genetics:
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A; Accession: T48336
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09ilw4 paeudomonas
087474 burkholder1
09m371 arabidopala
006348 mycobacter1
094ku9 brassica ca
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09a5e9 caulobacter
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01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
C-RF AMIDE.
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Q1-QCT-2001
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Bukaryota: Metazoa; Chordata: Craniata: Vertebrata; Buteleoatomi;

Actinopterygii: Neopterygii; Teleoatei; Buteleoatei; Ostariophysi;

Cyprintiormes: Cyprinidae: Carassius.

NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                      Satake H., Minakata H., Fujimoto M.:
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; EAA76662.1;
SEQUENCE 117 AA; 12879 MW: D5DC4CB22038C2B0 CRC64;
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Database

Max1mum Minimum

DB DB

Scoring table:

O97800 thermoplasm
O97642 stigmatella
O98d86 arabidopsis
O91022 pseudomonas
O80002 bordetella
O45375 bordetella
O45374 orocobacteri
O96183 drosophila
O9vp62 drosophila
O9vrv3 drosophila
O9vrv3 drosophila
O9vrv4 drosophila
O9vrv4 vibrio choi
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O9tz3 drosophila
O9tz3 drosophila
O9tz47 vibrio choi
O9tz53 drosophila
O95z56 telshmania
O9p441 xylella fas
O9a522 caulobacter
O50128 pyrococcus
O9ph76 xylella fas
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RC STRAIN-ATCC 15692 / PAOL;

RX MEDLINE-20437337; Pubmed-10984043;

RX MEDLINE-20437337; Pubmed-10984043;

RX Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warrener P.,

RA Stover C.K., Pham X.-Q.T., Evin A.L., Mizoguchi S.D., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lim R.M.,

RA Smith K.A., Spencer O.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Smith K.A., Spencer O.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAOl, an

opportunistic pathogen.",

RT opportunistic pathogen.",

RT opportunistic pathogen.",

RM Hickey M.J., Bacodé A., Schinla, act_bind.

DR Hickey M.J., Bacodé A., Schinla, act_bind.

DR Hickey M.J., Bacodé A., Schinla, act_bind.

DR Pfam: PF00128; alpha-amylase: 1.

DR Pfam: PF00128; alpha-amylase: 1.

DR Pfam: PF00128; alpha-amylase: 1.

DR Pfon: Pf00128; alpha-amylase: 1.

SO SEOUENCE 664 AA; 76329 MW; BF59FEED54C308AD CRC64;
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087474;
01-NOV-1998 (TrEMBLTel. (
01-NOV-1998 (TrEMBLTel. (
01-DEC-2001 (TrEMBLTel. )
                                                                                                                                                                                              Halgier B.E., Johnson G.R., Suen W.C., Blochenical and genetic evidence for multiplydroxytoluene in Burkholderia sp. (J. Bacteriol. 181:965-972(1999).
EMBL, AF076848, AAD12738.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suen W.C., Spain J.C.;
Cioning and characterization of Pseudomonas
2,4-dinitrotoluene degradation ";
J. Bacteriol. 175:1831-1837(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterla; Proteobacteria;
Burkholderla.
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Bacteria; P
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            SEQUENCE
                                                                                                                                                              InterPro;
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Pro; IPR000486; Extradiol_dioxygnse.
Pro; IPR004360; Gly_bleo_diox.
PP00903; Glyoxalase; 2.
m; PD000977; Extradiol_dioxygnse; 1.
m; PD000977; Extradiol_dioxygnse; 1.
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Pred. NO. 5;
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O9M371;
O1-OCT-2000
O1-OCT-2000
O1-DEC-2001
MEDIINE-98295987; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harrigordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekäla F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamiin N., Hoiroy. Hornsby T., Jageis K., Krogh A., McLean J., Houle S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barreil B.G.;

"Deciphering the biology of Mycobacterlum tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             006348
                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
Bacteria: Firmicutes: Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997 (TIEMBLICE1. 04, Created)
01-JUL-1997 (TIEMBLICE1. 04, Last sequence update)
01-DEC-2001 (TIEMBLICE1. 19, Last annotation update)
HYPOTHETICAL 33.2 XDA PROTEIN.
RV3485C OR MTCY13E12.38C.
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Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta: Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project; submitted (JAN-2000) to the EMBL/GenBank/DDBJ EMBL; AL132959; CAB71097.1; -.
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SEQUENCE 79
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16; Conservative
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10; Conservative
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E., Salanoubat M.
) the EMBL/GenBan
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Pred. No. 14;
3; M1smatches
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Bost Local S
Matches 11
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Best Local :
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PubMed-11351096;

MEDLINE-21249173; PubMed-11351096;

MEDLINE-21249173; PubMed-11351096;

MIN H.U., Wu S.S., Ratnayake C., Huang A.H.;

Kim H.U., Wu S.S., Ratnayake C., Huang A.H.;

Flarssica rapa Has Three Genes That Encode Proteins Associated Different Neutral Liplds in Plastids of Specific Tissues.";

Plant Physiol. 126:330-341(2001).

PHADL, AF290563; AAK57561.1; -.

EMBL, AF290563; AAK57561.1; -.

EMBL, AF290563; AAK57561.1; -.
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Q94KU9;
Q04KU9;
Q01-DEC-2001 (TrembLrel. 19, Created)
Q1-DEC-2001 (TrembLrel. 19, Last sequence update)
Q1-DEC-2001 (TrembLrel. 19, Last annotation update)
Q1-DEC-2001 (TrembLrel. 19, Last annotation update)
PLASTID-LIPID ASSOCIATED PROTEIN PAPI.
Brassica campestris (Field mustard).
Brassica campestris (Field mustard).
Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                             Q94F29 PRELIMINARY; PRT; 327 AA.
Q94F29;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLASTID-LIPID ASSOCIATED PROTEIN PAP1.
Brassica campestris (Field mustard).
Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots; Rosid,
eurosids II; Brassicales; Brassicaceae; Brassica.
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HSSP; P29132; 1DFI.
TUBETCULISH; RV3485c; -.
InterPro; IFR002188; ADH_short.
Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
COmplete protecome; Hypothetical protein; Oxidoreductase.
SEQUENCE 314 AA; 33194 MM; 26144BA917E09274 CRC64;
  SEQUENCE FROM N.A. MEDLINE-21249173; Klm H.U., Wu S.S.,
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Nature 393:537-544(1998).
-I- SIMILARITY: BELONGS TO
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  PubMed=11351096;
, Ratnayake C., H
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     A.H.;
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7.7;
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Ra Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Eiy B.,

Ra DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Ra Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Ra Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Ra Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Ra Liberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

"Complete genome sequence of Caulobacter cresce
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Best Local s
Matches 7
                                                                                                                    InterPro; IPR000700; PAS-assoc.
InterPro; IPR001799; Response_;
Pfam; PF002518; HATPase_c; 1.
Pfam; PF00795; PAC; 1.
Pfam; PF00795; PAC; 1.
Pfam; PF00512; signal: 1
Pfam; PF00512; signal: 1
Pfam; PF00512; signal: 1
SMART; SM00387; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00096; PAC; 1.
SMART; SM00096; PAC; 1.
SMART; SM00091; PAS; 1.
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Q9ASE9;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
SENSORY BOX HISTIDINE KIN
CC2501.
Caulobacter crescentus;
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InterPro; IPR003594; I
InterPro; IPR003661; I
InterPro; IPR004359; I
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EMBL; AF29056; AAK57564.1; -.

SEQUENCE 327 AA; 35644 MW; 6116E7F1B6C02C88 CRC64;
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InterPro;
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                                                               Complete
                                                                                                    SMART;
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7; Conser
                                                               proteome;
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IPR000014;
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                                                                                                PAS:
                                                               Kinase;
   68511 MW;
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His_kinA.
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                                                            Phosphorylation;
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Last annotation update)
E/RESPONSE REGULATOR.
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Pred. No. 7.7;
3; M1smatches
   OEDEEAF76FFA8611
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                                                               Sensory transduction;
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   CRC 64
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Query Match Best Local Similarity

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Score Pred.

53;

DВ 16;

16;

Length 637;

Matches

12;

Conservative

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9

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Streptomycineae; Streptomycetaceae; Streptomyces.

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A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Glibert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Olu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
A Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
Complete genome sequence of Methanobacterium thermoautotrophicum
T Complete genome sequence of Methanobacterium thermoautotrophicum
T deltaH: functional analysis and comparative genomics.";
AL J. Bacteriol. 179:7135-7155(1997).
R EMBL; ASD00805; AAB44680.1: ".
J. Bacterio: IPR000515; BPD_transp.
InterPro: IPR000515; BPD_transp.
InterPro: IPR000515; BPD_transp.
InterPro: IPR000515; BPD_transp.
InterPro: IPR0001610; PAC.
R InterPro: IPR000014; PAS.
InterPro: IPR000014; PAS.
R InterPro: IPR000014; PAS.
R InterPro: IPR000015; PAS-assoc_C.
R Ffam; PF00785; PAC; 1.
R Ffam; PF00999; PAS; 3.
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Best Local S
Matches 13
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Pfam; PF00512; 819nal; 1.
SMART; SM00387; HATPase_c; 1
SMART; SM00086; PAC; 1.
SMART; SM00081; PAS; 3.
                                                                             Q93L27;
01-DEC-2001 ()
01-DEC-2001 ()
01-DEC-2001 ()
CHAIN LENGTH ()
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01-JAN-1998 (TREMBLIRE)
01-DEC-2001 (TREMBLIRE)
SENSORY TRANSDUCTION I
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     Streptomyces aureofaciens
Bacteria; Flrmicutes; Act:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98037514; PubMed=9371463;
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13; Conservative
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785 AA;
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                                                                             (TrEMBLrel. 1:
(TrEMBLrel. 1:
(TrEMBLrel. 1:
H FACTOR-LIKE
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(TremBlrel. 05, Last sequence update)
(TremBlrel. 19, Last annotation update)
NSDUCTION HISTIDINE KINASE.
                                                                                                                                                                                                               PRELIMINARY;
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     Actinobacteria;
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19, Last annotation
PROTEIN.
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     Actinobacteridae;
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Matches 8
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Best Local S
Matches 11
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01-MAY-2000
01-MAY-2000
01-MAY-2000
01-MAY-300 (S
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
MEDLINE-2108560; PubMed-11217851;
Kawal J., Shinagawa A., Shibata K., Yoshino M.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Add
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kono
                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ data EMBL; AY033994; AAK61719.1; ".

SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1999)
EMBL; AL035608; CAB5:
NON_TER 54
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
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NCBI_TaxID=1894;
[1]
                                                                                                                        NCBI_TaxID=10090,
[1]
                                                                                                                                                          Eukaryota; Metazoa;
Mammalla; Eutheria;
                                                                                                                                                                                                Mus musculus (Mouse).
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000 (TrembLrel.
000 (TrembLrel.
3 (SUSHI-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AA; 6110 MW;
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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CAB55682.1;
                                                                                                                                                          Chordata;
Rodentla;
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Sciurognathi;
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Catarrhini; Hominidae;
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   Kondo S., Yaw
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   M., Ishii
... Fukuda
Yamanaka
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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Peacle G., Ouackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Peacle G., Ouackenbush J.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aonon H., Baldareili R., Barsh G.,

RA Blake J., Boffelii D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelii D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.N.,

RA Lyona P., Marchionni L., Mashima J., Mazzareili J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki N., Toyo-oka K., Wang K.N., Weltz C., Whittaker C., Wilming L.,

RA Navashirari V., Sohida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Navashirari V.,
                                                                                                                                                                             RA Kawai J. Shihadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Ahizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Kadota K., Matauda H.A., Ashburner M., Bataiov S., Casavant T.,

RA Kadota K., Matauda H.A., Ashburner M., Bataiov S., Casavant T.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Hake J., Boffelii D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Hake J., Boffelii D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Hake J., Batto K., Kandann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelii J., Wombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q9DAE5;
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01-JUN-2001
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Nature 409:685-690(2001).
EMBL; AKO08242; BAB25553.1; -.
MGD; MGI:1914185; 1700023802Rik.
SEQUENCE 277 AA; 31797 MW; 4
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Mammaiia; Eutheria;
                                                                                                                                                     Hayashizaki Y.;
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Metazoa, Chordata, C
Metazoa, Rodentia, C
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   1700023B02R1k.
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068003C5E894827B CRC64;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Airakawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi R., Staubii F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sachimi L.M., Staubii F., Suzuki R., Tonita M., Garariboidi M.,
RA Blake J., Boffeili D., Bojunga N., Carninci P., de Bonaido M.F.,
RA Blake J., Bult C., Pietcher C., Fujita M., Gariboid M.F.,
RA Blake J., Bult C., Fietcher C., Fujita M., Gariboid M.F.,
RA Gustincich S., Nili D., Hofmann M., Hume D.A., Kaniya M., Jee N.H.,
RA Lyons P., Marchionni L., Mashims J., Mazzarelii J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashtzaki Y., Storch K., Functor K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MGD; MGI:1914185; 1700023B02R1k.
InterPro; IPR000345; CYTC_heme_bind.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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EMBL; AK006260; BAB24488.1; -.
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1700023802R1K PROTEIN.
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                                Homo sapiens
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ns (Human).
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Eukaryota;

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OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_TaxID=9506;
RN [1]
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RA KUCSAWA H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
RA KUCSSAWA H., Inukai T., Look T.A.;
RA KUCSSAWA H., Naeve C.W., Look T.A.;
RA KUCSSAWA H., Naeve C.W., Look T.A.;
DR EMBL, AR060567; AAC15765.1; -
DR InterPro: IPR001128; Cyt.P450.
DR InterPro: IPR001240; HYR; 1.
DR Pfam; PP00404; HYR; 1.
DR Pfam; PP00004; Sushi SCR_CCP.
DR Pfam; PP00004; Sushi S.
DR SMART; SM00032; CCP; 3.
DR PROSITE; PS00006; CYTOCHROME_P450; UNKNOWN_1.
SQ SEQUENCE 465 AA; 52971 MW; 4D752B187FF3EFFB CRC64;
Query Motch
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
PROSITE: Hill | |
DB TPAVTPTWYAGSGYYP 33

Search completed: September 13, 2002, 09:29:16

Search completed: September 13, 2002, 09:29:16
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

DM protein - protein search, using sw model
Run on: September 13, 2002, 09:11:50; Search time 80.21 Seconds (without alignments)
14.965 William cell updates/sec
Title: US-09-446-543A-61
Perfect score: 171
Sequence: 171
Sequence: 17 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 105224 seqs, 38719550 reaiduea
Total number of hits satiafying chosen parameters: 105224
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Pred. No. 1a the number of resulta predicted by chance to have a acore greater than or equal to the score of the reault being printed, and is derived by analysis of the total score distribution.

Poat-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minlmum DB aeq length: 0
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SwissProt\_40:\*

## SUMMARIES

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019910	P30761	09 <b>pej7</b>	P31414	P04023	Q9zd28	P11227	P03356	Q9epk7	D9u1a9	P03357	P32770
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entities requires a license agreement (S or send an email to license@isb-sib.ch).  EMBL; AB015419; BAA29027.1;  EMBL; AB015419; BAA29027.1;  MIN; 602663;  HOrmone; Amidation; Signal.  SIGNAL 1 22  PEPTIDE 23 53 PROLACTIN-R  PEPTIDE 23 53 PROLACTIN-R  PEPTIDE 34 53 PROLACTIN-R  MDD_RES 53 53 AMIDATION ( SEDUENCE 87 AA; 9639 MW; 229A2F3F50C	nd an	RDM N.A. in; 268781; Habata Masuo ) ., Niahi in-relea; :272-270 CIFICITY 98338; FUKUSUM M., Kitz Fujino	STANI (Rel. 3 (Rel. 4 (Rel. 4 eleaalng ontaina: eptide p
BAA29027.1;	B3:1-10(1999).  Stimulates prolactin (PR no f prolactin through it pla directly to secrete pla pECIFICITY: MEDGILLA OBLONG  PROT entry 18 copyright. It Swiss Institute of Bioinf Bioinformatics Institute. Profit Institutions as I this statement is not rew	PubMed-9607765; Y., Fujli R., Kawamata Y., Aaano T., Matsumoto imura O., Onda R., Fujli asing peptide in the br. 6(1998). Y.	eated) int sec int sec int ar ide pi ide pi ide; ide; ide; ide; ide; ide; ide; ide
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90 - 1 - 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	(PRL) release and hits receptor GPR.  E PRL.  LONGATA AND HYPOTHS  IT is produced to contact and its contact are no ute. There are no ute. Usace utes.	amata Y., Hosoya umoto H., Sekigu Fujino M.; he brain."; he brain.";	87 AA. date) update) (PrRP) (Prolactin g peptide PrRP31; g peptide PrRP31; g peptide PrRP31;
http://www.lab-sib.ch/announce/ http://www.lab-sib.ch/announce/ ASING PEPTIDE PRRP31. ASING PEPTIDE PRRP20. 4 PROVIDE AMIDE GRDUP). 1B CRC64;	prolactin (PRL) release and regulates the tin through its receptor GPRIO. May stimulate to secrete PRL.  MEDULA OBLONGATA AND HYPOTHALAMUS.  MEDULA OBLONGATA AND HYPOTHALAMUS.  COPYPIGHT. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation its Institute. There are no restrictions on its titutions as long as its content is in on way entis not removed.	M., Fuchi M., chi M., chi M., fuchi M., chi M.	tin- 31; Bute
w.iab-sib.ch/announce/ww.iab-sib.ch/announce/	d regulates the RIO. May stimulate	Fukusumi S I., Hiouma S., H., P) and ita	tin-releasing 31; Protactin- Buteleostomi;
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PRRP_RAT STAHUARW;
PR1278;
90:178;
30-MAY-2000 (Rel. 39, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
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Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Hishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
"I FUNCTION: Stimulates prolactin (PRL) release and regula
expression of prolactin through its receptor GPRIO. May
lactotophs directly to secrete PRL.
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Pr
hormone) [Contains: Prolactin-releasing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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Mammalla; Eutheria; Ce
Bovidae; Bovinae; Bos.
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22
53 PROLACTIN-RE
53 PROLACTIN-RE
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                                                                                                                                                                                                                                                                                                                                                          92.48:
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0%;
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                                                                                                                                                                                                                                                                                                                                 Score 150; DB Pred. No. 9.6e 1; Mismatches
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Pred. No. 9.8e-19;
); Mismatches 0;
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.6e-17;
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                (Prolactin-releasing
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GPRIO. May St
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RESULT 4

NER3_H

ID NER3_H

AC 090049

AC 09-049

DT 01-MAR

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DT 01-MAR

DE (N-BCC

GH NEU3.

OS ENLARY

OC ENLARY

OC MAMMel

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RH [1]

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Matches 26
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PEPTIDE
MOD_RES
SEQUENCE
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SIGNAL
                                                                                   NER3_HUMAN STANDARD; PRT; 428 AA Q9UQ49; Q9HQE1; 01-MAR-2002 (Rei. 41, Created) 01-MAR-2002 (Rei. 41, Last sequence update) 01-MAR-2002 (Rei. 41, Last annotation update Sialidase 3 (EC 3.2.1.18) (Membrane sialida (N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eithe European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE-98268781; PubMed-9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Ho
Kitada C., Masuo Y., Asano T., Matsumoto H., So
Kitada C., Masuo Y., Asano T., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sumino Y., Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed-10498338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM H.A.
TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormone) [Contains: Prolactin-releasing releasing peptide PrRP20].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Tissue distribution of prolactin-releasing
                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                  ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression of prolactin through its receptor lactotrophs directly to secrete PRL. TISSUE SPECIFICITY: Widely expressed, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         medulia oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Stimulates
                                                                                                                                                                                                                        AB015418; BAA29026.1;
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                                                                                                                                                                                                                                                                                   Similarity
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232
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21
52
52
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52
9215 NW;
                                  Chordata;
Primates;
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83.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prolactin (PRL) release
                                                                                                                                                                                                                                                                                                                                                                                               Cleavage on
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                                                                                                                                                                                                                                                                                   Score 149;
Pred. Ho. 1
                                                                                                                                                                                                                                                                                                                                    PROLACTIN-RELEASIHG PEPTIDE PRRP31.
PHOLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-53 PROVIDE AMIDE GROUP
DOC75A264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                          Mismatches
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T., Nishimura
                                                                                                on update)
sialidase)
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                                                                                                                                                                                                                                                                                    DB 1;
.8e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide (PrRP) and
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Sekiguchi M
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; Murinae; Rat
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MBL outstation -
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                                                                                                 sialidase)
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RESULT 5
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ID Y587_PASMU
AC Q9CN56;
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Best Local (
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ACT_SITE
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MEDLINE-99335353; PubMed-10405317;
Wada T., Yoshikawa Y., Tokuyama S., Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as ions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to iicense@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Montl E., Bassi M.T., Papini N., Riboni M., Manzoni M., Croci G., Preti A., Balabio A., Tettamanti G., Borsani "Identification and expression of NEU3, a novel human slassociated to the plasma membrane.";

Blocham. J. 349:343-351(2000).
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"Cioning, expression, and
sialidase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
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                                                                                                                       195
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SUBCELLULAR LOCATION: Membrane-associated.

TISSUE SPECIFICITY: Highly expressed in skeletal muscle, adrenal gland and thymns, followed by pancreas, liver, he thymns. Weakly expressed in kidney, placenta, brain and length with the statement of the stateme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoconjugates.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal simile residues in alpha-(2->8)-glycosidic linkages of terminal simile residues in oligosaccharides, glycoproteins, glycollpids, colominic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Plays a role in modulating the ganglioside co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; AB008185; BAA82611.1;
; Y18563; CAB96131.1; AI
604617; -...
                                                                                                           KTRPHSLM1YSODLGVTWHHGRL1RPM
                                                                                                                                                     RTHRHSMEIRTPDINPAWYASRGIRPV
                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                                                              STANDARD;
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BNR
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BY SIMILARITY.
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BY SIMILARITY.
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Pred. No. 1
                    PRT;
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al mapping of a human 98
                    288
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| slalidase
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ganglloside
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RESULT

Y468_MYCPN

ID Y468_MYCPN

AC P75109; Q50317;

AC P75109 (P61. 35, Carrow)

O1-NOV-1997 (Rel. 35, Larrow)

"G-OCT-2001 (Rel. 40, Larrow)

"T158. "P158. "P1
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Best Local
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[1]
SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
MEDLINE-1-Aich R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (
16-OCT-2001 (
16-OCT-2001 (
Hypothetical
PM0587.
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                                                                                                                                                                                                                                           "Complete sequence pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pneumonlae.
Bacterla; Firmicutes;
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Hypothetical protein; Transferase; Kinsse; Complete proteome.
SEQUENCE 288 AA; 33778 MW; F4D2F6C26014D940 CRC64;
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-I- SIMILARITY: BELONGS TO THE FRECTOSAMINE KINASE FAMILY.
                                                                                                                                                                                                                           Nucleic Aclds
                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasmataceae; Mycoplasma
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nome of the bacterium
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Eukaryota; Metazoa; Cho
Mammalla; Eutherla; Cet
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
             This SWI
between
the Euro
                                                                                                                                                                          *Molecular cloning and characterization associated simildase specific for game J. Biol. Chem. 274:5004-5011(1999).

-i- FUNCTION: Plays a role in modulation the lipid bilayer at the level of
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O1-MAR-2002 (Rel. 4I, Last sequence up
O1-MAR-2002 (Rel. 41, Last annotation
Sialidase 3 (EC 3.2.I.18) (Membrane si
(N-acctyl-alpha-neuraminidase 3).
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EMBL: U34816; AAC43650.1; --
Hypothetical protein; Transu
TRANSMEM 16 36
                                                                                                                                                                                                                                                                     TISSUE-Brain;
MEDLINE-99143165;
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                                                                                                                                                                                                                                                Sawada M
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
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                                                         glycoconjugates.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
alpha-(2-8)-glycosidic linkages of terminal stalle residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid an
synthetic substrates.
SUBCELLULAR LOCATION: Membrane-associated (By similarity).
TISSUE SPECIFICITY: Expressed in brain.
SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
SIMILARITY: CONTAINS 3 BNR REPEATS.
            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Bioinformatics institute. There are no resti
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Cetartiodactyla; Ru
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gangliosides.*;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
N-acetyI-gamma-glutamyI-phosphate reductase (EC 1.2.I.38) (AGPR) (N-acetyI-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
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EMBL; AP001517; BAB06619.1; InterPro; 1PR000706; AGPR_a InterPro; IPR000534; Semial
                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch)
                                                                                                                                                                                                                                          "Complete genome sequence of the alkaliphilic bacterium 8a halodurans and genomic sequence comparison with Bacilius suncleic Acids Res. 28:4317-4331(2000).

-i- CATALYTIC ACTIVITY: N-acetyl-1-glutamate 5-gemialdehyd.
-phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
-i- PATHAR: THLME STEP IN ARGIAINE BIOSYNTHESIS.
-i- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
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Takami H., Nakasone K., Takaki Y.,
Fuji F., Hirama C., Nakamura Y., O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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REPEAT
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REPEAT
                                                                                                                                                         between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus/Staphylococcus
NCBI_TaxID=86665;
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                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through 
men the Swiss Institute of Bioinformatics and the EM
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POTENTIAL.
POTENTIAL.
BY SIMILARITY.
POTENTIAL.
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Pred. No. 5.9;
6; Mismatches
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                       ., Maeno G.,
Ogasawara N
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There are no restrictions
ong as its content is in
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RESULT 9
SOLITION CONTRACTOR CO
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Best Local
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                                                                                                                                           rlyBase; FBgn0000336; cnc.
InterPro; IPR001871; bZIP.
Pfam; PP00170; bZIP; I.
SMART; SN00336; BRLZ; I.
PROSITE; PS00036; BZIP_BASIC; 1
Transcription regulation; Activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila |
Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD003765; AGPR_act_site; I.

PROSITE; PS01224; ARGC; 1.

ARGC: 1.

Arginine blosynthesis; Oxidoreductase; NADP; Complete proteome ACT_SITE 149 DY SIMILARITY.

SEQUENCE 345 AA; 38188 MW; 3E9F45DD09FC68EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNC_DROME STA
P20482;
01-FEB-I991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                    EMBL; M37495; AAB59246.1;
PIR; A33111; A33111.
HSSP; P34707; ISKN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92001535; PubMed=1911393;
Mohler J., Vanl K., Leung S., Epsteln A.;

"Segmentally restricted, cephalic expression of a leucine zipper gene during Drosophila embryogenesis.";

Mech. Dev. 34:3-9(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Segmentation CNC.
                                                                                                                                                                                                                                                                                                                                                                                                                    or send an emall to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
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NCBI_TaxID=7227;
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16-OCT-2001
                                                                                                                                                                                                                                                                                           TRANSFAC; T01998;
                                                                                                                           Developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PLAYS A ROLE IN CEPHALIC PATTERNING. OF A HETERODIMERIC REGULATORY PROTEIN INVOLVED HEAD MORPHOCENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE BZIP FAMILY. CNC SUBFAMILY.
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PF02774;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Drachycera; Musca; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 17, Created)
(Rel. 33, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Semialdhyde_dhC; 1.
ξ
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45.5%;
  56948
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Activator; DNA-binding;
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Pred. No. 11;
2; Mismatches
                    BASIC MOTIF.
LEUCINE-ZIPPER.
GLN-RICH.
I -> L (IN REF.
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-> L (IN REF. 1; EADFF9A5D6CA5C5F
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AAB59246).
CRC64;
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Best Local S
Matches 9
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InterPro: IPR003753; Exonuc_VII_L.
InterPro: IPR002309; tRNA-synt_2.
Pfam; PF023601; Exonuc_VII_L; I.
Pfam; PF01336; tRNA_ant1; I.
Pfam; PF01336; tRNA_ant4; I.
SEQUENCE 402 AA; 43882 MW; 14592
                                                         EXL1_HUMAN Q92935;
                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outsuche EUropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as iong as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INT ACID-INSOLUBLE OLIGONDCLEOTIDES, WHICH ARE THEN DEGRADED FOR INTO SMALL ACID-SOLUBLE OLIGONDCLEOTIDES (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'-or 3'- to 5'-direction to yield 5'-phosphomononucleotides.
-1- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNI
                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                  or send an email to Ilcense@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seeger K.J., Har
Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuciease VII large sub
(Exonuclease VII large subunit).
XSEA OR SCK7.29c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9FBM3:
ī5-JUL-1998 (ReI. 36, Created)
15-JUL-1998 (ReI. 36, Last sequence update)
16-JCT-2001 (ReI. 40, Last annotation update)
Exostosin-like l (Exostosin-L) (Multiple exos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION:
-1- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
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                                                                                                                                                                     I7 PAWYASRG----IRPVG
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                                                                                                                                                                                                 Conservative
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                                                                       STANDARD;
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43882 MW; 145929A8372B4E08
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37.5%;
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47.6%;
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TO THE XSEA FAMILY.
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                                                                                                                                          109
                                                                                                                                                                     29
                                                                                                                                                                                               Score 47; DB
Pred. No. 15;
1; Mismatches
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Pred. No. 1
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  exostosis-like
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MBL outstation .
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MEDILINE-97189339; PubMed-9037597;

WISE C.A., Clines G.A., Massa H., Trask

"Identification and localization of the
of the multiple exostoses gene family.";

Genome Res. 7:10-16(1997).
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XU L., Deng H.X., Xia J.H.,
Mutations of the EXT genes
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Non-structural polyprotein (Contains: (EC 2.7.7.48); Helicase]
Hepatitis E virus (strain
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15-DEC-1998
15-DEC-1998
16-OCT-2001
                                                                                                        POLN_HEYBU STANDARD;
P29372;
01-DEC-1992 (Rei. 24, Creat
01-DEC-1992 (Rei. 24, Last
16-OCT-2001 (Rei. 40, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 388:539-547(1997).

1- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID [LPA] INTO PHOSPHAT ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION.

1- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate.

1- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate.

1- CATALYTIC ACTIVITY: BELOAUS STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS.

1- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).

1- SIMILARITY: BELOAUS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
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MEDLINB=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.&

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.&

Melson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

MCKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

MCKenney K., FitzGerald J.M., Lee N., Adams M.D., Hickey E.K.,

MCKenney K., FitzGerald J.M., Fujil C., Bowman C., Watthey L., Wallin

Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inner membrane; SEQUENCE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a coliaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as insured its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
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TIGR; HP1348; -.
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acyltransferase) (1-AGPAT) (Lysophosphatidic acid a
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Pfam; PF01553; Acyltransferase; 1.
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1-acy1-sn-glycerol 3-phosphate -
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No. 10
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Best Loc
Matches
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Fry
                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-93227573; PubMed-8470371;
Aye T.T., Uchida T., Ma M.Z., Ilda
Riklhisa T., Winn K.;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                           VITUS GENES 7:95-109(1993).
-I- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00506; Alpp; 1. Polyprotein; Transferase; ATP-binding.
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InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000606; Vlrai_heiicasel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length viral genome.";
Virology 185:120-131(1991).
-i- MISCELLANEOUS: HEPATITIS E VIRUS IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses, ssRNA positive-strand viruses, no NCBI_TaxID-31767;
                                                                                                                                                          "Sequence and gene
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Fry K.E., Reyes G.R.;
*Hepatitis E virus (HEY): molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92024067;
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PF00978; RNA_dep_RNApo12;
PF01443; Vlral_helicase1;
PF01660; Vmethyltransf; 1.
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37.08;
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InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR002588; V_ral_hellcasel.
Pfam; PF01561; Alpp; 1.
Pfam; PF00561; Alpp; 1.
Pfam; PF01443; V_tral_hellcasel; 1.
Pfam; PF01443; V_tral_hellcasel; 1.
SMART; SM00506; Alpp; 1.
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15-JUL-1999 ()
16-OCT-2001 ()
Hypothetical |
                  SEQUENCE OF 879-985 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.N., Hu P.-C., Bott K.F.,
                                                                                              Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Keiley J.M. Fritchman J.L., Weldman J.F., Small K.V., Sandusky M., Fuhrmann J. Nguyen D.T., Utterback T.R., Saudek D.M., Phililps C.A., Merrick J. Tomb J.-F., Dougherty B.A., Bott K.F., Hu R.-C., Lucler T.S., Peterson S.N., Smith H.O., Hutchlson C.A. III, Venter J.C.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed-7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fraser C.M., Gocayne J.D., White O., Sutton G., Kelley J.

Fritchman J.L., Weldman J.F., Small K.V., Sandusky M., Fuhrmann I.

Pritchman J.L., Weldman J.F., Small K.V., Sandusky M., Fuhrmann I.

Myuyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick

Myuyen D.T., Dougherty B.A., Bott K.F., Hu P.C., Lucler T.S.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.C., Lucler T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.",

Science 270:397-403(1995).
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SEQUENCE
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Mycoplasmataceae; Mycoplasma
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         Peterson S.N., Hu P.-C., Bott K.F., Hui
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Search completed: September 13, 2002, 09:30:42 Job time: 1132 sec
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TRANSMEM 16 36 POTENTIAL.

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T TRANSMEM 1010 1030 POTENTIAL.

T TRANSMEM 1064 1104 POTENTIAL.

T TRANSMEM 1060 1680 POTENTIAL.

T TRANSMEM 1709 1729 POTENTIAL.

T TRANSMEM 1709 1729 POTENTIAL.

T TRANSMEM 1752 1772

SEQUENCE 1783 AA; 200168 MW; 87BD575AEC2E374B CRC64;
                                                                                                                                                   Query Match 27.2%;
Best Local Similarity 29.0%;
Matches 9; Conservative
                                                                        1118 NRNENYKLNIQTPTEQSGWYA---IQPYSHF 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a coliaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U39728; AAC72488.1; -. EMBL; U01808; AAD12339.1; -. TIGR; MG468; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 175:7918-7930(1993).
-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-I- SIMILARITY: SOME, TO MG064.
                                                                                                                 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                            35

917

937

947

1010

1030

1084

1104

560

1680

1680

1789

1779

1750

1770

POT.

VA; 200168 MW;
                                                                                                                                                   6; Mismatches
                                                                                                                                                                 Score 46.5;
Pred. No. 92;
                                                                                                                                                                                   DB 1;
                                                                                                                                                   L
                                                                                                                                                                                   Length 1783;
                                                                                                                                                   Indels
                                                                                                                                                   'n
                                                                                                                                                   Gaps
                                                                                                                                                 <u>-</u>
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein protein search, using sw modei

September 13, 2002, 09:11:05 ٠. ; Search time 172.41 Seconds
(without alignments)
17.277 Million cell updates/

cell updates/sec

Title: Perfect score: US-09-446-543A-61 171

Sequence: SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 seqs, 95089334 residues

Searched:

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum 88

seq length: 0 scq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summarles

Database

PIR\_71:\*
1: piri:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* piri:

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	6	υī	4	ω	N	٢	Result
47	47	47	47	47	47.5	47.5	47.5	47.5		48	48	48	48	4.8	48	48.5	48.5	49	49.5	50	50	50.5	52	53	53.5	54	56.5	149	Score
27.5								27.8			28.1	28.1	28.1	28.1	28.1	28.4	28.4	28.7	28.9		29.2		30.4	:-		31.6	33.0	87.1	Query Match I
501	333	284	215	159	533	503	401	393	345	1084	455	348	335	220	118	1501	303	72	176	128	123	1882	785	637	314	790	664	83	Length I
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T48336	H82852	F71015	B87577	G82669	A33111	A82193	A97446	AB2664	D84012	T33759	D70885	T21648	S70671	C83292	AC3169	T45623	AH2016	E91002	867150	S76955	S77900	S73484	F69099	D87559	в70569	T47959	F83376	JC7607	
hypothetical prote	hydroxybenzoate oc	hypothetical prote	glutathione S-tran	ubiquinone biosynt	segmentation prote	Sun/nucleolar prot	hypothetical prote	conserved hypothet	N-acetylglutamate	hypothetical prote	probable aidC prot	hypothetical prote	lipopolysaccharide				hypothetical prote	~				•	sensory transduct1	box T		hypothetical prote	conserved hypothet	n-reieas	Description

5	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30
46	46	46	46	46	46	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	47	47
26.9	26.9	26.9	26.9	26.9	26.9	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.2	27.5	27.5
698	688	419	347	342	256	5262	4957	1693	1607	1495	957	779	240	4589	938
N	N	N	N	N	N	N	N	ب	N	N	N	N	N	N	N
T39050	AI2516	AH3166	H64371	B64395	F70812	T03454	T03455	HHMMNN	T13250	T31434	A84089	T49717	D64688	T14914	C84480
hypothetical prote	hypothetical prote	hypothetical prote	maiic acid transpo	mailc acid transpo	probabie lpgR prot	ALR protein - huma	ALR protein - huma	genome polyprotein	hypothetical prote	densin-180 - rat	hypotheticai prote	related to BCS1 pr	probabie 1-acyigiy	dynein beta heavy	hypothetical prote

# ALIGNMENTS

prolactin-releasing peptide - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Joate: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001
C.Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa. N.; Hashida, T.: Ishizuka, T.; Hosoya,
Blochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing poptide gene:
A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Rocession: JC7607
A;Rolecule type: DAR
A;Residues: 1-83 <YAM>
A;Residues: 1-83 <YAM>

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.

C; Genetics:

A; Introns: 33/1 A;Gene: PrRP

용 Ş Query Match
Best Local Similarity
Matches 26; Conserv Conservative 97.1%; 93.9%; ļ Score 149; DB 2: Pred. No. 8.5e-15; 1; Mismatches 4 Length 83; Inde1s ö Gaps 0

RESULT F83376

conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PAO C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000 C;Accession: F83376 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.: Hickey, M.J.: adman, S.: Yuan, Y.; Brody, L.L.; Coulter, S.N.; Foiger, K.R.: Kas, A.; Larbig, K.; L.; Lory, S.; Oison, M.V.
Nature 406, 959-964, 2000
A;Titie: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Accession: F83376
A;Accession: F83376

A:Status: preliminary A;Molecule type: DNA A:Residues: 1-664 <STO> A:Cresidues: references: GB:AE004642; GB:AE004091: NID:g9948163; PIDN:AAG05539.1; GSPDB:GN A:Experimental source: strain PAO1

PA2151

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                                                                                                                                                                                                 A;Gene: Rv3485c
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;46-227/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                A:Status: preliminary; nucieic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-314 <COL>
A;Cross-references: GB:295390; GB:AL123456; NID:g3261766; PIDN:CAB08708.1; PID:g2104408 A;Experimental source: strain H37RV
                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Sqares, R.; Suiston, J.E.; Taylor, K.; Whitehead, S.; Barreii, B.G. A;Title: Deciphering the blotogy of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: B70569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeiton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecuie type: DNA
A; Residues: 1-790 <DEH>
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A; Introns: 39/1; (
A; Note: F15G16.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AL132959
A; Experimental source: cultivar Co
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A; Accession: T47959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Rv3485c - Mycobacterium tubercuiosis (strain H37RV)
C;Species: Mycobacterium tubercuiosis
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Matches 11
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Matches 10; Conserv
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                                                                    1 SRTHR----
                            SNTHRWFGAYGVTKSAVDHMMKLAADELGPSWVRVNSIRP
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45.8%;
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                                                                    --- HSMEIRTPDINPAWYASRGIRP 27
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                                                                                                         pred. No. 4.2;
5; Mismatches
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Pred.
3; Mis
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Pred. No. 3.
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hypothetical protein K05_orf1882 - Mycopiasma pneumoniae (strain ATCC 29342) C:Species: Mycopiasma pneumoniae A;Variety: ATCC 29342 A;Variety: ATCC 29342 C:Date: 27-reb-1997 #soquence_revision 25-Apr-1997 #text_change 07-Dec-1999 C;Accession: S73484; S62840 H; Plagens, H.; Pirkl, E.; L1, B.C.; Herrmann, R. R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; L1, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996 A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma A;Reference number: S73327; MUID:97105885
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R; Smith, D.R.; Douce
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A; Molecule type: DNA
A; Residues: 1-637 <STO>
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Best Local Similarity
Matches 12; Conserv
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Matches 13; Conserv
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A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Deita H: fu A:Reference number: A69000; MUID:98037514

A:Recession: F69099

A:Status: proliminary; nucleic acid sequence not shown; translation not shown

A:Status: proliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-785 <MTH>

A:Residues: 1-785 <MTH>

A:Cross-references: GB:AE000805; GB:AE000666; NID:g2621213; PIDN:AAB84680.1; PID:g262

A:Experimental source: strain Deita H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: GB:AE005673; NID:gl3424056; PIDN:AAK24472.1; GSPDB:GN00148 C;Genetics:
A:Gene: CC2501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Saizberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sensory transduction histidine kinase - Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: D87559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldrodge, T.; Qlu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.: Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noeliing, J.; Reeve, J.N. J. Bacterioi. 179, 7135-7155, 1997
412 HRATERIRRPDGNYRWVEYVDRPIRTDG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 HRHSMEIRTPDINPAWYASRGIRPV 28
                                                               4 HRHSMEIRTPDINPAW--YASRGIRPVG 29
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48.0%;
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Pred. No. 19;
l; Mismatches
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pneumon

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A;Accession: $73484
A;Status: preliminary; nucleic acid sequence not shown; translation not ahown
A;Status: preliminary; nucleic acid sequence not shown; translation not ahown
A;Realdues: l-1882 <HIM>
A;Realdues: l-1882 <HIM>
A;Crobb: references: EMBL:AED00017; GB:D00089; NID:g1673812; PIDN:AAB95806.1; PID:g167381
A;Crobb: references: EMBL:AED00017; GB:D00089; NID:g1673812; PIDN:AAB95806.1; PID:g167381
A;Crobb: reference analysis of 56 %h from the genome of the bacterium Mycoplasma pneumoni
A;Reference number: $62797; MUID:96177562
A;Accession: $62840
A;Status: preliminary; nucleic acid sequence not ahown; translation not ahown
A;Residues: l-1848 <HIL>
A;Crobb: references: EMBL:U34816; NID:g1209514; PIDN:AAC43650.1; PID:g1209522
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
C;Genetics:
A;Genetic soci
                                                                             RESULT 9
$76955
hypothetical protein - Synechocystis sp. [arr--]
hypothetical protein - Synechocystis sp.
hypothetical protein - Synechocystis sp.
c; Speciea: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: $76955
C; Accession: $76955
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamacova Res. 3, 109-136, 1996
A; Accession: $76955
A; Status: preliminary
A; Molecule type: DNA
A; Residuce: 1-128 <KANY
A; Cross-references: EME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 1 - Clostridium barker1 (fragment) C;Species: Clostridium barker1 (C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change | C;Accession: $77900; $43551 C;Accession: $77900; $43551 R;Beatrix, B; Zeider, O.; Linder, D.; Buckel, W. Bur. J. Biochem. 221, 101-109, 1994 Pur. J. Biochem. 221, 101-109, 1994 A;Reference number: $43237; MUID:94222050 A;Accession: $77900
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A; Residues: 1-123 <BEA>
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Best Local Similarity 42.9

Matches 15; Conservative
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Beat Local :
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    EMBL: D90917;
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    GB:AB001339;
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Pred. No. 4.9;
2; Mismatches 1
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Pred. No. 82;
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  NID: g1653836;
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  PIDN:BAA18867.1;
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  PID: d10196d
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R;Hayashi, T.; Makino, n., C., Shiba, L., ...
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, L., ...
DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
                                                                                                                                                                                                                                                                                                                                                                       probable regulatory protein [imported] - Eacherichia coli (strain O157:H7, subatrain C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: E91002
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Beat Local Similarity
Fatches 9; Conserv
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A;Molecule type: DNA
A;Residues: 1-176 <JAU>
A;Cross-references: EMBL:275161; NID:g1420572;
A;Cross-reference: atrain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #aequence_revision
C;Accession: S67150
R;Jauniaux, J.C.; Polrey, R.
submitted to the Protein Sequence Datab
A;Reference number: S67143
A;Accession: S67150
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                                                                                                                                                                              A;Modecule type: DNA
A;Realdues: 1-72 <HAY>
A;Realdues: 1-72 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36412.1; PID:g13362458;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Map position: 15R
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                                                               Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local
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27 SRIANYELNIRTPGLNDCRMIVEGLRKLG 55
                               1 SRTHRHSMEIRTPDINPAWYASRGIRPVG 29
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26.1%;
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34.58;
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33 38;
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Pred. No. 3
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Pred. No. 8.6;
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C;Genetlcs:
A;Gene: all)
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C;Speciea: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45623
R;Bevan, M; Van Der Schueren, J; Chuang, Y; Voet, M; Robben, J; Volck
aubmitted to the Protein Sequence Database, December 1999
A;Accession: T45623
A;Accession: T45623
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
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T45623
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C;Species: Anabaena sp.
C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc ap. strain PCC 7120
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc ap. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_reviaion 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AH2016
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
                                                                                           R;Wood, D.W., Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                   hypothetical protein Atu5077 [imported] - Agrobacterium tumefaciena (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AC3169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: DNA
A:ResIdues: 1-1501 <BEV>
A:Cross-refcrences: EMBL:AL133421
A:Experimental source: cultivar Columbia; BAC
C:Genetics:
                                        A; Authors: Yoo, N.; Tao, Y.; Biddle, P.; Jung, M.; Kreapan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
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A;Molecule type: DNA
A;Residues: 1-303 <KUR>
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A;Accession: AH2016
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A; Introns: 64/1; 739/3; 785/2; 1302/2;
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A; Reference
                         A;Title:
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Best Local Similarity 29.5
Matches 13; Conservative
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                    The Genome
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number:
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of the Natural Genetic Englneer Agrobacterium tumefaciens AB2577; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.48
29.58
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; Pred. NO. 1.3e
7; Mismatches
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Pred. No. 22;
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9;
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R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas Beruginosa PA01, an A;Reference number: A82950; MUID:20437337
A;Accession: C83292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Accession: AC3169
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <KUR>
A:Residues: 1-118 <KUR>
A:Cross-references: GB:AE008687; PIDN:AAL45769.1; PID:g17743503; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:
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                             S
                                                                                                                                                        A;Gene: PA2821
C;Superfamily:
                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <SYD>
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1;
A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                             probable glutathlone S-transferase PA2821 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Decies: Pseudomonas aeruginosa C;Dete: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: C83292
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A;Genome: plasm
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Best Local Similarity 34.4
Matches 11; Conservative
                                                                    Matches
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Best Local
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28
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                    6 NSMEIRTPDINPAWYASRGIRPVGR 30
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                                                                  'n
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Pred. No.
50
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Title: Perfect Score: Sequence:

US-09-446-543A-61 171

1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF

OM protein - protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Com

Compugen

September 13,

2002, 09:10:35

; Search time 136.62 Seconds
(without alignments)
5.542 Million cell updates/sec

Scoring table:

Gapop 10.0 , BLOSUM62

Gapext 0.5

231628 seqs,

24425594 residues

Post-processing: Ninimum Natch 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Database

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2,

2: /cgn2\_6/ptodata/2,

3: /cgn2\_6/ptodata/2,

4: /cgn2\_6/ptodata/2,

5: /cgn2\_6/ptodata/2,

6: /cgn2\_6/ptodata/2,

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/cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/1aa/Packfiles1.pep:\*

Result

Pred. No.

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

18

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Score

Query Natch

Length

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Description

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US-09-105-678A-9
US-09-105-678A-3
US-09-105-678A-43
US-08-776-971-61
US-09-421-208-9
US-09-421-208-44
US-09-421-208-44
US-09-421-208-45
US-09-421-208-45
US-08-776-971-138
US-08-776-971-138
US-08-776-971-138
US-09-105-678A-3
US-09-105-678A-3
US-09-421-208-3

Indels

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Sequence 9, Appli
Sequence 61, Appli
Sequence 61, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 53, Appli
Sequence 135, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 32, Appli
Sequence 33, Appli
                                                                      TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 9
; SEQUIENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Noriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-105-678A-9
             Query Match
Best Local S
Matches 31
                                                                                                                                                                                                       APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-7UN-1998
PRIOR APPLICATION DATA: APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-7UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48456-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 W
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
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             100.0%;
ilarity 100.0%;
Conservative
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US-08-776-971-112
US-08-776-971-113
US-08-776-971-115
US-08-776-971-115
US-08-776-971-117
US-09-105-678A-37
US-09-105-678A-37
US-09-172-53-4
US-09-421-208-37
US-09-421-208-37
US-09-421-208-39
US-09-421-208-39
US-09-421-208-39
US-09-421-208-39
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US-09-421-208-39
US-09-421-208-39
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             Score 171; DB 3;
Pred. No. 6.1e-19;
; Mismatches 0;
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                                   Length 31,
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132. App
136. App
136. App
117. App
117. Appl
17. Appl
17. Appl
14. Appl
14. Appl
14. Appl
14. Appl
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15. Appl
16. Appl
17. Appl
18. Appl
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US-08-776-971-61
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                                                                                                                                                                        Sequence 61, Application Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ IO NO: 43:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION OATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: Iinear
MOLECDLE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE AODRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Nasato
APPLICANT: Noriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUNBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                    y Match 100.0%; Score 171; DB 3
Local Similarity 100.0%; Pred. No. 6.1e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRTHRHSNEIRTPOINPAWYASRGIRPVGRF 31
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                                                                 Hinuma, Shuji Habata, Yugo Kawamata, Yuji Hogoya, Nasaki Fujii, Ryo Fukusumi, Shoji
Fukusumi, Shoji
Fukusumi, Shoji
Ritada, Chieko
Ritada, Chieko
Ritada, POLYPROTEINS, THEIR PRODUCTION AND
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                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                            Sequence 9, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF P
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ TO NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        APPLICANT:
                                                                                                    CORRESPONDENCE ADORESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/JP96/03821
FILING OATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
                                                                 STREET:
              COUNTRY:
                             STATE:
                                                  CITY:
                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: FRAGNENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
NEDIUN TYPE: Olskette
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION OATA:
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MA
USA
                                                Boston
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OPERATING SYSTEM: OOS

OPERWARE: FastSEQ for Windows Version

TATA:

TATA 471B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/776,971B FILING OATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 31 amino acids
                                                                 130 Water
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                              DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Pred. No. 6.1e-19;
); Mismatches 0;
                                                                                    ROBERTS & CUSHMAN, LLP
                                                                                                                                        PRODUCING
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                                                                                                                                      A 19P2 LIGAND
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Approx. 8258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICATION NUMBER: US 09/105,678
FILING QATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING QATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION QATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Moriya, Takeo
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                            FILING OATE:
                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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Similarity 100.0%;
31; Conservative 0;
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Tanaka, Yoko
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Pred. No. 6.1e-19;
Wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 31;
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                                                                                        US-09-105-678A-44
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Ouery Match 100.0%; Score 171; DB 3; Length 32; Best Local Similarity 100.0%; pred. No. 6.3e-19; Matches 31; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
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REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy
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ADDRESSEE: DIKE, BRO
STREET: 130 Water St
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino
STRANDEDNESS:
                                                                                                                         TOPOLOGY:
                                                                                                                                      STRANDEDNESS
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                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27,026
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                                                                                                                                                                          LENGTH:
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r Street
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Pred. No. 6.1e-19;
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0:
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Gaps
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US-08-776-971-62
US-08-776-971-62
Sequence 62. Applicatio
Patent No. 6228984
Patent No. 6228984
GENERAL INFORMATION:
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                                                                                Ma tches
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION
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MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: PCT/JP96/0382I
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: PCT/JP96/0382I
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/34337I
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/5419
FILING DATE: 11-ANG-1996
APPLICATION NUMBER: JP 8/541805
FILING DATE: 11-ANG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                   Local Similarity
    Н
                     i SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAVID 6:
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                            FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440 WATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                TOPOLOGY: Iinear
                                                                                                                                                                                                                                                                                 TYPE; amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                        LENGTH: 32 amino acids
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Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
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idarity 100.0%:
Conservative
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Fujii, Ryo
Fukusumi, Shoji
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Kawamata, Yuji
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                                                                                                                                                                                                                          internal
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                                                                            Score I71: DB 4:
Pred. No. 6.3e-19;
Mismatches 0;
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                                                                                                                    Length 32;
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US-09-105-678A-45
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APPLICATION NUMBER; JP 172118/1997
APPLICATION NUMBER; JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                           Sequence 45,
Patent No. 6
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Best Local Similarity
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                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                               CORRESPONDENCE ADDRESS
                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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APPLICANT: Nishimura.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET; 130 GCITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                      1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 3I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                      SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 3I
                                                                                                                                                                             5, Application US/09I05678A 6103882
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E: DIKE, B
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Tanaka, Yoko
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liarity i00.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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BRONSTEIN,
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Pred. No. 6.3e-19:
                ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                          Length 32:
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RESULT 10
US-08-776-971-63
; Sequence 63, Ap
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: MOLECULE TYPE: peptide
US-09-105-678A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6228984
GENERAL INFORMATION:
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Uest Local Similarity
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APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 172118/1997
APPLICATION UMBER: JP 172118/1997
APPLICATION TOPPHARTION:
ANDER COALING DATE: ORNIATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
             COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 018kette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION OATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWAD
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hogoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADORESSEE: OIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
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                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
APPLICATION NUMBER: PCT/JP96/03821
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                                                                                                                                                                                                                                                                                                                                                                                Fukusumi, Shoj
Kitada, Chieko
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Pred. No. 6.6e-19;
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TYPE: amino acid
STRANDEONESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRACKENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-08-776-971-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          몽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JF 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CDRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-OEC-1995
APPLICATION NUMBER: JP 8/59419
FILING OATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 130 m
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                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02109
  REFERENCE/DOCKET NUMBER: 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              130 Water Street
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                                                                                                                                                                                                                                                                                                             Floppy disk
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100.0%; Pred. No. 6.6e-19;
tive 0; Mismatches 0;
                                                                                                                                                                                                              US/09/421,208
                48466-342
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US-08-776-971-59
; Sequence 59, Application; Patent No. 6228984
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match Tocal Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
             TELEFAX: 617-523-6440
INFORMATION FDR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        PRIDE APPLICATION DATA:

APPLICATION UNMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-AAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/216573

FILING DATE: 18-SEP-1996
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONPUTER: IBM compatible
OPERATING SYSTEM: DOS
SDETWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: 117-523-3400
                                                                                                        ATTDRNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUNBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
CONPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE ROF SEQUENCES: 140
ENGTH: 87 amino acids
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Fujii, Ryo
Fukusumi, Shoji
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Kitada, Chieko
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Kawamata, Yuji
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FRAGMENT TYPE: PROCEIN:
FRAGMENT TYPE: PROCEIN:
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-59
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GENERAL INFORMATION:
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Best Local Similarity 100.0%;
                                                                                                                                          INFORMATION FOR SEQ ID NO: 135:
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

PILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996
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                                                                                                                                                           TELEGDMMUNICATION INFORMATION:
TELEPHDNE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBN compatible
DPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
MDLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONPUTER READABLE FDRM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                    NAME: Conlin, David G. REGISTRATION NUMBER: 27.0 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
                                   TDPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                  LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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Habata, Yugo
Kawamata, Yuji
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Kitada, Chieko
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Pred. No. 2e-18;
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Query Match Best Local :

Local Similarity

DB 4; Length 87;

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/ MOLECULE TYPE: protein

/ FRAGMENT TYPE: internal

/ SEQUENCE DESCRIPTION: S

US-08-776-971-138
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US-08-776-971-138
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Best Local Similarity
Matches 31; Conserv
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GENERAL INFORMATION:
                                                                                                                                 INFORMATION FOR SEQ ID NO: 138: SEQUENCE CHARACTERISTICS: LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

EIP: 02109

COMPUTER READABLE FORM:
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WALER Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28 DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28 DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15 MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                           TOPOLOGY: linea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08776971B
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Hosoya, Masaki
Fujii, Ryo
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                   SEQ ID NO: 138:
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BER: 47176
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Pred. No. 2e-18;
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Search completed: September 13, 2002, 09:20:57 Job time: 622 sec
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                                                                                                                                                                                                                              ; TOPOLOGY: iinear
; MOLECULE TYPE: peptide
US-09-105-678A-7
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US-09-105-678A-7
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                                                                                                                                                Matches
                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PI
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatthle
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLID, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                               1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                            92.4%;
90.3%;
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100.0%; Pred. No. 2e-18;
tive 0; Mismatches
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                                                                                                                                                              Score 158; DB 3; Pred. No. 5.2e-17;
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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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110
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq iength:
seq iength:
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1: /SIDS1/gcgdata/ho
2: /SIDS1/gcgdata/ho
3: /SIDS1/gcgdata/ho
4: /SIDS1/gcgdata/ho
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20: /SIDS1/
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Match
                  1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT: *
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT: *
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT: *
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT: *
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT: *
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT: *
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT: *
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT: *
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT: *
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT: *
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT: *
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT: *
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT: *
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT: *
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT: *
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT: *
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT: *
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT: *
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT: *
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT: *
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
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27: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
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1.945 Miliion ceil updates/sec
Peptide PRRP8 frag
Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
19P2 ligand peptid
Human type G protein
Bovine G protein-
Bovine G protein-
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# ALIGNMENTS

AAB46955;

AAB46955 standard;

Protein;

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ID AAB4
XX AAB4
AC AAB4
XX GPR1
XX GPR1
KW GPR1
KW Cent
KW hypo
XX Unld
XX WO20
XX Unld
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2001 (first entry)
    WP1; 2001-182941/18
                                                                              Panula PAJ,
                                                                                                                                                                                                                                                03-AUG-1999; 99US-0365756.
20-MAR-2000; 2000US-0531567.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide PrRP8 fragment.
                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000WO-FI00664
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Best Local
                                                                                                                                                                                                                                                                     Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancrens; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-terminal fragments of prolactin-releasing peptide useful for regulating autonomic functions and in the manufacture of a medicament
                (TAKE ) TAKEDA CHEM IND LTD
                                                      28-APR-1997;
                                                                                             27-APR-1998;
                                                                                                                                      05-NOV-1998.
                                                                                                                                                                            WO9849295-AL
                                                                                                                                                                                                                                                                                                                                                                                                           Murine pituitary-derived ligand polypeptide antigenic epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANW95178 standard; Protein; 10
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4 pygrf 8
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nes 5; Conserv
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                                                                                                                                                                                                                                                     transgenic animal; epitope.
                                                      97JP-0109974.
                                                                                             98WO-JP01923
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100.0%; Pr
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0; Mismatches
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The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled cryphan receptor designated CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of CC the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Schizophrenia; disorders of growth hormone secretion; cancer: CC operative nutritional status and as vasopressor. Transgenic animais CC carrying the ingand polypeptide encoding DNA or its mutein are used to Study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC related sequences; in receptor-bindling assays; for production of Ab and CC canisters which can be used for the arremarking of activation of Ab and CC canisters which can be used for the arremarking of activation of Ab and CC canisters which can be used for the arremarking of activation of Ab and CC canisters which can be used for the arremarking of activation of Ab and CC canisters which can be used for the arremarking of activation of Ab and CC canisters which can be used for the arremarking of activation of Ab and CC canisters which can be used for the arremarking of activation of Ab and CC canisters which can be used for the arremarking of activation of the polypeptide canism of activation of Ab and considered to the canism of activation of the control of the control of the cont
Sequence
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AAW31400
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Best Local S
Matches 5
      18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                  G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; arc
                                                                                                                                                                                                                AAW31400 standard; Peptide; 15
                                                                     10-JUL-1997.
                                                                                       WD9724436-A2
                                                                                                        Synthetic
                                                                                                                        therapeutic
                                                                                                                                                            Synthetic ligand 19P2-L31 peptide II.
                                                                                                                                                                              06-APR-1998
                                                                                                                                                                                              AAW31400;
                                                   26-DEC-1996;
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5; Conserv
                                                                                                                         agent; antigen.
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      96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                   96WO-JP03821
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100.0%; Pred. No. 4.
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches S
                                                                                                                                                                            G protein-coupled receptor; GPCR; hypowvarianism: gonecyst cacogenesis; menopausai syndrome; euthyroid; hypomerabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea: galactorrhea; acromegaly; Chlari-Frommel syndrome; Argonz-del Castilo syndrome: Porres-Albright syndrome; lymphoma; Sheehan syndrome; dyszcospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus: abnormal saccharometabolism; oxytocia; prolactin secretion.
                                                                                                                                                                                                                                                                                                                                                                         C-terminai ligand polypeptide derived antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1999
                                                                                                              WO9858962-Al
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23-JUN-1997;
                                   22-JUN-1998;
                                                                         30-DEC-1998
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%; Score 28;
Llarity 100.0%; Pred. No.
Conscrvative 0: Mismatci
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                                   98WO-JP02765.
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                                                                                                                                      20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; 19P2 iigand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat
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                                                                               21-MAY-1998;
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                      Disclosure;
                                                               New monoclonal antibodies, u
studying diseases related to
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                        regulatory mechanism (e.g. promotion of prolactin secretion), cer nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its deri sequences AAY49290-302 represent peptide fragments of the 19P2 li
                                                                               The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central
                                                                                                                                                                       Disclosure; Page 27; 73pp; Japanese.
                                                                                                                                                                                                  New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
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regulatory mechanism; central nerv
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100.0%; Pr
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Sequence

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RESULT
AAW3 13
                      This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a composition or therapeutic agent for dementia, depression, hyperkinetic compositions, a central nervous system modulator or a pancreatic function CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic cutrauma, growth hormone secretory disease, hyper- and polyphagia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperilpidaemia, hypercholesterolemia, hyperglyceridaemia, hypergrolactinamia, disbetes, cancer, pancreatitis, renal disease, hyperprojection in the composis, asthma, rhoumatold arthritis, spinal injury, CC transient brain ischaemia, epilepsy, amylotrophic lateral scierosis, acute myocardial infarction, infertiiity, spinocerebellar degeneration, CC consistent brain ischaemia, epilepsy, amylotrophic lateral scierosis, acutivation of the binding activity of the ligand affecting cativitien of the floriding activity of the ligand affecting activity of the ligand affecting activity of the ligand affecting activity.
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Best Local Similarity
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28-DEC-1995;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                        Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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Y, Kitada C;
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100.0%; Pred. No.
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6.7;
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Query Match

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Score

28;

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Length

Query Match Best Local Similarity

93.3%;

Score 28; Pred. No.

DB 18; 8.9;

Length 20

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                                               This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 33 to 52 of the CR sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function cm coupletor. This sigand could have specific applications as a modulator. This sigand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, schizophrenia, compositions of the consciousness, anxiety syndrome, schizophrenia, compositions, growth hormone secretory disease, hyper- and polyphagia, hyperilpidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, panoreatitis, renai disease, hyperprolactinaemia, neurosis, asthma, rheumatoid arthritis, spinal injury, cutansient brain ischaemia, epilepsy, amylotrophic lateral scierosis, concertain disease, hyperglyceridaemia, rheumatoid arthritis, spinal injury, caute myocardial infarction, infertility, spinocerebellar degeneration, confirmed the demantitis, osteoporosis and/or collogogalactia, Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cativation of the 6 protein-coupled receptor protein.
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28-DEC-1995;
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modulator; pituitary; central nervous system; pancreas; prophylactic;
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   Sequence
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Y, Kitada C;
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                                                                                                                                                                                 CC derived ligand corresponding to amino acid residues 34 to 53 of the CC derived ligand corresponding to amino acid residues 34 to 53 of the CC sequence in AAW31368 and is used in an assay to monitor ligand binding CC to the G protein coupled receptor protein. Pharmaceutical compositions CC central nervous system modulator or a pancreatic function modulator. a CC central inguilation system modulator or a pancreatic function modulator. CC therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxlety syndrome, schizophrenia, trauma, CC growth hormone secretory disease, hyper- and polyphagia.
CC hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia, hypergrodactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperrolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC transient brain ischaemia, amylotrophic lateral Belerosis, acute myocardial infarction, spinocerabeliar degeneration, bone fracture, CC trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility CC and/or oliopogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
Query Match
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modulator; pituitary; central nervous system; pancreas; prophylactic;
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15-MAR-1996;
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DB; AAV02397.
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93.3%; Score 28;
iarity 100.0%; Pred. No.
Conservative 0; Mismatc
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95JP-0343371.
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                                                        The present sequence represents a bovine pltultary-derived ligand CC fragment. It is used in the course of the invention. The specification CC describes an agent for modulating prolactin secretion which comprises a citigand polypeptide or a salt, for a gprotein-coupied receptor (GPCR) CC protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal CC syndrome, euthyroid or hypometabolism. They can by used for promoting cc inhibiting prolactin secretion can be used for treating or promoting cc inhibiting prolactin secretion can be used for treating or preventing cc prolactinoma. Infertility, impotence, amenorrhea, galactorrhea, cc caromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Frombes, albright syndrome, lymphoma, Shechan syndrome or dyszoospermia. The inhibitory agents can also be used for treating or preventing cc choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prolactinoms; infertility; impotence; amenorrhea; galactorrhea; acromegaly, Chiari-Frommel syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; tyzoospermia; contraceptive; placental function; chorlocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97232;
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menopausal syndrome; euthyrold; hypometabolism; lactation;
pituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine pituitary-derived ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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16 pvgrf 20
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Conservative

93.3%; Score 28; 100.0%; Pred. No. 0

DB 20; Length 20;

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Sequence

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The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypoverianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pluvitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, cormegaly, Chiari-Frommei syndrome, Argonz-del Castilo syndrome, for The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
Query Match
Bost Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypocoaritanism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; prolactinoma; infertility; syndrome; amenorrhea; galactorrhea; acromegaly; Chlari-Frommel syndrome; Asyndrome; Asyndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; lruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
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n or placental function, e.g. for treating menopausal
, tumours, autoimmune disease or abnormal pregnancy
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                                             CC is used in the course of the invention. The specification describes
CC an agent for modulating prolactin secretion which comprises a
CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
CC protein. The agents for promoting prolactin secretion can be used for
CC treating or preventing hypocourianism, gonecyst cacogenesis, menopausal
CC syndrome, euthyroid or hypometabolism. They can by used for promoting
CC lactation in a domestic mammal and as an aphrodisiac. The agents for
CC inhibiting prolactin secretion can be used for treating or preventing
CC inhibiting prolactin secretion can be used for treating or preventing
CC prolactionma, infertility, impotence, amenorrhea, galactorrhea,
CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
CC forbes-Albright syndrome, lymphoma, Shechan syndrome or dyszoospermia.
CC The inhibitory agents can also be used as contraceptives. The agents for
CC modulating placental function can be used for treating or preventing
CC choricoarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

Abortion and approximation of preventing or preventing abortion and abortion and approximation of preventing the contraceptives.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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Sequence
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16 pvgrf 20
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                                       saccharometabolism,
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                                       abnormal lipidmetabolism or oxytocia.
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PVGRF 5

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RESULT |
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                                 The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the CC polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntigton's CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC carrying the ligand polypeptide encoding DNA or its mutchn are used to cstudy the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC enlated sequences; in receptor-binding assays; for production of Ab and CC enlated sequences; in receptor-binding assays; for production of Ab and CC enlated sequences; in receptor-binding assays; for production of Ab and CC enlated sequences; in receptor-binding assays; for production of Ab and CC enlated sequences; in receptor-binding assays; for production of Ab and CC enlated sequences; in receptor-binding assays; for production of Ab and CC enlated sequences; and content of the murine ligand-polypeptide.
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Sequence
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|16 ||pvgrf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide ligand for orphan G protein coupled receptors - used treating disorders of central nervous system, pituitary and creas, and for drug screening
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Query Match

93.38,

Score 28; 8 20;

Length 20;

Sequence

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RESULT 15
AAW95175
ID AAW951
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                                                   The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPRIO (human) or UHR-1 (rat). Cell; transformed with a vector containing CC the ligand polypeptide encoding DNN are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of CC the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; chalzophrenia; disorders of growth hormone secretion; cancer; CC diseases; schlzophrenia; disorders of growth hormone secretion animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC study the function of the polypeptide-expressing genes, as models of CC study the function of the polypeptide sayays; for production of Ab and CC polypeptide DNA is used as a source of probes and primers; to identify created sequences; in receptor-binding assays; for production of Ab and CC cantisers; in drug development; for gene therapy and to develop epitide epitotes which can be used for the preparation of anti-ligand polypeptide epitotes which can be used for the preparation of anti-ligand polypeptide
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disciosure; Page 26;
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Query Match 93.3%: Score 28; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 | | | | |
Db 16 pvgrf 20

Search completed: September 13, 2002, 09:18:34

Job time: 499 sec
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Run

017234 caenorhabdl Q96sd4 homo sspien

homo sspien

O9d3v7 mus musculu
O9c2p5 mus musculu
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O20294 csenorihabdl
O9rj10 streptomyce
O19879 caenorihsbdi
O9385 spiroplasma
O99289 streptococc
O9pke7 chlamydia m
O9s892 csulobacter
O9ew96 streptomyce
O91802 bacilen mos
O9k802 bacilius ha
O33440 pseudomonas
P74747 synechocyst
O96925 homo saplen
O9v0q3 pyrococcus

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12.204 Million cell updstes/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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 O9w624 carassius a
O9ilw4 pseudomonss
O9m371 arabidopsis
O93127 streptomyce
O9ilf9 homo saplen
O9ph76 xylella fss
O60687 homo ssplen
O9lg20 oryaa sativ
O20170 caenorabaii
O95zb5 leishmania
O91212 pseudomonas
O50128 pyrococcus
O9y276 homo ssplen
O9sd86 arabidopsis
O9sd86 arabidopsis
O9sz21 deinococcus
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  RESULT
Q911W4
ID Q9
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O9W624;

O1-NOV-1999 (TIEMBLIEL 12, C

O1-NOV-1999 (TIEMBLIEL 12, I

O1-DEC-2001 (TIEMBLIEL 19, I

C-RF AMIDE.
 Q911W4;
Q911W4;
Q1-MAR-2001
Q1-MAR-2001
Q1-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

TISSUE-BRAIN;
Satake H., Minaksta H., Fujlmoto M.;
Satake H., Minaksta H., Fujlmoto M.;
"Carassius RFamide (C-RF amlde).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databsses.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Carassius auratus (Goldfish).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrsta; E
ActInopteryg11; Neopteryg11; Teleoste1; Euteleoste1;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID-7957;
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                                                                                                                              1 TPDINPAWYXXRGIRPVGRF 20
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56 SPEIDPFWYVGRGVRP1GRF 75
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6 Q9A7W7
Q55020
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L Q9EPF7
Q9P5J9
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Q19879
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Euteleostoml;
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13; Length 117;

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                                                                                           SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL132959; CAB71097.1; -.
                                                                                                                                                                                                                              Q9M371 PRELIMINARY; PRT; 790 AA.
Q9M371.
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL B7.4 KDA PROTEIN.
F15G16.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-
                                                                             Hypothetical protein. SEQUENCE 790 AA; 8
                                                                                                                                        De Haan M., Maarse A.C., Grivell L.A.,
Mayer K.F.X., Quetier F., Salanoubat M.
Submitted (NOV-1999) to the EMBL/GenBan
                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudlcots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabldopsis.
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PA2151.
Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                    SEQUENCE FROM N.A.
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366
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|78 TPDINP-WFLQRSGRP
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PPHNPRTYGSRGLQPHGRW
                PDINPAWYXXRGIRPVGRF
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                                            Similarlty
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                                   Conservative
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                                                                             87376 MW;
                                           45.08;
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62.58;
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384
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                                                                                                                                          EMBL/GenBank/DDBJ
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                                 Pred. No. 9.5;
3; Mismatches
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Pred. No. 6
                                                  Score 49;
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                                                                                                                                                        H.W., Lemcke
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                                                                            CRC64
                                                   Length 790
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                                                                                                                                                                                                                                                                                                                                                                                664;
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, Yuan Y.,
Lim R.M.,
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RESULT
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Best Local
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Best Local :
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                   Q9PH76;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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01-DEC-2001
01-DEC-2001
01-DEC-2001
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01-MAY-2000 (TrEMBLrei. 13, Last sequence update)
01-MAY-2000 (TrEMBLrei. 13, Last annotation update)
DJ479J7.3 (SUSHI-REPEAT PROTEIN (SRPUL)) (FRAGMENT)
DJ479J7.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kormanec J., Bistakova J., Novakova R., Homerova D., Rei
"Cloning and characterization of a new polyketide gene of
Streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY033994; AAK61719.1; -.
SEQUENCE 420 AA; 43011 MW; 3C27E22BEBBCZDEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces
                                                                                                       Q9PH76
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1999) to the EMBL; AL035608; CAB55682.1;
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Mammalla; Eutheria;
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Homo sapiens (Human).
Homo sapiens (Human).
Chordata;
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STRAIN-CCM3239;
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    HYDROXYBENZOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawior
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                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                    1 TPDINPAWYXXRGIRP
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 54 AA;
(TremBLrel. 15, Created)
(TremBLrel. 15, Last sequence update)
(TremBLrel. 19, Last annotation updat
DATE OCTAPRENYLTRANSFERASE.
                                                                                                                                                                                                                                                                                             Congervative
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Pred. No. 1.8;
1; Mismatches
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Pred. No. 13;
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                   update)
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RA HO P.L., Hoheisel J.D., Junquelra M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Lalgret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Machado M.A., Martins E.A.L., Martins E.M.F., Marsino C.L.,
RA Monck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T., Pariis A.,
RA Quaggio R.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA da Silva A.C., da Silva R.M., da Silva F.R., Silva M.A.,
RA da Silva A.C., da Silva H.M., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RHAL, Addosa G. J.S., Pereira P.G., Silva M.A., Setubal J.C.;
RHAL, Addosa G., Arezaelli, -.
RA Lagousco I.S., Meidanis J., Setubal J.C.;
RHAL, Addosa G., Arezaelli, -.
RA Lagousco I.S., Dankunda I.
RA PROSITE. PS00043: Unita, Dankunda I.
RA PROSITE. PS00443: Unita, Dankunda I.
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Best Local
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O60687;
O1-AUG-1998 (
01-AUG-1998 (
01-JUN-2001 (
SUSHI-REPEAT
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SEQUENCE FROM N.A.

KUTOSAWA H., Inukai T., Inaba T., Goi K., Chang K. S., Sinjyo Rakestraw K.M., Naeve C.W., Look T.A.;

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF060567; AAC15765.1; -.
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                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01040; UblA; 1.
PROSITE; PS00943; UBIA; DNKNOWN_1
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                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                     NCBI_TaxID=9606;
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8; Conserv
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8 (TrEMBLrel. 07,
1 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                 (Human).
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Primates;
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53.3%;
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Last annotation updat
                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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020170;
01-NOV-1996
01-NOV-1996
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Q9LGZ0;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
                                                                                                                                                                                                        Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poaies; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TIEMBLIE1. 15, Last sequence update)
EST AU070209(R3722) CORRESPONDS TO A REGION OF THE PREDICTED GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001128; Cyt_P450.
Interpro; IPR00310; HYR.
Interpro; IPR000316; Sushi_SCR_CCP.
Pfam; PF02494; HYR; 1.
Pfam; PF00084; sushi; 3.
SMART; SM00032; CCP; 3.
PROSITE; PS00086; CYTCCHROME_P450; UNKNOWN_1.
SEQUENCE 465 AA; 52971 MW; 4D752B187FF3EFB8 CRC64;
                                                                                                                                                     Interpro; IPR000608; UBQ_conjugat.

Pfam; PF00179; UQ_con; 1.

SMART; SM00212; UBCQ: 1.

PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.

Ligase; Ubiquitin conjugation.

SEQUENCE 540 AA; 60487 MW; 5DELFF4EEB7
                                                                                                                                                                                                                                                                                                         "Oryza sativa nippombare(GA3) genomic DNA, chromosome clone:P0702F03.";
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T
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(TrEMBLrel. 15,
(TrEMBLrel. 19,
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                           PRELIMINARY;
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Last sequences
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Pred. No.
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Pred. No. 17;
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EMBL; 268342; CAA92775.1;

InterPro; IPR000536; Cation_chan_non_lig.
InterPro; IPR001522; Channel_pore_K.
InterPro; IPR001522; Channel_pore_K.
InterPro; IPR00595; cNMP_binding.
Pfam; PF00027; CNMP_binding; 1.
Pfam; PF00020; cNMP_binding; 1.
SMART; SM00100; CNMP; 1.
SMART; SM00100; CNMP; 1.
PROSITE; PS00088; CNMP_BINDING_1; UNKNOWN_1.
PROSITE; PS00042; CNMP_BINDING_3; 1.
SEQUENCE 767 AA; 89988 MW; F7ECF69DBBEAACE
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O952B5
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OFFICE OF
                                                                                                                                                                                                                                                                                         Ivens A.C., Lewis S.M., Bagherzad Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schaefer N., Mueller-Auer S., Gabel C., Fuchs M., Rieger lvens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
NCBI_TaxID=6239;
                                                                                                                                                       Hypothetical
SEQUENCE 14
                                                                                                                                                                                                             "A physical map of the Leishmania Genome Res. 8:135-145(1998).
EMBL; AL596272; CAC44727.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FRON N.A.
STRAIN-FRIEDLIN;
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STRAIN-FRIEDLIN;
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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Caenorhabditis.
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RESULINE-20437337; PubNed-10984043;

XX NEDLINE-20437337; PubNed-10984043;

XX NEDLINE-20437337; PubNed-10984043;

XX Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

XX A H.Ckey N.J., Brinkman F.S.L., Hufnagie W.O., Kowalik D.J., Lagrou M.

XX A H.Ckey N.J., Brinkman F.S.L., Hufnagie W.O., Kowalik D.J., Lagrou M.

XX A H.Ckey N.J., Brinkman F.S.L., Hufnagie W.O., Kowalik D.J., Lagrou M.

XX A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

XX A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

XX A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XX A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XX A Reizer J., Saier M.H., Hancock R.E.W., Lory S., Oison M.Y.;

**Complete genome sequence of Pseudomonas aeruginosa PAO1, an

**Opportunistic pathogen.";

XX A REVIET ABOU4622; AAGO5340.1;

XX A REVIET ABOU4622;

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01-JUN-1998
01-JUN-2001
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                                       Kawarabayasi Y., Shwada M., Norikawa N., Haikawa Y., Hino Y. Yamamoto S., Sekine M., Baba S.-I., Kosuyi H., Hosoyama A., Sakai M., Oyura K., Otsuka R., Nakazawa N., Takamiya M., Ohi Funshashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Aoki K.-1., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-OT3;
MEDLINE-98344137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota;
NCBI_TaxID-53953;
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Pseudomonas
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Bacteria; Proteobacteria;
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8; Conserv
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Last annotation updat
IN PH1420.
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Pred. No. 19;
2; Mismatches
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horikoshii OT3.";
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                                                                                                                                                                                                                                                 , Ohfuku Y.,
N., Oguchi A.,
oshi K.,
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O9Y276;
O1-NOY-1999 (TrEMBLrel. 12, Created)
O1-NOY-1999 (TrEMBLrel. 12, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O7SI (BCS] (YEAST HOMOLOG)-LIKE).

Vertebrata
SEQUEHCE FROM 1
TISSUE-MUSCLE,
Strausberg R.;
                                                                                                                                                                                                      de Lonlay P., Valnot I., Barrientos A., Gorbatyuk M., Tzagoloff A., Benayoun E., Chretten D., Kadhom H., Lombes A., Ogler de Baulny H., Hiaudet P., Munnich A., Rustin P., Rotig A., "Mutations in bosi, a mitochondrial respiratory chain assembly gene, are responsible for the complex III deficiency of patients with tubulopathy and liver fallure.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLIHE-96207227; PubMed-8619474;
Andersson B., Wentland M.A., Ricafrente
"A 'double adaptor' method for improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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Pfam; PF00433; prenyltrens; 2.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UHKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 284 AA; 32319 MW; 8E0E7BC3711D3815
                                                                                         Strausberg R.;
Submitted (HOV-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLIHE-97264341; PubMed-9110174;
Yu W., Anderson B., Worley K.C., Muzny D.M., Dir
Rlasfrente J.Y., Wentland M.A., Lennon G., Gibbs
"Large-scale concatenation cDHA sequencing.";
Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    construction.
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                                                                                                                                         TISSUE-RHABDOMYOSARCOMA;
                                                                                                                                                             SEQUENCE FROM H.A
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification and characterization of human cDHAs PET112, SCO1, COX15, and COX11, five genes involved and function of the mitochondrial respiratory chain Genomics 54:494-504(1998).
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                        RHABDOMYOS ARCOMA;
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Pred. No. 22;
3; Mismatches
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shotgun library
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bbs R.A.;
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Bevan M., Van Der S
Volckaert G., Bancre
Submitted (DEC-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSSUB6;
OSSUB6;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 16, Last sence update)
O1-MAR-2001 (TrEMBLrel. 16, Last senctation update)
HYPOTHETICAL 164.4 KDA PROTEIN (GEHOMIC DNA, CHRO
CLOHE:MXM12).
1184
                                                                                                                                                                                               DNA Res. 4:215-230(1997).
EMBL; ALU33421; CAB62610.1;
EMBL; AB005249; BAB09962.1;
Hypothetical protein.
SEQUENCE 1501 AA; 164360
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-COLUMBIA;
STRAIN-COLUMBIA;
MEDLIHE-97471969; PubMed-9330910;
MEDLIHE-974711 H., Hakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                 Sato S., Kotani H., Hakamura Y., Kaneko T., Asamizu E., Fui Miyajima N., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. features of the 1.6 Mb regions covered by twenty physicall:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
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SPOMAPSWYSOYGTFKHGLVQPVHDTGRF
                                       TPDIHPAWYXXRG----IRPV---GRF 20
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Similarity 34.5%;
10; Conservative
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7; Conserv
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G., Bancroft I., N
(DEC-1999) to the
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Mewes H.W., Lemcke
e EMBL/GenBank/DDBJ
                                                                               Score 43.5; D
Pred. Ho. 1.5e
5; Mismatches
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Pred. NO. 33;
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Ho. 1
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Cke K., Mayer
DBJ databases.
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CHROMOSOME
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                                                                                   Indels
                                                                                                                                                                                                 CRC64;
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yer K.F.
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Search completed: September 13, Job time: 1062 sec
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RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 15692 / PAQ1;

RX MEDLINE-20437337; PubMed-10984043;

RX MEDLINE-20437337; PubMed-10984043;

RA MEDLINE-20437337; PubMed-10984043;

RA MEDLINE-20437337; PubMed-10984043;

RA Hickey M.J., Pham X.-Q.T., Erwln A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Relzer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT complete genome sequence of Pseudomonas aeruginosa PAQ1, an

opportuniatic pathogen. ";

RI Nature 406:959-964(2000).

DR EMBL, AE004709, AAG06209.1; -.

DR InterPro; IPR004045; GST_N.

CM Transferase; Complete proteome.

KW Transferase; Complete proteome.

SQ SEQUENCE 220 AA; 24716 MW; 6596183EA6CAA050 CRC64;
                                                                                                                                                           Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivislon; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=287;
                                                                                         9
                                                                                                                         6
                                                                                       PAWY -- REISPLGR 50
                                                                                                          PAWYXXRGIRPVGR 19
                                                                                                                                                                             39.48;
                  2002, 09:29:17
                                                                                                                                                         Score 43; DB 16; Length 220;
Pred. No. 25;
1; Mismatches 2; Indels
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                                                                                                                                                             Gaps
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GonCore version 4.5 Copyrlght (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:30:42 ; Search time 80.21 Seconds (without alignments) 10.620 Million cell updates/sec

US-09-446-543A-73 109

Title:
Perfect score:
Sequence: 1 TPDINPAWYXXRGIRPVGRFXX 22

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Searched:

Total number of hits satisfying chosen parameters: 105224

Minlmum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

45	4	3	42	41	40	39	38	37	36	ယ	34
38	38	38	38	38	38	38.5	38.5	38.5	38.5	38.5	38.5
34.9	34.9	34.9	34.9	34.9	34.9	35.3	35.3	35.3	35.3	35.3	35.3
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HMPA_BACSU	LYTB_MYCLE	Y587_PASMU	PHSC_ECOLI	118B_HUMAN	RL15_AERPE	POLG_ZYMVR	CAD2_RAT	CAD2_MOUSE	CAD2_HUMAN	CAD2_BOVIN	DPO1_THEFL
P49852	Q9x781		P77409							P19534	P30313
bacillus s	mycobacter	pasteurella	escherichia	homo sapier	aeropyrum p	z genome po	rattus norv	ສນອ muscul	homo sapie	bos taurus	thermus agu

## ALIGNMENTS

RESULT 1  IN PRIC_HUMAN  STANDARD; PRT; 87 AA.  A. P81277. AA. P81277. BY 30-MAY-2000 (Rel. 39, Created) BY 30-MAY-2000 (Rel. 39, Last sequence update) BY 30-MAY-2000 (Rel. 39, Last sequence update) BY 30-MAY-2000 (Rel. 39, Last sequence update) BY 50-MAY-2000

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8
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PRRP_R
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                                                   Query Match
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Matches 18
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Matches 18
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a coliaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRRP_RAT
P81278;
30-MAY-2000
                                                                                                                PEPTIDE
PEPTIDE
MOD_RES
                                                                                                                                                                                                                                                                                                                                        Sumino Y., Fujino M.; "Tissue distribution of prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2000 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31; Prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                           Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAT
                                                                                                      SEQUENCE
                                                                                                                                               SIGNAL
                                                                                                                                                                 EMBL; AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                              regui. Pept. 83:1-10(1999).
-i- PUNCTION: Stimulates or
                                                                                                                                                                                                                                                                                                                                                                                  PubMed~10498338:
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           releasing peptide
                                                                                                                                                                                                                                                                                                                                  receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                           PUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulactotrophs directly to secrete PRL. TISSUE SPECIFICITY: Widely expressed, with highest levels in mediala oblongata and hypothalamus.
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                       TPD1NPAWYXXRG1RPVGRF 20
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            TPDINPAWYTGRG1RPVGRF
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21
52
52
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Rodentia;
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., Kurokawa
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-53 PROVIDE AMIDE
DOC75A264EEE4F29 CRC64;
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Sciurognathi; Muridae; Murinae; Rat
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                                                e 104; DE NO. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                            Kawamata Y., Habata
T., Nishimura O., Or
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No. 1.3e-10;
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Sekiguchi M.,
                                                                     Length 83;
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                                                                                                                        PEPTIDE PRRP31.
PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                and regulates the GPR10. May stimulate
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RESULT 3
PRRP_BOVIN
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Best Local S
Matches 18
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P81264:
30-MAY-2000
30-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
PEPTIDE
PEPTIDE
MOD_RES
                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
nature 393:272-276(1998)
-I- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPRIO. May stimulates the control of the prolactin through its receptor of the prolactin lactotrophs directly to secrete PRL.
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30-MAY-2000 (Rei. 39, Last sequence update)
01-MAR-2002 (Rei. 41, Last annotation update)
Projactin-releasing peptide precursor (PrRP) (Prhormone) [Contains: Projactin-releasing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                                                                           EXTL1 OR EXTL.
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Hormone; Amidation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDLINE-98268781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYXXRG1RPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
                                                                                                                                                                                                                                                                                                                          TPD1NPAWYAGRG1RPVGRF
                                                                                                                                                                                                                                                                                                                                                                                               Similarity 90.0
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide PrRP20]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>$</u>
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
 PubMed=9037597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9607765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
22
53
53
53
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Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROLACTIN-RELEASING PEPTIDE PRAMIDATION (G-54 PROVIDE AMIDE 08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROLACTIN-RELEASING
                                                                     Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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PEPTIDE PRRP20.
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RESULT
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Best Local 9
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OPSILLIMPO STANDARD; E
P3536;
P3536;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequate-
16-OCT-2001 (Rel. 40, Last announce tateral eye opsin.
Limulus polyphemus (Atlantic homework)
Eukaryota; Metazoa; Arthropoda;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutations of the l
Chinese.";
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

WHYTS W., Spieker N., Van Roy N., De Paepe A., De Boulle K.,

Willems P.J., Van Hul W., Versteeg R., Speleman F.;

Willems P.J., Van Hul W., Versteeg R., Speleman F.;

"Refined physical mapping and genomic structure of the EXTL1 genum structure of the EXTL1 genum interface (MAY-199) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wise C.A., Clines G.A., Massa N., Trask B.J., Lovett M.; 
*Identification and localization of the gene for EXTL, a third member of the multiple exostoses gene family.*; 
Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-oncogene;
TRANSMEM I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>:</del>
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L; AF08363; AAD02840.1;
L; AF083624; AAD02840.1;
L; AF083625; AAD02840.1;
L; AF083625; AAD02840.1;
L; AF083626; AAD02840.1;
L; AF083627; AAD02840.1;
L; AF083628; AAD02840.1;
L; AF083629; AAD02840.1;
L; AF083631; AAD02840.1;
L; AF083632; AAD02840.1;
L; AF083631; AAD02840.1;
L; AF083632; AAD02840.1;
L; AF083631; AAD02840.1;
L; AF083631; AAD02840.1;
L; AF083632; AAD02840;
L; AF08362; AAD02840;
L; AF08362; AAD02840;
L; AF08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reticulum (By similarity).
SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  TPDINPAWYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pro; IPR004263; Exostosin.
PF03016; Exostosin; 1.
oncogene; Multigene family
MEM IO 30 SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
676
      Metazoa; Arthropoda;
Limulus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family; Transmembrane; Signal-anchor.
   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
   (POTENTIAL).
   N-LINKED (GLCNAC. . .) (POTENTIAL).
3 MW; B5E006A8762E5633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          419
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                     sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46;
Pred. No.
                                                              horseshoe crab)
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                               Chelicerata; Merostomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M1smatches
                                                                                                                                                 update)
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                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L03791; AAA28273.1; -. EMBL; L03781; AAA02498.1; -. PIR; B48197; B48197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMIS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROFEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR000276; GPCR_Rhodpsn.
InterPro: IPR001760; Opsin.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation, G-protein
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[1]
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FUNCTION: VISUAL PIGNENTS ARE THE LIGHT-ABSORBING MOLE MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, LINKED TO CIS-RETINAL.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: LATERAL EYE.

PTM: SOME OR ALL OF THE CARBOXI-TERMINAL SER OR THR R
BE PHOSPHORYLATED (BY SIMILARITY).

BIS PHOSPHORYLATED (BY SIMILARITY).

MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bloinformatics and the EN European Bioinformatics Institute. There are no restructed the control of th
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                                Similarity
     Conservative
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1123
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42139
                                39.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; Transmembrane; Glycoprotein; Vision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL)
Score
Pred.
2: Mis
                                                                                                                                            5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (POTENTIAL)
EXTRACELLULAR
3 (POTENTIAL)
CYTOPLASMIC
4 (POTENTIAL)
EXTRACELLULAR
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1 of the horseshoe
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                                                           Length 376,
                                                                                                                                            . .) (POTENTIAL)
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
Photoreceptor; Retinal protein; Transmer
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    EMBL; L03792; AAA28274.1;
EMBL; L03782; AAA02499.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Limulus polyphemus.";

Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).

-I- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Median oceIIi;
MEDLINE=93317641; PubMed=8327495;
Smith W.C., Price D.A., Greenberg
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Limulidae;
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16-OCT-2001
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SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: OCCLLAR CELLS; MEDIAN OCCLLI.

PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES PERFORMENT OR STATIANTY).

BE PHOSPHORYLATED (BY SIMILARITY).

MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 530 NM.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                       A48197;
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Limulus.
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EXTRACELLULAR.
7 (POTENTIAL).
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N-LINKED (GLCNAC. . .) (P
FA9647C40531CBF8 CRC64;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COISON G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi W., Qin H., Allen R., Knaff D.B.;

"Primary structure of genes encoding light-harvesting and reaction center proteins from Chromatium vinosum.";

Submitted (MAR-1998) to the EMBL/Genbank/DDBJ databases.

-1- FUNCTION: TNE REACTION CENTER OF PURPLE BACTERIA CONTAIN A TIGHTLY BOUND CYTOCHROME DANCE WHICH RE-REDUCES THE PHOTO OXIDIZED PRIMARY ELECTRON DONOR.

-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPÏD ANCHOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no
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P30143;
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                                                                                     ECOGENE; EG11555; yaaj.
Interro; IPR001293; AA_rel_permease_1.
Interro; IPR001463; Na_ala_symp.
Pfam; PF01235; Na_Ala_symp; 1.
PRINTS; PR00175; NAALASMPORT.
                                                                                                                                                                                                                                                                                                                                                                               Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rei. 26,
01-JUL-1993 (Rel. 26,
16-OCT-2001 (Rei. 40,
                                                              PROSITE; PS00873; NA_ALANINE_SYMP;
Hypothetical protein; Transmembrane
                                                                                                                                          EMBL; D10483; -; NOT_ANNOTATED_CDS EMBL; AE000111; AAC73118.1; - ECOGene; EG11555; yaaJ.
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                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coil K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; "Systematic sequencing of the Escherichia coli genome: analysi the 0-2.4 min region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92334977; PubMed-1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; 
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAAJ OR B0007.
Escherichia coli
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                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SODIUM:ALANINE SYMPORTER FAMILY (SAF). STRONG, TO H. INFLUENZAE HI0183.
                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                              Potential).
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7; Conser
                                                  Complete
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iiarity 36.8
Conservative
 141
174
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                                                  proteome.
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161
194
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                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
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                                                                                                                                                                                                                                                                                                                                         Integrai membrane
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Pred. No. 8.8;
3; Mismatches
POTENTIAL.
POTENTIAL.
POTENTIAL.
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96BCD91FF1B9AE7E CRC64;
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                                                                membrane;
                                                                                                                                                                                                                                                                                                                                        protein. Inner membrane
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NRP1_YEAST
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Best Local S
Matches 8
Interpro; IPRO00504; RRM.

Interpro; IPRO01875; 2nf-RanBP.

Pfam; PP00075; rrm; 1.

Pfam; PP00641; zf-RanBP; 2.

SMART; SM00360; RRW; 1.

SMART; SM00367; znF_RB2; 2.

PROSITE; PS01030; RRM; 1.

PROSITE; PS01030; RRM; 1.

PROSITE; PS01030; RRM, NP_1; FALSE_NEG.
PROSITE; PS01039; ZF_RANBP2_1; 2.

PROSITE; PS01099; ZF_RANBP2_2; 2.

Nuclebr protein; Zinc-finger; RNA-binding
                                                                                                                                                EMBL; X68020; CAA48159.1; -.
EMBL; 267750; CAA91579.1; -.
EMBL; 774215; CAA98741.1; -.
PIR; S31139; S31139.
HSSP; P04170; 6RXN.
SGD; S0002336; NRP1.
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SEQUENCE
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                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases -- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS. -- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wehner E.P., Rao E., Brendel M.;

Molecular structure and genetic regulation of SFA,
responsible for resistance to formaldehyde in Sacchi
cerevisiae, and characterization of its protein pro-
mol. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                             or send an
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Pohl T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93247548;
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                                                                                                                                                                                                                                         requires a license agreement (See http://www.lsb-sib.ch/announce/an email to license@isb-sib.ch).
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Pred. No.
    RNA-binding;
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in product.";
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Best Local 5
Matches 5
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Best Local :
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EX7L_STRCO
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ZN_FING
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COMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the EUropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGI ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARTY).

-1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield 5'-phosphomononucleotides.
-1- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PP02601; Exonuc_VII_L; 1.

Pfam; PF01336; tRNA_ant1; 1.

Hydrolase; Nuclease; Exonuclease.

SEQUENCE 402 AA; 43882 MW; 14
                                                                                                                                                       EMBL; AL391754; CAC05901.1; -.
InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR002309; tRNA-synt_2.
                                                                                                                                                                                                                                                                                                                         +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coellcolor.

Bacterla; Firmlcutes; Actinobacterla; Actinobacteridae;
Actinomycetales; Streptomyclneae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuclease VII large subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales;
NCBI_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Exonuclease VII large subunit). XSEA OR SCK7.29c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9F8M3;
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89
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                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE XSEA FAMILY.
PEWYAPRGQLSLRAAEIKPVG
                    PAWYXXRG-----IRPVG
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                                               Similarity
9; Conser
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6; Conserv
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355
581
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                                               Conservative
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610
564
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79299 .
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Pred. No. 16;
3; Mismatches
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RANBP2-TYPE
RANBP2-TYPE
                                                          Score 42;
Pred. No.
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                                                                                                           145929A8372B4E08 CRC64;
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ADA9BC09FD582669
                                             Mlsmatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomycetaceae; Streptomyces
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                                                           DB
13;
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RESULT 12
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Best Local !
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InterPro; IPR000706; AGPR_act_site.
InterPro; IPR000534; Semia1dh_dh.
Pfam; PF01118; Semia1dhyde_dh; 1.
Pfam; PF02774; Semia1dhyde_dh6; I.
ProDom; PD003765; AGPR_act_site; 1.
PROSITE; PS01224; ARGC; 1.
                                                                                                             01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                       Y762_METJA
Q58172;
                                                                                                                                                                                                                                                                                                                                                                        Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome. ACT_SITE 149 149 BY SIMILARITY.
SEQUENCE 345 AA; 38188 MW; 3E9F45DDD9FC6BEA CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as ing as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
STRAIN-C-125 / JCM 9153;
MEDILINE-20512502; PubMed-I1058132;
Takaml H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last amotation update)
N-acety1-gamma-glutamy1-phosphate reductase (
                                                                                 Hypothetical MJ0762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        halodurans and genomic sequence comparison with Bacillus sub-
Nuclelc Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus haiodurans.
Bacteria: Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acety1-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase). ARGC OR BH2900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACHD
SEQUENCE FROM N.A
                                                    Methanococcus jannaschli.
Archaea; Euryarchaeota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entitles requires a ilcense agreement (S or send an email to license@isb-slb.ch).

    -!- PATHWAY: THIRD STEP IN ARGININE BIOSYNTHESIS.
    -!- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fuji F., Hirama C., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Staphylococcus
NCBI_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KBV2;
                         NC8I_TaxID-2190;
                                          Methanococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horikoshi K.;
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat)
protein MJ0762.
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                                                                                                                                                                      STANDARD;
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Pred. No. 14;
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FltzGeraid L.N., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Ovcrboek R., KIrkness E.F., Wainstock K.G., Merrick J.N., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
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                                                               STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999, PubMed+8688087;
Bult C.J., White O., Olsen G.J., Zhou
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Science 27
                                                                                                     SEQUENCE FROM N.A.
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Methanococcus.
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RESULT 14
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P11528;
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MEDLINE-88318927; Put
Singh S., Lowe D.G.,
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01-OCT-1989 (Rel.
16-OCT-2001 (Rel.
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TIGR; MJ0576; -
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between the
the European
                 This SWISS-PROT entry is copyright. It is produced through a collaborative between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                        Nature 334:708-712(1988).
                                                                                                                                                                                                                                            Singh S., Lowe D.G., Thorpe D.S., I
Dangott L.J., Chinkers M., Goeddel
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Echino
Echinoidea; Euechlnoidea;
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Eukaryota, Metazoa, Echinodermata, Eleutherozoa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed
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to protein kinases.";
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Klenk H.-P.,
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                                                             FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON FOR TRESACT A CHENOTACTIC PEPTIDE, AND ON VARIOUS AS A RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphc SUBCELUILAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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SIMILARITY: STRONG, TO
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Fraser C.M., Smith H.O., Woese C.
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G., Thorpe D.S.,
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PIR; S05480; OYURGA.

InterPro; IPR001828; ANF_receptor.

InterPro; IPR0010719; Euk_pkinase.

InterPro; IPR001054; Guanylt_cyclase.

Pfam; PF01034; ANF_receptor; 1.

Pfam; PF00211; guanylate_cyc; 1.

PROSITE; PS50011; PRDTEIN_KINASE_DOM; 1.
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Ol-OCT-1996 (Rel. 34, Created)
Ol-OCT-1996 (Rel. 34, Last sequence update)
Ol-OCT-2096 (Rel. 40, Last annotation update)
Ilypothetical 35.4 kba protein Rv0493c.
RV0493c DR MT0513 DR MT072069.19c.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Corynebacterineae; Mycobacteriaceae; Mycobacteriaceaeae; Mycobacteriaceae;
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SEQUENCE
                 SEQUENCE FROM N.A.

STRAIN-COC 1551 / Dshkosh;

Flelschmann R.D., Alland D., Eisen J.A., Carpenter L., White O

Flelschmann R.D., Nickey

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Naft D., Nickey

Kolonay J.F., Nelson W.C., Umayam L.A., Ermoiaeva M.D., Salzbe

Delcher A., Otterback T., Weldman J., Khouri N., Gill J., Miku
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or send a
                                                                                                                                                             complete genome sequence. Nature 393:537-544(1998).
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NCB1_TaxID-1773;
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EXTRACELLULAR (POTENTIAL).
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SEQUENCE 329 AA; 35427 MW; B
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                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tube laboratory strains.", submitted (APR-2001) to the EMBL/GenBank/DDBJ-!- SIMILARITY: SOME, TO M.LEPRAE B2168_F2_93.
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                                               Similarity 42.9%; Similarity 42.9%; 6; Conservative
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Search completed: September 13, 2002, 09:30:43
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US-08-776-971-64

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                             US-09-105-678A-40
S-09-421-208-40
S-09-105-678A-28
S-09-105-678A-35
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S-09-421-208-47
S-09-105-678A-48
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S-09-105-678A-48
S-09-776-971-52
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393 Appl
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RESULT 1
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Patent No. 6228984
GENERAL INFORMATION:
                      INFORMATION FOR
                                                                                                                                                                             APPLICATION NUMBER: US/08/776.971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DT/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-AWR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-AWR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-AWR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY_AGENT INFORMATION:
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MEDIUM TYPE: D1skette
COMPUTER: 1BM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wil
                                                                NAME: CON1in, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 477
TELECOMMUNICATION IMFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTE:
STREET: 130 Water Street
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SEQUENCE
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STATE: MA
                                              TELEFAX: 617-523-6440
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Fukusumi, Shojl
Kitada, Chleko
OF INVENTION: POLYPROTEINS,
R OF SEQUENCES: 140
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Hosoya, Masaki
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
AVEREEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Datase
16 PYGRF 20
                                                         Local Similarity
Local Similarity
Conserv
                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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les 5; Conserv
                            1 PVGRF 5
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6103882
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                                                                                                                                                                                                        20 amino acids
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Tanaka, Yoko
Nishimura, Osamu
                                                        Conservative
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                                                   93.3%; Score 28; DB
100.0%; Pred. No. 2.1
tive 0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                    DB 3;
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RESULT 4
US-09-105-678A-46
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                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                        Sequence 46, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-TUN-1998
PRIOR APPLICATION DATA: APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON110, DAV1d G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CNARACTERISTICS:
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APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
TITLE OF INVENTION: 52
                                                                                CORRESPONDENCE ADDRESS
                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: F10ppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                            ClTY: Boston
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CITY: Boston
STATE: MA
                                                   STREET:
                                                                ADDRESSEE:
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COUNTRY:
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                                                130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                            DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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RESULT 5
US-08-776-971-8
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REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAC: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/0877697IB Patent No. 6228984 GENERAL INFORMATION:
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Uest Local Similarity
Matches 5; Conserv
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLIID, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ref. CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1995
FILING DATE: 28-DEC-1995
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I PVGRF 5
                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                       Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: KA
                                                                                                                                                                                                                                                                         COUNTRY: USA
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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I00.0%; Pred. No.
tive 0; Mismatc
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2.8;
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Query Match
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GENERAL INFORMATION:
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TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,97IB
FILING DATE: 06-Feb-1997.
CLASSIFICATION: <UNKnown>
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                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JF 7/343371
FILING DATE: 28-DEC-1995
FILING DATE: 28-DEC-1995
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REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 8/246573

RILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAVId G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukusuni, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                 APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
APPLICATION NUMBER: JP 8/211805
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Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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Habata, Yugo
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RESULT 7
US-08-776-971-64
US-08-776-971-64
Sequence 64, Application
Patent NO. 6228984
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/776,97IB
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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ATTORNEY/AGENT
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CON111, David G.
REGISTRATION NUMBER: 27,0:
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVGRF 20
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       APPLICATION NUMBER: PCT/JP96/03821
PILLING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILLING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILLING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILLING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILLING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08776971B
6228984
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5; Conserv
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ZIP: 02109
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Habata, Yugo
Kawamata, Yuji
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Fujii, Ryo
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Pred. No.
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MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-776-971-64
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GENERAL INFORMATION:
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Best Local
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nes 5; Conserv
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TELECOMMUNICATION INFORMATION:
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                                                              ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND DSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ninuma, Shuji
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                                                                                                            APPLICATION NUMBER: PCT/JP96/0382I FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
          NAME: Conlin, David G. REGISTRATION NUMBER: 27, REPERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                              APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEN:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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llarity IOO.0%; Pred. No. 2.
Conservative 0; Nismatches
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Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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; MOLECULE TYPE:
US-09-421-208-34
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US-09-421-208-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 517-523-6440 INFORMATION FOR SEO ID NO: 98: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUM-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                         NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
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mea 5; Conserv
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ZIP: 02109
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   I PVGRF 5
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amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
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130 Water Street
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Tanaka, Yoko
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100.0%; Pr
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                         93.3%; Score 28;
100.0%; Pred. Mo.
tive 0; Mismatc!
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pred. No. 2.8
matches
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                            Mismatches
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2.8;
                                       DB 4; Length 20; 2.8;
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US-09-421-208-40
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                                                                                                            Patent No.
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Sequence 46, Application US/09421208 Patent No. 625856I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/ACENT INFORMATION:
NAME: Conlin, David G.
REGISTRATIOM NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-523-34
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Mariya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: MEHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/421,208
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
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OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%;
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INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
FRIGTH: 20 amino acids
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                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                         APPLICATION NUMBER: US/0:
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE - CORRESSEE - CORRESSE - COR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, yoko
APPLICANT: Nishimura. Osa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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ATTORNEY/AGENT INFORMATION:
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STREET:
STREET:
41
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PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PVGRF 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DQS
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STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                02109
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I00.0%; Pr
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                                                                                                  US/09/105,678A
JP 172118/1997
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RESULT 13
US-09-105-678A-35
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Best Local Similarity 100.
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/09105678A Patent No. 6103882
          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLID. DAVID G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #I.30
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suc..., Takeo
APPLICANT: Horiya, Takeo
APPLICANT: Tanaka, Yoko
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APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 1992 LIGAND
NUMBER OF SEQUENCES: 52
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
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STANDENNESS:
TOPOLOGY
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ATTORNEY/AGENT INFORMATION:
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16 PVGRF 20
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CITY: Boston
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
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                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                 130 Water Street
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21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Masato
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TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-35
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                                                                                                                                    STRANDEDNESS:
TOPOLOGY: linear
HOLECULE TYPE: peptide
US-09-105-678A-41
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIGR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLITE DATA:
                                               Ouery Match 93.3%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 2. Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 41, Application US/09105678A Patent No. 6103882
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Best Local Similarity 100.0%; Pred. No.
Matches 5; Conservative 0; Mismatci
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TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
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LENGTH: 21 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                              NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
1 PVGRF 5
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Tanaka, Yoko
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2.9;
                                                                                 DB 3; Length 21;
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RESULT 15
US-09-105-678A-47
Sequence 47, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
Search completed: September 13, 2002, 09:20:57 Job time: 622 sec
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                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-47
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PILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, Dav1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                   Best Local Similarity Matches 5; Conserva
                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440
INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DC SOFTWARE: Patentin ReleCURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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ADDRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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                                                                                         16 PVGRF 20
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                                                                                                                                                                93.3%; Score 28; DB 3; ilarity 100.0%; Pred. No. 2.9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0, Version #1.30
                                                                                                                                                                                                       Length 21;
                                                                                                                                                                   Indels
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Title:
Perfect score:
Sequence:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                 Total number of hits satisfying chosen parameters:
                                                                                     Searched:
                                                                                                                                       Scoring table:
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                                                                                     96089334 residues
                                                                                                                       Gapext 0.5
                                                                                                                                                                                                                                                                             2002, 09:23:58;
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(without alignments)
3.901 Million cell updates/se
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PIR\_71:\*
1: pir1:\*
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Database

Post-processing: Minimum Match
Maximum Match

Maximum Match 100% Listing first 45 su

summaries

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	L U	12	11	10	· w	· œ	7	o	ហ	4	Ç.	N	· -	Result
28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	Score
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Query Match Best Local Similarity

93.3%;

Score 28; Pred. No.

36; 2

Length 154;

45	44	43	42	41	40	39	38	37	36	G	34	w w	ω 23	31	30	
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probable membrane	dehydrogenase Atu3	L-iditolsorbitol d	MotA/TolQ/ExbB pro	hypothetical prote	NADH dehydrogenase	_	hypothetical prote		zonadhesin - pig	natriuretic peptid	guanylyl cyclase A	natriuretic peptid	atrial natriuretic	membrane glycosylt	periplasmic glucan	

## ALIGNMENTS

prolactin-releasing peptide - rat C:Species: Rattus norvegicus (Norway rat) C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C:Accession: JC7607

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RESULT
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A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Accession: JC7607
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A; Residues: 1-83 </ANA
A; Cross-references: DDBJ: AB040612; DDBJ: AB040613
C; Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.
 A;Gene:
                           A;Cross-references: EMBL:AL021530; PIDN:CAA16482.1; GSPDB:GN00070; SCOEDB:SC2E9.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: PTRP
A;Introns: 33/1
                                                                A; Molecule type: DNA
A; Residues: 1-154 <OLI>
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Best Local Similarity 100
Matches 5; Conservative
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SCOEDB:SC2E9.14
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0; Mismatches
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hypothetical protein B4 [imported] C;Species: human herpesvirus 6 A;Variety: strain Z29 C;Date: 21-Jan-2000 #sequence_revis
                                                                      RESULT
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DNA Res. 3, 109-136, 1996
A;Title: Sequence
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                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S74322;
A; Accession: S76779
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protain - Synechocystis sp. (strain PCC 6803)
(/Specias: Synechocystis sp.
A;Varlety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Dct-1999
C;Accession: S76779
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A;Accession: S76067
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <KAN>
A;Residues: 1-170 <KAN>
A;Cross-references: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10045.1; PID:d101069
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Residucs: 1-173 <KAN>
A;Residucs: 1-173 <KAN>
A;Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18691.1; PID:d10194:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Dct-1999
C;Accession: S76067
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; }
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; }
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Takeuchi, C.; Wada, T.; Watanabe,
                                                                                                                                                                                                            0
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Pred. No.
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da, M.; Yasud
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Science 274, ____
A; Authors: Yoo, H.; Tao, Y.; Drunn, Ster, E.W.
A;Title: The Genome of the Natural
A;Title: The Genome of AB2577; PMID:17
                                                                                                                       C;Accession: AI2990
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Glilet, W.; Grant, C.; Guenthmer, D.; Kutyavin, T.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                       RESULT 7
3.0x0acyi-(acyl-carrier-protein) reductase [imported] - Agrobacterium tumefactens
C.Species: Agrobacterium tumefaciens
C.Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Gene: AGR_L_2601
A/Map position: iinear chromosome
C/Superfamily: ribitol dehydrogenase;
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-246 <KUF
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R;Dominguez, G; Dambaugh, T.R.; Stamey, F.R.;
J. Viroi. 73, 8040-8052, 1999
A;Tltle: Human herpesvirus 6B genome sequence:
A;Reference number: Z22734, MUID:99412318
A;Accession: T44148
A;Status: preliminary; transiated from GB/EMBL/
A;Molecule type: DNA
A;Molecule type: DNA
                                             A; Reference number: A; Accession: AI2990
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A;Accession: H98292
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3-oxoacyi-(acyi-carrier-protein) reductase VC202i [Imported] - Agrobacterium C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: H98292
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A; Cross : references: EMBL: AF157
A; Experimental source: strain
C; Genetics:
A; Note: B4
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A; Residues: 1-246 < XUR>
A; Cross-references: GB:
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A; Title: Genome Sequence of the Plant Pa
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ce: strain 229;
                                                                                                        Y.; Biddle,
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PMID:11743193
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variant B
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T.; Levy, R.; L1, )
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Nature 406, 959-964, 2000
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A; Accession: FB3104
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hypothetical protein Rv0712 - Mycobacterium tuberculosis (strain H37RV) C:Species: Mycobacterium tuberculosis C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T36846
R;Ollver, K.; Harris, D.; Parkhill, J.; Barrell, B. submitted to the EMBL Data Library, September 1998 A;Reference number: Z21615
A;Accession: T36846
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable dehydrogenase - Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Date: 03-Dec-1999 *sequence_revision 03-Dec-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
T36846
                                                                                                                                                                                                                                                                             A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana A; Reference number: A84420; MUID: 20083487 A; Accession: F84922
                                                                                                                                                                                                                                                                                                                                R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VenAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-260 <OLI>
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-294 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: F84922
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                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                                                       Gene: At2g48040
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Matches
                                                                                   Query Match
Best Local
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Best Local
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Pred. No.
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September 1998
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#text\_change 22-Oct-1999

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cobalamin blosynthesis protein [imported] - Bacillus megaterium (Species: Bacillus megaterium C;Species: Bacillus megaterium C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T44687 R;Raux; E.; Lanols, A.; Warren, M.J.; Rambach, A.; Thermes, C. Blochem. J. 335, 159-166, 1998 A;Reference number: Z2829; MUID:98416126 A;Reference number: Z2829; MUID:98416126 A;Accession: T44687
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C;Superfamily: Conserved hypothetical protein MJ1225; CBS homology
C;Keywords: duplication
F;13-61/Domain: CBS homology <CBS1>
F;92-140/Domain: CBS homology <CBS2>
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A;Authors: Sqares, R.: Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: C70643
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                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-367 <RAU>
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A; Residues: 1-300 < KJE>
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A: Accession: S08244
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R:Coie, S.T.; Brosc
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     :Cross-references:
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EMBL:AJ000758; NID:g3724036; PIDN:CAA04311.1; PID:g3724042
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Search completed: September 13, Job time: 773 sec

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3 Ketoacyi-CoA thiolase (fadA-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05:Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Jun-1999
C:Accession: D69399
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, Q.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne. J.D.; Weidman, J.F.: McDonaid, L.
Nature 390. 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.: Sykes,
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.: Sykes,
A:Authors: Utterback, T.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Artic: The complete genome sequence of the hyperthermophilic, suifate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: D69399
A:Accession: DA3
A:
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A; Note: cbin
C; Superfamily: Methanobacterium cobal
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

Run

September 13, 2002, 09:30:43; Search time 80.21 Seconds (without alignments)
3.379 Million cell updates/sec

Title: Perfect score: US-09-446-543A-73\_COPY\_16\_22 30 1 PVGRFXX 7

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number Of hits satisfying chosen parameters: 105224

Minimum DB Maximum DB seq length: 0 length: 2000000000

POst-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database SwigsProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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PINE_ECOLI	IGF2_PIG	IGF2_RAT	IGF2_MOUSE	IGF2_HUMAN	IGF2_SHEEP	RL22_AERPE	IGF2_BOVIN	Y17K_BPP4	RL3_PIG	IGE2_MUSVI	IGF2_CAVPO	SP3E_BACSU	PCAF_PSEPU	DCUP_AQUAE	OPT_HUMAH	LINC_PSEPA	NUE2_RHIME	YP15_STAAU	ZAN_PIG	AHPA_HUMAN	AHPA_RAT	AHPA_MOUSE	MDOH_ECOLI	CATA_BRARE		AR73_HUMAN	AR72_HUMAN	YR33_THEPE	Y4AD_RHISN	PRRP_BOVIN	PRRP_HUMAN	PRRP_RAT	ID
P03014 escherichia		ratt	5 mus m	P01344 homo sapien	4	Q9yf76 aeropyrum p	o	4 bact	Q29293 sus scrofa	4 mustel		P21458 bacillus su	051956 pseudomonas	aquit		pseudomona	н	ъ	ene:	homo s	P18910 rattus norv		P33137 escherichia	brachydani	3 rhizo	4 homo	œ	9 thermofilu	1 rhiz	54 bos 1	1277 homo sa		Description

# ALIGNMEHTS

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PREPLAY  STANDARD: PREP: 83 AA.  DE PREP: ANY  STANDARD: PREP: 83 AA.  RC 981278;  30 -MAY-2000 (Rel. 39, Created)  DY 30 -MAY-2000 (Rel. 41, Last annotation updates; Profactin-releasing peptide in the Sekiguchi M., Katada C., Kasumata Y., Hosoya M., Eukusumi S., Ratida C., Kasumata Y., Habata Y., Yayin Y., Habata Y., Habata Y., Habata Y., Habata Y., Habata Y., Habata Y., Yayin	

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PRRP_HUMAN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                       PEPTIDE
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[2]
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Fujii R., Fukusumi S.
Sekiguchi M., Kitada
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Mammalia; Eutheria;
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49 PVGRF
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les 5; Conserv
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FINCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May stitactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: MEDULIA OBLONGATA AND HYPOTHALAMUS.
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Fuku9umi S., Hom
Ritada C., I
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.., Kurokawa
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Pred. No.
                                                             Score 28;
Pred. No
                                                                                                           BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GRODP

229A2F3F50CF981B CRC64;
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                                                 Mismatches
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T., Nishimura
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6.3;
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Sekiguchi M.,
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a O., Qnda H.,
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RESULT 4
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Matches 5; Conserv
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- BOVIN

- PRIP BOVIN

- PRISON

- PRIS
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P55351;
01-NOV-1997
01-NOV-1997
15-JDL-1998
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PEPTIDE
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MOD_RES
SEQUENCE
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Kitada C., Masuo Y., Asano T., Matsumoto H., S.
Kurokawa T., Nishimura O., Onda H., Fujino M.,
"A projactin-releasing peptide in the brain.";
Nature 393:272-276(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB015417; BAA29025.1; -.
Hormone; Amidation; Signal; Cleavage on Signal; Cleavage on 2 2 PROLACTIN-R PEPTIDE 23 53 PROLACTIN-R PEPTIDE 33 53 AMIDATION (
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                                                                Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
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Bovidae; Bovinae; Bos.
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          releasing peptide PrRP20].
SEQUENCE FROM N.A.
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TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                      PVGRE
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sym pNGR234a
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100.0%; Pr
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Pred. No.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP
OBAC35A13B0FA908 CRC64;
                                                                                                                                                                                    Y4AD
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Sekiguchi M.,
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                                                      PIR; S08244; S08244.
InterPro: IPR000644; CBS.
Pfam; PF00571; CBS; 4.
SMART: SM00116; CBS; 4.
Hypothetical protein; Repeat; C
DOMAIN B 61 CE
                                                                                                                                                                                                                                                                              STRAIN-NV3 / DSM 2475:
Kjems J., Leffers H., Olesen T., Ingelore
Sequence, organisation and transcription
and the downstream tRNA and protein genes
Thermofilum pendens.":
Syst. Appl. Microbiol. 13:117-127(1990).
-i- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rei. 14, Created)
01-APR-1990 (Rei. 14, Last sequence update)
16-OCT-2001 (Rei. 40, Last annotation update)
Hypothetical 33.4 kDa protein in ribosomal RNA operon.
Thormofilum pendens.
Archaea; Crenarchaeota: Thermoprotesies; Thermofiliace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97305956; PubMed=9163424:
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenth Ferret X.;
Perret X.;
"Molecular basis of symbiosis between Rhizobium and legumes."
Nature 387:394-401(1997).
-1- FUNCTION: PRODABLY PART OF AN OPERON Y4AABCD INVOLVED IN SYNTHESIS OF AN ISOPRENOID COMPOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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                                                                                                                                                                                                          This SWISS-PRDT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Dioinformatics Institute. There are no restrictions use by non-profit institutions as iong as its content is in
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 SEQUENCE
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              DOMAIN
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P15889:
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ilarity 100.0%:
Conservative
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140
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276
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RESULT 6
AR72_HUMAN
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Matches 5
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                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2000) to the EMBL/GenBank/DdbJ databases.
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
-INFOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINGEN:
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDENYDE
             Oxidoreductase.
ACT_SITE 112
CONFLICT 113
                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (see http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Praml C., Savelyeva L., Perri P., Schwab M.; "Cloning of the human aflatoxin Bl-aldehyde reductase gene 1p36.1 in a region frequently altered in human tumor ceils. Cancer Res. 58:5014-5018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ireland L.S., Harrison D.J., Neai G.E., Hayes J.D.;
"Molecular cloning, expression and catalytic activity of a human ARR7
member of the aldo-keto reduces superfamily: evidence that the
major 2-carboxybenzaidehyde reductase from human liver is a homologue
of rat aflatoxin B1-aldehyde reductase.";
Blochem. J. 332:21-34(1998).
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16-OCT-2001 (Rel. 40, Last annotation update)
Afiatoxin Bi aldehyde reductase 1 (EC 1.-.-.) (AFB1-AR (Aldoketoreductase 7).
AKR7A2 OR AFR OR AKR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini: Nominidae; Nomo.
                                                                                               EMBL; Y16675: CAA76347.1; -.
                                                                                                                         EMBL; AF026947; AAC52104.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
MEDLINE-99040634: PubMed-9823300;
                                                        Pfam;
                                                                    MIM; 603418:
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                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYtoplasmic.
SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                         REDUCTASE
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                                                     PF00248; aldo_ket_red;
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Pred. No.
          HYDROGEN-BOND DONOR (PROBABLE).
A -> T (IN REF. 1).
3BBFB7ED0CAF4D54 CRC64
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AR73. HUMAN STANDARD,
AR73. HUMAN STANDARD,
O95154; Q9NUC3;
16-OCT-2001 (Re1. 40, Crested)
16-OCT-2001 (Re1. 40, Last sequence update)
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16-OCT-2001 (Re1. 40, Last annotation updste)
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CONFLICT
SEQUENCE
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or send a
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EMBL; AL035413; CAB72322.1: -.
INTERPO: | IPR001195; Aldo_ket_red
Pfam; PF00248; aldo_ket_red; I.
                                                                                                                                                                                                                                                                                                                                                                                                    between the Swlss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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Msmmaiia; Eutheria;
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FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHYDRODIOL BY FORMING NONBIHDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
EFFECTS OF AFLATOXIN B1.
SUBCELLULAR LOCATION: CYtoplasmic.
SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
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331 AA;
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Pred. No.
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E -> D (IN REF. 1).
V -> M (1H REF. 1).
A -> ADGSPEGCGSFWGTLGPGADCCFPS
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Catarrhini;
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-> A (IN REF. 1).
B9C32C33C7102AB3 CRC64;
                                                   ore 28; DB;
red. No. 25;
Mismatches
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i; Hominidae; Homo.
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P58393;
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56 PYGRE
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Eukaryota; Metazoa: Chordats: Craniata; Veri
Acthopterygii; Heopterygii; Teleostei; Eut
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by snd for commercial entities requires a license agreement (See http://www.isb-shb.ch/announce/or send sn email to license@isb-shb.ch).
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GIGA1 OR RO2B46 OR SMC03924.
Rhizobium meiiloti (Sinorhizobium meiiloti).
Bacteria; Proteobacteria; aipha subdivision;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
BLND1HG 15
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5; Conserv
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MDOH OR B1049 OR 21684 OR ECS1427.
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InterPro; IPR002226; Catalase.
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sequence analysis
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ALMOST ALL AEROBIC
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.O.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kitkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Milier L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome **Sarrances**
                                                                                                                                                                                                                                                                            Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishil K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Y Ilda T., Takami H., Honda T., Sasakawa C., Ogasawara H., Y Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia D157:H7 and genomic comparison with a laboratory strain K-DHA Res. 8:11-22(2001).

DHA RES. 8:11-22(2001).

COULO BE A GLUCOSYL TRANSFERASE OR SIMPLY A SUBUHIT OF
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kashimoto K.
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito
Sampel G., Seki Y., Tagami N., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Noriuchi T.;
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Bacteria, Proteobacteria,
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MEDLINE-21156231; PubMed-11258796;
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"A 718-kb DHA sequence of the Escherichia corresponding to the 12.7-28.0 min region
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MEDLINE-97426617; PubMed-9278503;
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Nature 409:529-533(2001).
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                     SWISS-PROT entry is copyright. It is produced through a collab
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InterPro: 1PR001173: Glycos_transf_2:
Pfam: Pr00535; Glycos_transf_2: 1.
Transmembrane: Inner membrane: Transf
                                                             Pandey K.N., Sligh S.:
"Molecular cloning and expression of murine natriuretle factor receptor cDNA.";
J. Biol. Chem. 265:12342-12348(1990).
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MEDLINE-90324219; PubMed-1973687;
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Rodentla;
                                                                                                                                                                                                                                                                                                                                                                                                                                             93.3%; br
100.0%; Prr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    license agreement (See http://www.lsb-sib.ch/announce/
license@isb-sib.ch).
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  for three species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28;
Pred. No.
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CYTOPLASMIC.
POTENTIAL.
PERIPLASMIC.
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PERIPLASMIC.
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PERIPLASMIC.
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CYTOPLASMIC.
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P -> L (IN REF. 1).
; 7DCAF93640180944 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERIPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC.
                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathl; Murldae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  M1smatches
  Burnicr J.P., Lowe D.G.; cies of natriuretic pepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                         guanylate cyclase/atriai
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  EMBL; J05504; AAA37670.1; ..

EMBL; L31932; AAA66945.1; ..

P1R; A36568; CYMSAR.

P1R; A3088; A33088; A1988; HSSP, 002846; 1AWL.

MGD; MG1:97371; NPT1.

InterPro; 1PR001170; ANF_receptor.

InterPro; 1PR001828; ANF_receptor.

InterPro; 1PR001054; EWL_DKIMASE.

InterPro; IPR001054; Guannylt_cyclase.

Pfam; PF01094; ANF_receptor; 1.

Pfam; PF00069; pkinase; 1.

Pfam; PF00069; pkinase; 1.

PRINTS; PR00255; NATPEPTIDER.

SMART; SM00044; CYCG; 1.
 CARBOHYD
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COMPLICT
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SMART; SM00044; CYCG; 1.
PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50015; GUANYLATE_CYCLASES_2;
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
BY SIMILARITY
BY SIMILARITY
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FECEPLOY-A.\*;

MOI. PHAITMACCI. 47:172-180(1995).

MOI. PHAITMACCI. 47:172-180(1995).

MOI. PHAITMACCI. 47:172-180 (1995).

POINTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANF.

CYCLASE ACTIVITY ON BINDING OF ANF.

SUBCELLIAHAR LOCATION: Type I membrane protesin.

MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO HITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE

ANP RECEPTORS: TWO
-B) AND ONE (ANP-C)
E OF ANP FROM THE

SIMILARITY: CONTAINS I PROTEIN KINASE-LIKE DOMAIN.

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Glycoprotein; Phosphorylation; Lyase;

N-LINKED (GLCNAC...) (
N-LINKED (BLCNAC...) ( ATRIAL NATRIURETIC PEPTIDE EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE). GUANYLATE CYCLASE PROTEIN KINASE-LIKE. (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL)

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RESULT 1
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         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDIJAN-91352095; PubMed-1679239;

MEDIJAN-91352095; PubMed-1679239;

Duda T., Goraczniak R.M., Sharma R.K.;

"Site-directed mutational analysis of a membrane guanylate c
cDNA reveals the atrial natriuretic factor signaling site.";

Proc. Natl. Acad. Sci. U.S.A. 88:7882-7886(1991).

PROC. NATLACAL NATRIURETIC PEPTIDE. HAS G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chinkers M., Garbers D.L., Chang M.S., Goeddei D.v., Schulz S.,
"A membrane form of guanylate Cyclase peptide receptor.";
Nature 338:78-83(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANPA_RAT
P18910;
                                                                                                                                                                     CYCLASE ACTIVITY ON BINDING OF ANE:

- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
- I- SUBCELLULAR LOCATION: Type I membrane protein.
- II- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: THE GLANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-MICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM THE WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
- IS IMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
- I- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE-91056089; PubMed-1978722;
Yamaguchi M., Rutledge L.J., Garbers D.L.;
"The primary structure of the rat guanylyl
natriretic peptide receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxiD=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (Rei. 16, Created)
01-NOV-1990 (Rei. 16, Last sequence update)
16-OCT-2001 (Rei. 40, Last annotation update)
Atriai natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.I.2) (NPR-A) (Atrial natriuretic peptide
                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EV
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MEDLINE-89143770; PubMed-2563900;
Chinkers M., Garbers D.L., Chang M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bioi. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A-type receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
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53A544FB2C8EF253 CRC64;
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                                                                                                                                                                       CYCLASE CLASS-4/GUANYLYL CYCLASE
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EMBL; J05677; AAA41200.1;
EMBL; M74535; AAA41202.1;
PIR; S03348; OYMTR.
HSSP; Q02846; LAWL
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CONFLICT
SEQUENCE
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CARBOHYD
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DOMAIN
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OI-APR-1990 (Rei. 14, Last sequence update)
OI-MAR-2002 (Rei. 14, Last sequence update)
OI-MAR-2002 (Rei. 14, Last sequence update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
A-type receptor).
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Interpro; IPR001828; ANF_receptor.
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR001054; Guanyit_cyclase.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF00211; guanylate_cyc; 1.
                  TISSUE-Kidney;
MEDLINE-89356605; PubMed-2569967;
Lowe D.G., Chang M.S., Hellmiss R.,
Goeddel D.V.;
                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; /
                                                                                                                                                                                                                                                                                                                                  PI6066;
0I-APR-1990
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PROSITE; PS00453; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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PRINTS; PR00255; NATPEPTIDER.
SMART; SM00044; CYCC; 1.
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Human atriai natriuretic peptide receptor defines
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114
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100.0%; Pr
                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteieostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No.
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CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE-LIKE.
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BY SIMILARITY
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-> P (IN REF. 3).
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Mismatches
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                                    Chen E.,
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    Phosphoryiation;

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a new paradigm for
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(POTENTIAL).
(POTENTIAL).
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                                    Garbers D.L.,
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This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Dsage by and for commodified and this statement is not removed.
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                                                                                                                EMBL, 
                                                        HSSP;
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1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. NAS GDANYLATE

CYCLASE ACTIVITY ON ENDOING OF ANF.

-1- CATALYTIC ACTIVITY: GTP - 3',5'-cyclic GMP + diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pardhasaradhi K., Kutty R.K., Gentieman S., 
"Expression of mRNA for atrial natriuretic 
cyclase (ANPRA) in human retina."; 
Celi. Mol. Neurobiol. 14:1-7(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maeda N., Andware v.T., "Identification of functional polymorphisms in noncoding the human natriuretic peptide receptor A gene."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takahashi Y., Nakayama T., Soma M., Izumi Y., Kanmatsuse K.; "Organization of the human natriuretic peptide receptor A gene."; Blochem. Biophys. Res. Commun. 246:736-739(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send
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MEDLINE-95042574; PubMed-7954658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a
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                                                                                                    SU, ABO10482; BAA31199.I

LL; ABO10483; BAA31199.I

SU; ABO10484; BAA31199.I

SU; ABO10485; BAA31199.I

SU; ABO10486; BAA31199.I

LL; ABO10486; BAA31199.I

SU; ABO10489; BAA31199.I

SU; ABO10489; BAA31199.I

SU; ABO10490; BAA31199.I

SU; ABO10490; BAA31199.I

SU; SO1459; OXPHAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOOS: TNERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO MITH GUANYLATE CYCLASE ACTIVITY (AND-A AND AND-B) AND ONE (AND-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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AB010491; BAA3119,
AB010471; BAA3119,
AB010471; BAA3119,
AB010472; BAA3119,
AB010473; BAA3119,
AB010474; BAA3119,
AB010475; BAA3119,
AB010475; BAA3119,
AB010477; BAA3119,
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AB010479;
AB010480;
AB010481;
                                                                               Q02846; 1AWL.
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. 8:1377-1384(1989).
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an email to license@isb-sib.ch)
  IPR001170;
IPR001828;
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ANF_receptor.
ANF_receptor
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Pfam; PF00021; guanylate_cyc; 1.
Pfam; PF00069; pkinase; I.
PRINTS; PR00255; NATPEPTIDER.
SMART; SM00044; CYCG; 1.
PROSITE; PS00459; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS0015; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS0015; GUANYLATE_CYCLASES_2; 1.
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Q28983;
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DOMAIN
-(- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNE
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOC
SIGNALING.
-(- SUBDATT: PROBABLY FORMS COVALENT OLIGOMERS.
-(- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTE
APICAL REGION OF THE SPERM HEAD (BY SIMILAN
                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890; 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1658-1667; 1777-1795 AND 1914-1921.
STRAIN-MEISHAN: TISSUE-Testis; MEDLINE-96064658; PubMed-7592795;
                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9823;
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                                                                     "A sperm membrane protein that binds the egg extracellular matrix is homor factor.";
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5; Conserv
                                       Chem. 270:26025-26028(1995).
TION: BINDS IN A SPECIES-SPECIFIC
NE EGG. MAY BE INVOLVED IN GAMETE
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IPR001054; Guanylt_cyclase.
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100.0%; Pr
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Cetartiodactyla; Suina; Suidae;
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INTERCNAIN (PROBABLE).
N-LINKED (GLCNAC...)
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EXTRACELLLAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE-LIKE.
GUANYLATE CYCLASE.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No.
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  I MEMBRANE PROTEIN,
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Togous to von Willebrand
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                                         MANNER TO THE RECOGNITION
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AND/OR
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InterPro: IPRO00561; EGF-11ke.
InterPro: IPRO00998; MAM.
InterPro: IPRO00998; TIL.
InterPro: IPRO0328: TILA.
InterPro: IPRO0328: TILA.
InterPro: IPRO01007; VWFC.
InterPro: IPRO01007; VWFC.
InterPro: IPRO01007; VWFC.
InterPro: IPRO01046; VWG.
Pfam; PF00629; MAM; 2.
Pfam; PF00629; MAM; 2.
Pfam; PF00629; TILA; 5.
Pfam; PF00629; TILA; 5.
Pfam; PF0094; VWG; 4.
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
SMART; SM00216; VWC; 2.
SMART; SM00216; VWC; 2.
SMART; SM00216; VWC; 2.
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PRDSITE; PS011B6: E
PRDSITE; PS00740: N
PROSITE; PS0060: N
Signal: Giycoproted
Repeat.
SIGNAL 1
SIGNAL 1
CHAIN 30
DOMAIN 2419
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ID DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESIDN TO THE ZDNA PELLUCIDA.

ID DOMAIN: DURING SPERN MIGRATION THRDUGH THE REPRODUCTIVE TRACTS, THE MUCCIN-LIKE DDMAIN MIGHT INHIBIT INAPPRDPRIATE TRAPPING DF SPERMATOZDA DR PROMDTING ADHESIDN TO THE OVIDUCTAL ISTEMUS.

ID DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT DLIGOMERIZATIOH (BY SIMILARITY TO HUMAN INTESTINAL MUCI).

IPTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZDHADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX. PROCESSING MIGHT OCCUR DURING SPERM MATBRATIDN AND/OR CAPACITATION.

IS SIMILARITY: CONTAINS 2 MAM DOMAINS.

IS SIMILARITY: CONTAINS 1 EGF-LIKE DOMAINS.
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DOMAIN
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EGF_2:
MAM_1:
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GUCIN-LIKE DDMAIN).

VWFD 1 (PARTIAL).

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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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EXTRACELLULAR
PDTENTIAL.
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                                                                                                           EMBL; X13290;
PIR: S04165;
Hypothetical
SEQUENCE 14
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDILINE-89343620; PubMed-2548057;

ROUCH D.A., Messeroti L.J., Loo L.S.L., Jackson C.A., Skurray R.A.:

"Trimethoprim resistance transposon Tn4003 from Staphylococcus auree encodes genes for a dihydrofolate reductase and thymidylate synthetase flanked by three copies of IS257.";

MOI. Microbiol. 3:161-175(1989).

-1- SIMILARITY: TD B.SUBTILIS DEGV.
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PI3977;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
01-FEB-1995 (Rel. 31, Last annotation
Hypothetical 15.5 kDa protein.
Staphylococcus aureus.
                                                                                                                                                                       This SWISS-PRDT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/Bannounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes: Bacilius/Clostridium group, Bacilius/Staphylococcus group; Staphylococcus. NCBI_TaxID-1280;
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S-> K (IN REF. 1: AA SEQUENCE).
S-> K (IN REF. 1: AA SEQUENCE).
S-> K (IN REF. 1: AA SEQUENCE).
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Search completed: September 13, 2002, 09:30:44

Job time: 1134 sec

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Perfect score:
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Post-processing: Minlmum Match 0% Maxlmum Match 100% Listing first 45 s Maximum summarles

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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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14	28	93.3	258	H	Q921C1	Q921cl mus muscul
15	28	93.3	260	N	88068	O88068 streptomyce
16	28	93.3	294	N	006001	

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1 PYGRF 5 ||||| 18 PYGRF 22

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Gaps

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### ALIGNMENTS

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SOURCE RESERVE OF CONTRACT OF 
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MEDILINE-98155132; PubMed-9495744:

Eulberg D., Lakner S., Golovleva L.A., Schlomann M.;

Characterization of a protocatechuate catabolic gene cluster from Rhodococcus opacus ICP: evidence for a merged enzyme with 4-carboxymuconolactone-decarboxylating and 3-oxoadipate enol-lactone-hydrolyzing activity.",

J. Bacteriol. 180:1072-1081(1998).

EMBL; AP003947; AAC38248.1; -.

HSSP; PF00108: thiolase.

Piam: PF00108: thiolase.
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067984;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3-OXOADIPYL COA THIOLASE HOMOLOG (EC 2.3.1.) (FRAGMENT).
Transferase; Acyltransferase.
NON_TER 106 106
SEQUENCE 106 AA; 10856 MW;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardlaceae; Rhodococcus.
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     10856 MW;
     7C0A24EDE86E9C2F CRC64;
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RESULT
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Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
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054139,
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF365406: AAK60139.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
YIP3-LIKE PROTEIN (FRAGMENT).
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STRAIN-B207;
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NCBI_TaxID=5476;
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HYPOTHETICAL
SC2E9.14.
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Q922Z1;
Q1-DEC-2001 (TIEMBLIE1. 19, Created)
Q1-DEC-2001 (TIEMBLIE1. 19, Last sequence update)
Q1-DEC-2001 (TIEMBLIE1. 19, Last annotation update)
SIMILAR TO HYPOTHETICAL PROTEIN FROM CLONE 24796.
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Streptomyces coelicolor.
Bacteria: Firmicutes; Actinobacteria; Actinobacterida
Bacteria: Firmicutes; Actinobacteria; Actinobacterida
                                                                                                                                                                                                                                                                                           Strausberg R.;
SEMBL; BC006689; AAH066891; -.
SEQUENCE 161 AA; 17643 MW;
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL021530; CAA16482.1; -.
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Parkhill J., Barrell
Submitted (JAN-1998)
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Mammalia; Eutheria;
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Submitted (JAN-1998)
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01-NOV-1996
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"Sequence analysis of the genome of the unicellular cyanobacterlum Synechocystis sp. strain PCC6803. I. Sequence features in the 1 mb region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).
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                                                          "Sequence analysis of the genome of the unicellular cyanobacterium Syncchocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions." DNA Res. 3:109-136(1996).
                                                                                                                                                                                                               Kaneko T., Sato S., Kotani H., Tanaka A., Agamiz
Miyajima N., Nirosawa M., Sugiura M., Sasamoto S.
Nosouchi T., Mateuno A., Muraki A., Nakazaki N.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yan
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ori Y., Ota T., Suzuki
T., Nakamura Y.,
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Nosouchi T., Matsuno A., Muraki A., Nakazaki N.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yam
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Hypothetical protein; Complete proteome.
SEQUENCE 173 AA; 20509 MW; 2E2414F099C882F7 CRC64;
"Numan herpesvirus 68 genome with human herpesvirus 6A.";
J. Virol. 73:8040-8052(1999).
EMBL; AF157706; AAD49620.1;
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                                                                                                                 Dominguez G., Pellett P.E.;
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20.5 KDA PROTEIN.
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amada M., Ya
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                                                                 RA Adams M.D., Celniker S.E., Nolt R.A., Evana C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Nilk R.A., Wonkins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blaze! R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Beyraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Baltek R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
Burtls K.C., Busam D.A., Butler H., Calleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borthox K.C., Busam D.A., Butler H., Calleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Davies P., Harris M., Glasser K.,
RA Cherry J.M., Cayley S., Davies P., Harris M., Glasser K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., kenlson J.A., Ketchum K.A.,
RA Harris M.L., Harvey D., Heilman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krantz J., Liang Y., Lin X.,
RA Harris M., Walson K.A., Nixon K., Musskern D.R., Nelson D.L.,
RA Harris M., Walson K.A., Nixon K., Musskern D.R., Santh T.,
RA Polley S., Marsial R., Ferral R.D.C.,
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Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warry

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., L
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Homo sapiena (Numan).
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Submitted (JUL-2000) to the
EMBL; AL365408; CAB96952.1;
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                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
MammaIla; Eutheria; R
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EMBL; AE004849; AAG07718.1; -
Isomerase; Complete proteome.
SEQUENCE 257 AA; 28152 MW; F4CFCEB4AD9D1BB7 CRC64;
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STRAIN-MAFF303099;
MEDLING-21082930; PubMed-11214968;
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Phyllobacterlaceae; Mesorhizobium.
       SEQUENCE
                                                                     NCBI_TaxID-10090
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PUTATIVE DEHYDROGENASE.
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SEQUENCE 260
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EMBL; AL03154T; CAA20822.1;
HSSP; P19992; IHDC.
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Soehl G., Elberger J., Jung Y., Kozak C., Nillecke K.;
Soehl G., Elberger J., Jung Y., Kozak C., Nillecke K.;
"The mouse gap junction gene Connexin29 is highly expressed scientific nerve and regulated during brain development.";
Blo1. Chem. 382:973-978(2001).
EMBL; AJ297318; CAC29245.1; -
SEQUENCE 258 AA; 28982 MW; 26D13AB3AC009458 CRC64;
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Pfam; Pr00106; adh_short; I.
Pfam; Pr00080; SDRFAMILY.
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STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kleser H.M., Denapalte D.,
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Bacteria; Firmlcutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCB1_Tax1D=1902;
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"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelloolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).

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96.1	96.1	96.1	96.1	96.1		٠	٠	٠	96.1	٠	96.1		96.1		97.1	97.1	97.1	97.1	97.1	97.1	.7	97.1	97.1	97.1	.7	.7	97.1	.7	.7	.7	97.1	97.1	97.1	
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AAB46954	AAB90996	AAB90994	AAG62527	AAG62519	AAY49302	AAY49301	AAB10358	AAB10350	AAW95175	AAW95191	AAW97234	AAW97232	AAW31374	AAW31387	AAG62530	AAB10361	AAW97226	AAW31390	AAG62533	AAB10364	AAW31393	AAG62532	AAB10363	AAW31392	AAB90995	AAB90991	AAG62531	AAY49291	AAB10362	AAW87615	AAW97235	AAW31391	AAG62536	
-		Prolactin releasin	H rel		ligand	19P2 ligand peptid	Rat oxytocin secre	Bovine oxytocin se	Murine pituitary-d	tuitary	pe ligand p	pituitary-	Ŗ	G	Human CRH releasin	0	type 1	type	CRH	oxytoc	type	CRH	oxytoci	Ō			n CRH re	$\vdash$	o	19P2	Ξ	Human type G prote	Human CRH releasin	

# ALIGNMENTS

AAW31394 standard; Peptide;

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RESULT
AAW313
AW313
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AC AAW3
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XX G PI
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XW Indu
XW Homcu
XW Homcu
XX Homcu Fujii R, Fu Kawamata Y, 18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996; G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; WPI; 1997-363672/33. N-PSDB; AAV02431. W09724436-A2 therapeutic agent. Human type G protein-coupled receptor ligand fragment 4. 06-APR-1998 (first entry) AAW31394; (TAKE ) TAKEDA CHEM IND LTD. 26-DEC-1996; 10-JUL-1997. Homo sapiens Fukusumi S, Y, Kitada C 96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805. 96WO-JP03821. Habata к Hinuma <u>.</u> Hosoya 3

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RESULT AAW97236 ID AAW97236 ID AAW97236 PUT 06-M XX AAW9 XX Rat KW G pitu KW Poitu AXX Poitu 30-1 XX Poitu 30-1 XX Poitu AXX Poitu 30-1 XX Poitu 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc ligand polypeptide corresponding to amino acid residues 34 to 53 of the Cc asquence represented in ANW31390 and is used in an assay to monitor ci ligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function commodulator. This ligand could have specific applications as a control in the representation of prophylactic or therapeutic sgent for dementia, depression, hyperkinetic cs yndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, cc syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, cc trauma, growth hormone secretory disease, hyper- and polyphagla, cc hyperripidaemia, hypercholesterolaemia, hyperripyceridaemia, hypercholesterolaemia, hyperripyceridaemia, cc hyperrolactinaemia, diabetes, cancer, pancreatitis, renal disease, cc hyperripidaemia, brian ischemia, epilepsy, amyjotrophic dateral sclerosis, cacute myocardial infarction, infertillty, spinocerebellar degeneration, co bone fracture, trauma, atopic dermatitis, osteoporosis and/or coigogalactia. Assaya can also be developed to screen compounds which are cc apable of altering the binding activity of the ligand affecting cactivation of the G protein-coupled receptor protein.
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                            Fujii R,
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nes 17; Conaery
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89,58;
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Pred. No. 1.8e-10;
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Compared in the course of the invention. The specification deacribes

an agent for modulating prolactin secretion which comprises a

Compared polypeptide or a salt, for a grotein-coupled receptor (GPCR)

Compared polypeptide or a salt, for a grotein-coupled receptor (GPCR)

Compared polypeptide or a salt, for a grotein-coupled receptor (GPCR)

Compared polypeptide or a salt, for a grotein-coupled receptor (GPCR)

Compared protein. The agents for promoting prolactin secretion can be used for promoting

Compared protein in a domestic mammal and as an aphrodialac. The agents for

Compared protein in a domestic mammal and as an aphrodialac. The agents for

Compared protein in a domestic mammal and as an aphrodialac. The agents for

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Compared protein in a domestic mammal in a secretion and a secretories.

Compared protein in a domestic mammal in a secretion and a secretories.

Compared protein in a domestic mammal and as contraceptives. The agents for

Compared protein in a domestic mammal input mode, abortion, unthrifty fetus,

Compared protein in a domestic mammal input mode, abortion, unthrifty fetus,

Compared protein in a domestic mammal input metabolism or oxytocis.
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Natches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of as druga for diseases relating to oxytocin secretion and in wedletne
                                                                                                                                                                                                                                                                                                                 WQ200038704-A1,
                                                                                                                                                                                                                                                                                                                                                                                                    Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bieeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal
                                                                                                                            Mataumoto
                                                                                                                                                                                                                                                                             06-JUL-2000
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                                                                                                                                                                                                                                         22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                      veterinary medicine;
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89.5%;
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                                  of oxytocin,
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Matches 17
The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodles can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of projectin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in ciarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarcan section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                          Hew monoclonal antibodies, studying diseases related
                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                 Matsumoto H,
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0; Mismatches 2;
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central nervous system; pancreat
                                                                                                                                                                                                                                                                as drugs and
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                        its derivative
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RESULT
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Best Local s
Matches 17
                                             Matches
                                                      Ouery Match
Best Local (
                                                                                                                                  The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor iigand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                         Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                              18-NOV-1999; 99JP-0327900.
26-SEP-2000; 2000JP-0297073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                   Sequence
                                                                                                                                                                                                                                                   Claim 4; Page 75; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                    Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000; 2000WO-JP08119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-2001
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                                                                                                                           Invention
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          1 PDIHPAWYXXRGIRPVGRF 19
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pdinpawyasrgirpvgrf
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                                            Similarity 89.5
L7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     releasing protein related
                                                                                                                                                                                                                                                                                                                                   Matsumoto H,
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89.5%;
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                                           Score 100; DE Pred. Ho. 1.8e 0; Mismatches
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Pred. Ho. 1.8e-10;
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                                                        DB 22;
.8e-10;
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                                                                Length
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                                                                                         AAW31395
                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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10-SEP-1999;
15-OCT-1999;
AAW31395;
                                                          AAW31395 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-112059/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prolactin releasing peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB90992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CONJ-) CONJUCHEM INC.
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                                                                                                                                                                                                                                                                                                                          Local Similarity 89.1
nes 17; Conservative
                                                                                                                                                                                                                                       1 PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                                                                           2 pdinpawyasrgirpvgrf 20
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                  97.1%;
89.5%;
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                                                          21
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Pred. No. 1.8e-10;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                              Length 20;
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CC ligand polypeptide corresponding to amino acid residues 34 to 54 of the CS sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein harmoceutical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a cc prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, cc trauma, growth hormone secretory disease, hyper-and polyphagia, cc hyperlipidaemia, hypercholesterolaemia, hyper-lyceridaemia, cc hyperrolactinaemia, diabetes, cancer, pancreatitis, renal disease, cc Turner's syndrome, neurosis, asthma, rheumatold arthritis, spinal injury, cc transient brain ischaemia, epilepsy, amylotrophic lateral scierosis, collegaiactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cativation of the C protein-coupled receptor protein.
                                            AAB10366
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Best Local S
Matches 17
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
AAB10366;
                             AAB10366 standard; peptide; 21 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saplens.
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modulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human type G protein-coupled receptor ligand fragment
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                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                         Local Similarity
nes 17; Conserv
                                                                                                         2 pdinpawyasrgirpvgrf 20
                                                                                                                                        1 PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y, Kitada
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                                                                                                                                                                                                                                                      21
                                                                                                                                                                         Conservative
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95JP-0343371.
96JP-0059419.
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                                                                                                                                                                                      97.1%;
89.5%;
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                                                                                                                                                                       Score 100; DB 18;
Pred. No. 1.9e-10;
0; Mlsmatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hosoya M;
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RESULT
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Best Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as drugs
medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Physiologically-active polypeptide recognized as ilgand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; oxytocin secretion promoter: G protein-coupled receptor proteinsent; disease; pain; atonic bleeding; uterine recovery failucassarcan section; artificial fertilization; galactostasis; goat:
                                                                                                                                                                                                                                                                                                            AAG62535 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                         analgesic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200038704-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human oxytocin secretion promoting peptide SEQ
                                                            Homo sapiens.
                                                                                                                                         Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
                                                                                                                                                                                      Human
                                                                                                                                                                                                                                24-AUG-2001
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                                                                                                                                                                                    CRH releasing protein
                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.1%;
milarity 89.5%;
Conservative
                                                                                                                         hyperaldosteronism;
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                                                                                                                                                                                                                           (first
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                                                                                                    adrenal
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Pred. No. 1.9e
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                                                                                                 hypercortisolaemia; hypoadrenocorticism; d hyperfunction; obesity.
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|.9e-10:
|es 2;
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RESULT 1
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Best Local S
Matches 17
Fujii R,
Kawamata
                                                             18-SEP-1996:
28-DEC-1995:
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                             G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                               06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                  AAW31396 standard; Peptide;
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26-SEP-2000;
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                 therapeutic
                                                                                                                                                                                                                                                                                     Human type G protein-coupled receptor ligand fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                        10-JUL-1997.
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                                    (TAKE ) TAKEDA
                                                                                                                              26-DEC-1996;
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             Fukusumi S,
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2000JP-0297073
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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89.58;
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Pred. No. 1.9e-10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC ligand binding to the g protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipideemia, hypercholesterolaemia, hypergiyceridaemia, renai disease, CC Turner's syndrome, neurosis, asthma, rheumarold arthritis, spinal injury, CC translent brain ischaemia, epiiepsy, amyiotrophic laterai sclerosis, CC translent brain ischaemia, epiiepsy, amyiotrophic laterai degeneration, CC acute myocardial infarction, infertiiity, spinocerebellar degeneration, CC consolation, translent kesays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting
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Physiologically-active polypeptide recognized as ligand by protein-coupled receptor protein, for promoting secretion.
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ligand binding to the G
                                                                                                    (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                22-DEC-1999;
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                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                   veterinary medicine;
                                                                                                                                                                                                                                                                                                                                                        Human oxytocin secretion promoting peptide SEQ ID
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DB; AAV02433.
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                                                                                                                                                                                                                                                                                                               oxytocin secretion promoter; G protein-coupled receptor protein;
ent: disease; pain; atonic bieeding; uterine recovery failure; co
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17; Conser
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of the G
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89.58;
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                                                                                                      LTD
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Pred. No. 2e-10;
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oxytocin
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present
                                     The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G proteir receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hyposdrenocorticism, Addison's hypercortisolaemia, secondary or chronic hyposdrenocorticism, Addison's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as drugs
medicine
                       hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison disease (including boredom, naisea, pigmentation, hypogonadism, hair
                                                                                                                                                                         Use of G protein receptor ligand or peptide for corticotropin releasing hormone secretion .
                                                                                                                                                                                                                                          Kitada C,
                                                                                                                                           Disclosure; Page
                                                                                                                                                                      corticotropin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
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26-SEP-2000; 2000JP-0297073.
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and hypotension), adrenal gland
nt sequence is a peptide used in
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17; Conserv
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RESULT IAAW31391
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              compositions containing this ilgand may be used as a pituitary function compositions containing this ilgand may be used as a pituitary function modulator. First ilgand could have specific applications as a prophylactic or therspeutic agent for dementia, depression, hyperkinetic prophylactic or therspeutic agent for dementia, depression, hyperkinetic cyprophylactic or therspeutic agent for dementia, depression, hyperkinetic cyprophylactic or therspeutic agent for dementia, depression, hyperkinetic cyprophylactic or therspeutic agent for dementia, polyphagia, hypercholesterolaemia, hyperglyceridsemia, hypercholesterolaemia, hyperglyceridsemia, hypercholesterolaemia, hyperglyceridsemia, hyperglyceridsemia, hyperglyceridsemia, hyperglyceridsemia, cyprophylactinacim, diabetes, cancer, pancreatitis, renal disease, cyprophylactinacim, hypercholesterolaemia, hyperglyceridsemia, hyperglyceridsemia, composition, the curosis, sethma, rheumatoid arthritis, spinal injury, canute myocardisl inferction, infertility, spinocerebellar degeneration, content processes and/or collogisiscia. Assays can also be developed to screen compounds which are content on a fittering the binding activity of the ligand affecting activity of the ligand affecting activity of the ligand affecting
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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modulator; pituitary; centrsl nervous system; pancress; pro
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of aitering ion of the G
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          CC The present sequence represents a human type ligand fragment. It
CC is used in the course of the invention. The specification describes
CC an agent for modulating prolactin secretion which comprises a
CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
CC protein. The agents for promoting prolactin secretion can be used for
CC tresting or preventing hypocovarianism, genecyst escogenesis, menopausal
CC syndrome, eurhyroid or hypometabolism. They can by used for promoting
CC inhibiting prolactin secretion can be used for treating or preventing
CC inhibiting prolactin secretion can be used for treating or preventing
CC pituitary adenomatosis, brain tumour, emmeniopsthy, autoimmune discase,
CC prolactinoms, infertility, impotence, amenorrhes, gsisctorrhea,
CC prolactions, infertility, impotence, amenorrhes, gsisctorrhea,
CC prolacting syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
CC The inhibitory sgents can also be used so contraceptives. The sgents for
CC modulating placental function can be used for treating or preventing
CC choriocarcinoms, hydatid mode, irruption mole, abortion, unthrifty fetus,
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Best Local S
Mstches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; sutoimmune disesse; proiactinoms; infertility; impotence; amenorrhes; gsisctorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Csstilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocsrcinoms; hydstid mole; furuption mole; abortion; unthrifty fetus; sbnormal saccharometabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                  Use of G protein-coupled receptor ligands - for modulating proisctin secretion or placental function, e.g. for treating menopsusal syndrome, tumours, autoimmune disease or abnormal pregnancy
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3PCR; hypoovarianism; gonecyst
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Pred. No. 2.9e-10;
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OX
                                            This is the amino acid sequence of the human pituitary G
CC protein coupled receptor ligand 19P2L. A method suitable for
CC commercial high-level production of 19P2L comprises expressing
CC the ligand in host cells as a recombinant fusion protein e.g. with
CC human basic fibroblast growth factor (see AAV83796-97) that has
CC been modified to include an N-terminal cysteine residue. The
CC ligand is released from the fusion by cysnylation followed by
CC ammonolysis. 19P2L has prolectin secretion-stimulating and (at
CC high doses) prolactin secretion-inhibiting properties. It can be
CC used in the treatment and prevention of various diseases including:
CC senile dementia, cerebrovascular dementia, and dementia associated
CC with: geneslogical disorders (e.g. Alzheimer's disease, Parkinson's
CC disease, Pick's disease, Huntington's disease), infectious diseases
CC diseases (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism,
CC intoxication by drugs, metal and organic compounds), tumourigenic
CC subarachnoidal heamorrhage, and other types of dementia, depression,
CC hyperactive child syndrome (microencephalopathy) and disturbance of
CC consciousness. It is also useful for prevention and treatment of
CC disease associated with projectice and autoimmune disease
CC (hypersecretion disorders), and sentinal vesicle hypothesiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clsim 5; Page 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WP1; 1999-047884/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19P2 iigand; G protein coupled receptor; pituitary; prolactin releasing peptide; human; dementia; breast cancer;
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impotence and autoimmune disease and seminal vesicle hypoplasis
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                                                                       1 PDINPAWYXXRGIRPVGRF
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-105-678A-48
US-09-105-678A-8
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US-09-105-678A-8
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uery Match 97.1%; Score 100; DB 3; Length 2 est Local Similarity 89.5%; Pred. No. 1.3e-10; fatches 17; Conservative 0; Mismatches 2; Indels	O9-105-678A-46 O9-105-678A-46 O9-105-678A-46 O9-105-678A-46 Sequence 46, Application US/09105678A Setent NO. 6103882 GENERAL INFORMATION: APPLICANT: Suenegs, Massato APPLICANT: Tanaks, Yoko APPLICANT: Tanaks, Yoko APPLICANT: Nishimura, Osemu TITLE OF INVENTION: METNOD OF PRODUCING A 19P2 LIGAND KUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 water Street CITY: Boston STATE: MA COUNTRY: USA LIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION NUMBER: JP 172118/1997 ATTORNEY/AGENT INFORMATION: NAME: CON110, David G. REFIRENCE/DOCKET NUMBER: 48466-342 TELECOMMUNICATION INFORMATION: TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 46: SEQUENCE CNARACTERISTICS: LENGTH: 20 amino acids STRANDEDNESS: TOPOLOGY: 1inear MOLECULE TYPE: peptide  09-105-678A-46	28 99 96.1 20 4 US-08-776-971-98 29 99 6.1 20 4 US-09-421-208-34 30 99 96.1 20 4 US-09-421-208-40 31 99 96.1 21 3 US-09-105-678A-35 32 99 96.1 21 4 US-08-776-971-51 35 99 96.1 21 4 US-08-776-971-51 36 99 96.1 21 4 US-09-421-208-35 37 99 96.1 21 4 US-09-421-208-35 38 99 96.1 21 4 US-09-421-208-41 37 99 96.1 22 3 US-09-105-678A-42 39 96.1 22 3 US-09-105-678A-42 40 99 96.1 22 4 US-08-776-971-10 40 99 96.1 22 4 US-08-776-971-52 41 99 96.1 22 4 US-08-776-971-52 42 99 96.1 22 4 US-09-421-208-36 43 99 96.1 31 3 US-09-105-678A-7 44 99 96.1 31 3 US-09-105-678A-8 45 99 96.1 31 3 US-09-105-678A-3 46 99 96.1 31 3 US-09-105-678A-3
20;		Sequence
Gaps		e 98, Apple e 34, Apple e 35, Apple e 51, Apple e 41, Apple e 41, Apple e 42, Apple e 42, Apple e 52, Apple e 52, Apple e 52, Apple e 52, Apple e 54, Apple e 54, Apple e 54, Apple e 36, Apple e 6, A
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PDINPAWYXXRGIRPVGRF 19

PDINPAWYASRGIRPVGRF 20

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                                                                                                          ; MOLECULE TYPE: protein
FRACMENT TYPE: Internal
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SEQUENCE DESCRIPTION: SE
US-08-776-971-64
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US-08-776-971-64
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Patent No. 6228984
GENERAL INFORMATION:
                                               Matches
                                                                     Query Match
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 64: SEQUENCE CHARACTERISTICS:
                                               Local Similarity
hes 17; Conserv
          1 PDINPAWYXXRGIRPVGRF 19
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OPERATING SYSTEM: DOS
SOFTWARE: PostSED for Windows Version 2.0
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, RDBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukusumi, Shoji
Kitada, Chieko
Title of invention: Polyproteins, Their Production and USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinume, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
PDINPAWYASRGIRPVGRF 20
                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                        STRANDEDNESS: single
TDPOLOGY: linear
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                                               Conservative
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Fukusumi, Shoji
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                                                       Score 100; DB 4;
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Matches
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILLING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COD110, David G.
REGISTRATION NUMBER: 48466-342
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, App.
                                                                                                                                                    Sequence 47, Application US/09105678A Patent No. 6103882
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
COMPUTER: IMM PC COMPATIBLE
DPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0,
CURRENT APPLICATION DATA:
                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
MDLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Boston
STREET:
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les 17; Conserv
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                             ADDRESSEE:
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             130 Water Street
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                             DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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89.5%;
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COUNTRY:

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Best Local Similarity
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Sequence 65, Application No. 6228984
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INFORMATION FOR SEQ 1D NO: 47
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, DAV1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMHUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 21 amino a
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: pept:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/I05,678A
FILING DATE: 26-JUN-1998
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                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                               APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
                                                                                                                                                                                                                                                                                                                            Fukusum1, Shoj1
Kitada, Chieko
Title OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                    CITY: Boston
STATE: MA
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                     STREET: 130 Water Street
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                                                                                                                                                                                                                                                                                                                      OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                               Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                     Kawamata, Yuji
Hosoya, Masaki
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.4e-10;
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SEQUENCE DESCRIPTION: SEQ ID NO: 65: US-08-776-971-65
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Patent No. 6258561
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                          PRIOR APPLICATION UNDER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CON111, Dav1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4717
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
               NAME: COnlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 02109
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                                                                                                                                                                                                                              APPLICATION NUMBER:
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FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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FILING DATE: 28 - DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
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89.5%;
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                      48466-342
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                                                                                                                                                 : TOPOLOGY: Iinear
; MOLECULE TYPE: peptide
US-09-105-678A-48
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US-09-105-678A-48
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Best Local S
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION THEORY APPLICATION:
APPLICATION THEORY APPLICATION:
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APPLICATION THEORY APPLICATION:
                                                                     Matches
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Best Local 9
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Patent No. 6
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                                                                                                                                                                                                                                TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIN: 22 amino acids
                                                                                                                                                                                                                                                                             NAME: CONIIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
TELEPNONE: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CNARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                 1 PDINPAWYXXRGIRPVGRF 19
     PDINPAWYASRGIRPVGRF 20
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                                                                  I Similarity
17; Conserv
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                                                                                                                                                                                                                                22 amino acids
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                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                   97.I%;
89.5%;
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89.5%;
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                                                                Score 100; DB 3;
Pred. No. 1.4e-I0;
0; Mismatches 2
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Pred. No. 1.4e-10;
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RESULT 9
US-09-421-208-48
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                                                                                                                                                                      / MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
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                                                                         Query Match
Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGIN: 22 amino acids
 N
                                   I PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukusumi, Shoji
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
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APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
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PDINPAWYASRGIRPVCRF
                                                                           L Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujii, Ryo
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                                                                                        97.18;
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 20
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                                                                         Score 100; DB 4;
Pred. No. 1.4e-10;
0; Mismatches 2
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                                                                                                          Length 22;
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; MOLECULE TYPE: peptide
US-09-421-208-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CONLIA, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                    Sequence 9, Application Patent No. 6103882
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Ogamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LIP
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                                                                                                                                                                                                                                                                                                                                                                              PDINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                 9, Application US/09105678A
5. 6103882
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                                                      Boston
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                                                                      130 Water Street
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89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
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Pred. No. 1.4e-10;
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; WOLECULE TYPE: peptide
US-09-105-678A-9
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                                                                     COUNTRY: USA

2IP: 02109

2IP: 02109

COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, Day1d G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6103882
GENERAL INFORMATION:
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Best Local S
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TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                          STREET: 100
                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3, Application US/09105678A 6103882
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                                                                                                                                                                                                                                                                                                                                                                                      130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/105,678A
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                                      48466-342
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Mismatches
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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ENGTN:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 61: SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                             APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON111, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 47176
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 PDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B
FILING DATE: 05-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUKUSUMI, Sh0ji
K1tada, Chleko
TITLE OF INVENTION: POLYPROTEINS,
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ninuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
                                       LENGIN: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 amino acids
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Fujii, Ryo
Fujii, Shoji
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Kawamata, Yuji
Nosoya, Masaki
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RESULT

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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SI
US-08-776-971-61
                          S
                                                                                                                         ; MOLECULE TYPE: US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                       Matches
                                                                    Query Match
Best Local :
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                          TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CNARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172I18/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPAT
OPERATING SYSTEM: PC-DC
SOFTWARE: Patentin Reig
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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13 PDINPAWYASRGIRPVGRF 31
                                                       Local Similarity
les 17; Conserv
                                                                                                                                                       TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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mes 17; Conserv
                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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                                                                                                                                                                                               CENGTN:
                1 PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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Conlin, David G.
27,026
                                                                                                                                                                                amino acid
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                                                                                                                                                                                                31 amino acids
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Tanaka, Yoko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suenaga, Masato
                                                       Conservative
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                                                                                                                                                       linear
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                                                                   97.1%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHOD OF PRODUCING A 19P2 LIGAND
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89.5%;
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                                                                    Score 100; DB 4;
Pred. No. 2.1e-10;
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Pred. No. 2.1e-10;
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                                                       Mismatches
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                                                                              Length 31;
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APPLICANT: MOTLYB, ALL...

APPLICANT: Tanaka, Yoko

APPLICANT: NIShImura, Osamu

TITLE OF INVENTION: METNOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                    RESULT 15
US-09-I05-678A-44
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FOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-43
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                                                                                                                                                                                                                             Sequence 44, Apr. No. 6103887
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE,DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION: 617-523-3400
TELEPAN: 617-523-3440
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Suenage
                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT:
                                                  CORRESPONDENCE ADDRESS:
AQDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CNARACTERISTICS:
LENGTN: 31 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                              APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #I.30 CURRENT APPLICATION DATA:
            STATE: N
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                                          Boston
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MA
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                                                                                                                                                               Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
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89.58;
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Pred. No. 2.1e-IO;
O; M1smatches 2; Indels
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECONMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTN: 32 amino acids
                                                                                                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS:
                                                                                     13 PDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 1
FILING DATE: 27-JUN-1997
                                                                                                        PDINPAWYXXRGIRPVGRF 19
                                                                                                                                                            Conservative
                                                                                                                                                                         97.18;
89.58;
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                                                                                                                                                        Score 100; DB 3;
Pred. No. 2.2e-10;
0; Mismatches 2
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                                                                                                                                                                                          Length 32;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 09:23:58; Search time 172.41 Seconds (without alignments)
11.147 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_2\_21 103

1 PDINPAWYXXRGIRPVGRFX 20

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	Ç	4	w	2	_		Result
41	41	41	41	41	41	41	41	41.5	42	42	42.5	42.5	43	43	43	43	43	43	43	43	43	44	44	44.5	45	46	49	99		Score
39.8	39.8		٠	39.8	39.8	9	9.8	40.3	40.8	40.8	41.3	41.3	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	12.7	12.7	13.2	43.7	44.7	47.6	96.1		Query
545	476	347	343	342	338	284	226	345	433	428	1501	443	719	476	476	476	376	376	<b>90</b> 6	232	220	284	250	664	767	333	790	83		Tenath
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A87448	AG0502	H64371	T46534	B64395	T20100	A75117	A87664	D84012	н87660	F81694	T45623	T21499	S61046	G85480	G90629	G64720	B48197	A48197	T32376	G75608	C83292	F71015	G83400	F83376	T21969	H82852	T47959	JC7607		∄
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# ALIGNMENTS

Query Match Query Match Best Local Similarity 89.5%; Pred. No. 2.3e-09; Best Local Similarity 89.5%; Pred. No. 2.3e-09; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps Qy 1 PDINPAWYXXGIRPVGRF 19               Db 34 PDINPAWYXGGIRPVGRF 52  RESULT 2 T47959 hypothetical protein F15G16.60 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T47959 R;De Haan, M; Maarse, A.C.; Grivell, L.A.; Newes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, January 2000 A;Reference number: Z24480 A;Reference number: Z24480 A;Residues: 1-790 <deh> A;Residues: 1-790 <deh> A;Residues: DNA A;Residues: DNA A;Residues: EMBL:AL132959 A;Experimental source: Cultivar Columbia; BAC cione F15G16 C;Genetics: A;Map position: 3 A;Introns: 39/1; 678/2; 698/3; 773/2 A;Note: F15G16.60</deh></deh>	RESULT 1  JC7607  prolactin-releasing peptide - rat C:Species: Rattus norvegicus (Norway rat) C:Decies: 30-Jun-2001 *sequence_revision 30-Jun-2001 *text_change 30-Jun-2001 C:Accession: JC7607 R;Yanmada, M; Ozawa, A.; Ishil, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya Biochem. Blophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 A;Contents: Spleen A;Accession: JC7607 A;Molecule type: DNA A;Residues: 1-83 <yam> A;Residues: 1-83 <yam> A;Cross-references: DDNA A;Cross-references: DDNJ-AB040612; DDBJ:AB040613 C:Comment: This peptide induces arachidonic acid metabolite release from rat anterio C:Genetics: A;Gene: PFRP A;Title: Telease from rat anterio</yam></yam>
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A; Experimental source: strain 9a5c

A; Experimental source: strain 9a5c

R; Simpson, A,J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

Briones, M.R.S.; Bueno, M.R.P.; Faclincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A, Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, R

A, Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Diiveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

M,; Mibako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2

M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
                                                                                                                                                                                                                                                                                                        C;Accession: 1
                                                                                                                                                                                                                                                                                                                                              hypothetical protein F30El1.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-767 <WIL>
                                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: Z19495 A; Accession: T21969
     A; Introns: 50/2
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                                                      A;Gene: CESP:F38E11.7
                                                                                                                         A;Cross-references: EMBL:Z68342; PIDN:CAA92775.1; GSPDB:GN00022; CESP:F38E11
                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The genome sequence of the plant pathogen xyleila fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 bel
A;Accession: H82852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; anonymous, The Xylelia i
Nature 406, 151-157, 2000
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A;Experimental source: strain 9a5c
R,Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Aivarenga, R.; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-333 <SIM>
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     50/2; 118/1; 139/2;
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     189/3;
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Pred. No.
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Pred. No.
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226/1; 248/1; 287/2; 375/2; 432/3; 465/3;
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3.9;
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  548/1;
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Best Local S
Matches 8
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PALNCAWEDLRALRPSG PDINPAWYXXRGIRPVG Similarity 8; Conserv

249

Conservative

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Mismatches

7

0;

Gaps

0

42.78; 47.18;

Score 44; DB Pred. No. 9.6;

2

Length

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C;Accession: G83400
R;Stover, C.K.; Pham, X.D.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Couiter, S.N.; Folger, K.R.; Kas, adman, S.; Yuan, Y.; Brody, L.L.; Couiter, S.N.; Folger, K.R.; Kas, adman, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163;
A;Experimental source: strain PAO1
                                                                                                    A; Liory S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an
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A;Aceference number: A82950; MUID:20437337
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C;Accession:
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                                                                                                                                                                                                                                                               hypothetical protein PA1952 [imported] - Pseudomonas aeruginosa (strain PAD: C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A;Gene: PA2
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                                                                                          A; Status: preliminary
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                  A;Experimental source: strain PAOI
                                A;Residues: 1-250 <STO>
A;Cross-references: GB:AE004622; GB:AE004091; NID:g9947948;
                                                                        A; Molecule type: DNA
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Best L
Genetics:
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Best Local Similarity
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Pred. No.
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Pred. No. 21;
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                                    PIDN: AAG05340.1;
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Larbig,
                                    GSPDB:GN
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-220 <STO>
A; Cross-references: GB: AE004709; GB: AE004091;
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA2821
C; Superfamily: plaice glutathione transferase
hypothetical protein - Deinococcus radiodurans (strain R1)
c;Species: Deinococcus radiodurans
c;Date: 03-Dec.1999 #sequence_revision 03-Dec.1999 #text_change 31-Mar-2000
C;Accession: G75608
c;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalis,; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                     RESULT
G75608
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Nature 406, 959-964, 2000
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1420
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A;Residues: 1-284 <KRAW>
A;Cross references: GB:AP000006; NID:g3236133;
A;Experimental source: strain OT3
A;Note: this accession replaces an interim acce C;Genetics:
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A;Title: Complete sequence snd gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
A;Accession: F71015
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Reference number: A82950; MUID:20437337
A;Accession: C82392
A;Status: preliminary
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Best Local Similarity 44.*
Conservative
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Best Local Similarity
Matches 9; Conserv
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Pred. No.
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Pred. No. 12;
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                      J.D.; Dodson,
T.; Zalewski,
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A.; Larbig,
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K.; Lim,
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R; Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid K10r12.
A; Reference number: Z21157
A; Accession: T32376
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
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A; Rolecule type: DNA
A; Residues: 1-232 < WHI>
A; Cross-references: GB: AE001862;
A; Cross-references: Strain R1
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A48197
A;Cross-references: EMBL:L03792; NID:g156644; PIDN:AAA28274.1; PID:g156645 C;Superfamily: vertebrate rhodopsin C;Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor; F;318/Binding site: retinal (Lys) (covalent) #status predicted
                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-376 <SMI>
                                                                                                                                                                    R;Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A. Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
A;Title: Opsins from the lateral eyes and ocelli of the horseshoe A;Reference number: A48197; MUID:93317641
                                                                                                                                                                                                            opsin, oceilar - Atiantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
C;Accession: A48197
R;Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A;Reference number: A75250;
A;Accession: G75608
A;Status: preliminary
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A; Map position: 3
A; Introns: 31/3; 123/
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A; Map position: 2
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C; Keywords: amino acid transport; transmembrane protein C; Keywords: amino acid transport; transmembrane protein F;10-26/Domain: transmembrane #status predicted <TM1>F;91-107/Domain: transmembrane #status predicted <TM2>F;142-158/Domain: transmembrane #status predicted <TM4>F;142-158/Domain: transmembrane #status predicted <TM4>F;208-224/Domain: transmembrane #status predicted <TM5>F;308-224/Domain: transmembrane #status predicted <TM6>F;303-319/Domain: transmembrane #status predicted <TM6>F;303-319/Domain: transmembrane #status predicted <TM7>F;301-407/Domain: transmembrane #status predicted <TM8>F;414-430/Domain: transmembrane #status predicted <TM9>
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R;Blattner, F.R.; Plunkett 111, G.; Bloch, C.A.; Perna, N.T.; E
A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reforence number: A64720; MUID:97426617

A;Accession: G64720
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C;Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor;
F;318/Binding site: retinal (Lys) (covalent) #status predicted
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A; Residues: 1-476 <BLAT>
A; Cross-references: GB:AE000111; GB:U00096; NID:g1786181;
A; Experimental source: strain K-12, substrain MG1655
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A;Molecule type: mRNA
A;Residues: 1-376 <SMl>
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
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les 6; Conservation
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G;Accession: G85480
R;Perna, N.T.; Plunkett 111, G.; Burland, V.; Mau, B.; Glasner,
C;Accession: Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane transport protein [imported] - Escherichia coii (strain 0157:H7, subst
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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C:Superfamily: sodium-dependent D-alanine/glycine transport protein
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G;Species: Escherichia coli
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A;Experimental source: strain O157:H7, substrain EDL933
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A;Tittle: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90629
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A; Residues: 1-476 <STO>
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A;Molecule type: DNA
A;Resldues: 1-476 <HAY>
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Shiba, T.; Hattori,
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RIMD 0509952
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M.; Shinagawa,
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OM protein - protein search, using sw model
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September 13, 2002, 09:30:44; search time 80.21 seconds (without alignments) 9.655 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_2\_21 103 1 PDINPAWYXXRGIRPVGREX 20

Run on:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Searched:

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Oatabase : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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P44408	P55386	0922v4	016368	P25747	P23525	067625	046908	089330	P20471	09y4k1	P07118
haemophilus	rhizoblum 8	<b>ՊԱՑ ՊԱՑԸս</b> ևս	caenorhabdl		spinacia ol		gulliardia	z genome po	rhizobium m	<u>.</u>	escherichia

### ALIGNMENTS

01-M 01-M	RESULT 1 PRRP_HUMAN ID PRRP_ AC P8127 OT 30-MA
Ol-MAR-2000 (Rel. 3), Last Ol-MAR-2002 (Rel. 4), Last Prolactin releasing peptide prepared (Rel. 4), Last Prolactin releasing peptide releasing peptide prepared (Relaxins: Prolact releasing peptide prepared (Ruman).  Eukaryota; Metazoa: Chorda Mammalia; Eutheria: Primat Relaxing-9606; [1]  TISSUE-Brain:  SEQUENCE FROM N.A.  TISSUE-Brain:  Nishimura O., Masuo Y., Asano Kurokawa T., Nishimura O., Masuo Y., Asano Kurokawa T., Nishimura O., **  "A prolactin-releasing pep Nature 393:272-276(1998).  "ITSSUE SPECIFICITY.  PUMMed-1049838; Fuyill R., Kitada C., K Sumino Y., Fujino M.;  "Tissue distribution of probediation of president for prolaction of president for prolaction of president for propared directly the suropean Bioinformatic the European Bioinformatic the Europea	T 1 HUMAN PRRP_HUMAN P81277; P81277;
-2002 (Rel. 4 -2	(Re
Ol-Min-2000 (Net. 3), Last sequen Ol-Min-2002 (Reil. 4), Last annota prolactin releasing peptide precu hormone) [Contains: Prolactin rel releasing peptide prep20]. PRH. Body Metazoa; Chordata; Cra Mammalia; Eutheria; Primates; Cat. MCBI_TaxiO-9606; [1] TISSUE-Brain; MEDLINE-92868781; PubMed-9607765; MEDLINE-92868781; PubMed-960776 n. TISSUE SPECIFICITY; PUBMed-1049838; TISSUE SPECIFICITY; PUBMed-1049838; TISSUE SPECIFICITY; MEDULAD SERGIAL 183:1-10(1999). 1-1-FUNCTION: Stimulates prolactin receptor: "Tissue distribution of prolactin throu lexpression of prolactin lexpression of	
Ol-MAR-2002 (Rel. 4), Last anotation update) Prolactin releasing peptide precursor (PRR) (Prolactin-releasing bormone) [Contains: Prolactin-releasing peptide PrRP3]; Prolactin-releasing Primates; Catarrhini; Hominidae; Homo. (REJ.TAXIO-9806; [1] PREMISUE-BRAIN; PubMed-9607765; MEDITER-99266781; PubMed-9607761; MEDITER-99266781; PubMed-9607761; MEDITER-99266781; MEDITER-99268781; PubMed-9607761; MEDITER-99268781; PubMed-9607761; MEDITER-9926881; PubMed-96078818; PubMed-9607881; PubMed-96078818; PubMed-	PRT;
notation update) recursor (PrRP) (Prolactin-re- releasing peptide PrRP31; Pr releasing peptide PrRP31; Pr Catarrhinl; Hominidae; Homo.  Catarrhinl; Hominidae; Homo.  Kawamata Y., Hosoya M., Fu , Matsumoto H., Sekiguchi M., Fu , Matsumoto H., Sekiguchi M., Fu  And H., Fujino M.; Ectin Citin (PRI) release and regul hrough its receptor GPRIO. Ma ecrete PRL.  And DIONOATA AND HYPOTHALAMUS  Tight. It is produced through of Bloinformatics and the fustitute. There are no rest ions as long as its content should by an greement (See http://www.isb sb-sib.ch)  By SIMILARITY.	87 AA
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releasing prolactin- leostom1; to.  Fukusum1 S., H., H., H., H., H., EMBL outstate EMBL outstate strictions on to 1s in no and for comme b-sib.ch/anno prRPP20.	
e) (Prolactin-releasing tide PrRP31; Prolactin- trebrata; Euteleostom1;  pulnidae; Homo.  Hosoya M., Fukusumi S.,  Sekiguchi M.,  Sekiguchi M.,  M.;  M.;  M.;  M.;  Peptide (PrRP) and its  peptor GPR10. May stimulate  eptor GP	

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RESULT
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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hi
Kitada C., Masuo Y., Asano T., Matsumoto H., Si
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                             Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rei. 39, Created)
30-MAY-2000 (Rei. 39, Last sequence update)
30-MAR-2002 (Rei. 39, Last sequence update)
01-MAR-2002 (Rei. 41, Last annotation update)
Prolactin-releasing poptide precursor (PrRP) (Profactin-releasing hormone) [Contains: Profactin-releasing peptide PrRP31; Profactin-
                                                                                                                                                     SIGNAL
                                                                                                                                                             Hormone;
                                                                                                                                                                         EMBL: AB015418; BAA29026.1;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          releasing peptide PRH.
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30-MAY-2000
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"Tissue distribution
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PDINPAWYTGRGIRPVGRE
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                                           17; Conservative
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., Kurokawa T., Nishimura
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-53 PROVIDE AMIDE
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Sekiguchi M.,
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16-OCT-2001 (Rel.
Exostosin-11ke 1 (
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01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Pr
hormone) [Contains: Prolactin-releasing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRP
SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                                   Eukaryota: Metazoa:
Mammalia: Eutheria;
                                                                                                                                                    EXTL1 OR EXTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPRIO. May stimulate lactotrophs directly to secrete PRL.
-i- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98268781; PubMed-9607765;
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Bovidae; Bovinae; Bos.
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                                                              NCBI_TaxID=9606;
                                                                                                                                Homo sapiens (Human)
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none; Amidation; Signal; C
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FIDE 33
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17: Conserv
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. 39, Last
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                                                                                                                                                                                          36, Created)
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PubMed-9037597
                                                                                Chordata;
Primates;
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pred. No. 1.3e-09;
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PROLACTIN-RELEASING F
AMIDATION (G-54 PROVI
: 08AC35Al3B0FA908 CRC
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actyia; Ruminantia; Pecora;
                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                    PRT:
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he brain.";
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                                                                                   Hominidae;
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ASING PEPTIDE PRRP20.
4 PROVIDE AMIDE GROUP)
908 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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Lateral eye ops1n.
Limulus polybemus
Eukaryota; Metazoa;
Limuldae; Limulus.
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Anti-oncogene; M
TRANSMEM 10
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SEQUENCE
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MAYLE W., Spieker N., Van Roy N., De Paepe A., De Boulle K.,

Willems P.J., Van Hul W., Versteeg R., Speleman F.;

Willems P.J., Van Hul W., Versteeg R., Speleman F.;

"Reff.ned physical mapping and genomic structure of the EXTL1 gene.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- SUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratic between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu L., Deng H.X., "Mutations of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wise C.A., Clines G.A., Massa H.. Trask B.T., Lovett M.; "Identification and localization of the gene for EXTL, a of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
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                                                                                                                                                                               401
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-: AF083633; AAD02840.1: JOINED
L: AF083623; AAD02840.1: JOINED
L: AF083624; AAD02840.1: JOINED
L: AF083625; AAD02840.1: JOINED
L: AF083626; AAD02840.1: JOINED
L: AF083626; AAD02840.1: JOINED
L: AF083628; AAD02840.1: JOINED
L: AF083628; AAD02840.1: JOINED
L: AF083629; AAD02840.1: JOINED
L: AF083629; AAD02840.1: JOINED
L: AF083630; AAD02840.1: JOINED
L: AF083631; AAD02840.1: JOINED
L: AF153980; AAF73172.1: JOINED
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SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                  PDINPAWYXXRG1RPVGRF
                                                                                                                                                                             PODFPFYYLQQGSRPEGRF 419
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Similarity 47.4%:
9; Conservative
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676 /
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                                                                                                                                                                                                                                                                                                                                   Multigene family; Transmembrane; Signal-anchor.

Signal-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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EXT
                             (Atlantic horseshoe crab)
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74673 MW;
                Arthropoda;
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Pred. No.
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N-LINKED (GLCNAC.
B5E006A8762E5633
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                Chelicerata;
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on update)
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               Merostomata; Xiphosura;
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                                                                                                                                                                                                                                                        Length 676,
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                                                                                                                                                                                                                                                                                       PRINTS: PR00237; GPCRRHODOPSN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1:
PR0SITE: PS00238; GPR0TEIN_RECEP_F1_2:
PR0SITE: PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                         EMBL: L03791: AAA28273.1: -.
EMBL: L03781: AAA02498.1: -.
PlR: B48197: B48197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Limulus polyphemus.";

Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).

-I- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93317641; PubMed-8327495;
Smith W.C., Price D.A., Greenberg
"Opsins from the lateral eyes and
                                                                                                                                                                                                                                                                                                                                InterPro: 1PR000276: InterPro; 1PR001760: Pfam; PF00001: 7tm_1;
                                                                         CARBOHYD
                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                              Photoreceptor:
                                                                                                                                                                                                                                                                                                                                                                  GCRDb;
                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_Tax1D~6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBSCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: LATERAL EYE.
PTM: SOME OR ALL OF THE CARBOYL-TERMINAL SER OR THR
BE PHOSPHORYLATED (BY SYMILARITY).
MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM A
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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Similarity 46. 6; Conservative
                                                                         Retinal protein; Transmembrane;
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                                               G-protein coupled receptor.
          41.78;
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Score 43: DB
Pred. No. 8.1:
2: Mismatches
                                                  RETINAL CHROMOPHORE (B)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
, CCE401766AB06F26 CRC6
                                                                                           CYTOPLASMIC.
BY SIMILARITY
                                                                                                               EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                    CYTOPLASMIC.
6 (POTENTIAL).
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EXTRACELLULAR
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          8.1:
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1 of the horseshoe
                    ۲,
                  Length 376;
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01-JUN-1994 (R
16-OCT-2001 (R
Oceliar opsin.
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TRANSMEM
DOMAIN
  CARBOHYD
SEQUENCE
                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith W.C., Price D.A., Greenberg R.N., Battelle B.-A.;

**Opsins from the lateral eyes and ocelli of the horseshoe crab,
Llmulus polyphomus.";

Proc. Natl. Acad. Scl. U.S.A. 90:6150-6154(1993).

-!- FUNCTION: VISUAL PIGNENTS ARE THE LIGHT-ABSORBING NOLECULES THAT
MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
LINKED TO CIS-RETINAL.

-!- SUBCELLULAR LCCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: OCELLAR CELLS; NEOIAN OCELLI.

-!- PIN: SONE OR ALL OF THE CONSISTON TERMINAL SER OR THR RESIDUES MAY
BE PHOSPHOYLATED (BY SIMILARITY).

-!- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 530 NM.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COOPLEO RECEPTORS.
                                                                                               TRANSNEM
DOMAIN
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00232; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                        EMBL; L03792; AAA28274.1;
EMBL; L03782; AAA02499.1;
PIR; A48197; A48197.
                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc
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Smith W.C., Price D.A., Greenberg
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Limulidae; Limulus.
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                                                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Ops1n.
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                        CARBOHYD
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            (Atlantle
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annotation
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EXTRACELLULAR.
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CYTOPLASMIC.

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MBL outstation -
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P30143;
01-JUL-1993
01-JUL-1993
16-OCT-2001
Pfam; PF01235; NB_A1a_Symp;
PRINTS; PR00175; NAALASNPORT
PROSITE; PS00873; NA ALANTWP
                                                                                                                                                        EMBL; O10483; -; NOT_ANNOTATEO_CDS.
EMBL; AE000111; AAC73118.1; -.
ECOGEne; EG11555; yaaJ
InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR001463; Na_ala_aymp.
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a coilable between the Swiss Institute of Bioinformatics and the ENBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Wage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley N., Collado-Vldes J., Glasner J.O., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden N.A., Rose O.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                  <del>:</del>
                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92334977; PubMed-1630901;
Yura T., Nor1 H., Nagal H., Nagata T., Ish
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia
the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
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Escherichia c
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Slmilarity 46.2%;
6; Conservative
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                                                                                                              Transmembrane;
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                                                                                                               Inner
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                                                                                                              membrane; Transport;
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SEQUENCE
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
-I- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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932770; Q12228;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Asparagine-rich protein (ARP protein).
NRP1 OR ARP1 OR ARP OR YDL167C.
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Pfam; PF00641; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a copyred the swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
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                                                                                                                                                                                                               PROSITE; PS50102; RRM; 1
PROSITE; PS00030; RRM_RN
PROSITE; PS01358; ZF_RAN
PROSITE; PS50199; ZF_RAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P04170; 6RXN.
SGD; S0002226; NRP1.
InterPro; 1PR000504; RRM.
InterPro; 1PR001876; Znf-RanBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X68020; CAA48159.1; -.
EMBL; Z67750; CAA91579.1; -.
EMBL, Z74215; CAA98741.1; -.
EMBL, Z74215; CAA98741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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E; PS00030; RRM_RNP_1; FALSE_NEG.
E; PS01358; ZF_RANBP2_1; 2.
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E; PS50199; ZF_GANBP2_2; 2.
Frotein; Zinc-finger; RNA-binding RNA-Bindin
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Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01
Hydrolase;
SEQUENCE
  09K8V2;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL391754; CAC05901.1;
InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR002309; tRNA-synt_2.
Pfam; PF02601; Exonuc_VII_L; 1.
Pfam; PF01336; tRNA_ant1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC
(Exonuclease VII large subunit).
XSEA OR SCK7.29c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001
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                                           ARGC_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURT
INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
-I- CATALYTIC ACTUITY: Exonucleolytic cleavage in either 5'- to
or 3'- to 5'-direction to yield 5'-phosphomononucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EX7L_STRCO
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                                                                                                                                                             6 AWYXXRG1RPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE XSEA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED
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9; Conserv
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(Rel. 41, Created)
                                                                                                                                                                                                                                                         Conservative
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                                             STANDARD;
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50.0%;
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                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                               Score 42;
Pred. No.
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Pred. No.
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15;
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RESULT 11
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                                                                                                                                                                                   Y762_METJA
Q58172;
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SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAIN=20512582; PubMed=11058132;
MEDLINE=20512582; PubMed=11058132;
Takaml H., Nakasone K., Takaki Y., Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ul-MAK-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate aemialdehyde dehydrogenase) (NAGSA dehydrogenase).
ARGC OR BH2900.
         STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
NEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L.,
Sutton G.G., Blake J.A., FitzGerald L.M.,
                                                                                            Archaea; Euryarchaeota;
Nethanococcua.
                                                                                                                                                   01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the alkaiiphillic bacterlum Bacillus halodurans and genomic sequence comparison with Bacillus subtilia Nucleic Acida Res. 28:4317-4331(2000).

-I- CATALYTIC ACTIVITY: N-acetyl-T-glutamate 5-semialdehyde + NAI + phosphate - N-acetyl-5-glutamyl phosphate + NADPH.
-I- PATHANY: THIND STEP IN ARGININE BIOSYNTHESIS.
-I- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baciilus halodurans.
Bacterla; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=86665;
                                                                                 NCBI_TaxID=2190;
                                                                                                                 Methanococcus
   Kerlavage
                                                          SEQUENCE FROM N.A.
                                                                                                                                        Hypothetical
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an email to license@iab-sib.ch).
   i.G., 191
le A.R.,
                                                                                                                                                                                                                                                                                                   Similarity 52.9
9; Conservative
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                                                                                                                                                                                                STANDARD;
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MJ0762.
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us group; Bacillua.
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   B.A.,
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Pred. No. 1
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   Tomb
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Mismatches
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동
, Flelschmann R.I
, Clayton R.A., (
F., Adama M.D.,
                                                                                                       Methanococcaceae;
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Q57996;
Q1-NOV-1997
Q1-NOV-1997
16-OCT-2001
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TIGF, MJ0762; -
HyDOThetical pr
TRANSMEM 8
TRANSMEM 79
TRANSMEM 108
TRANSMEM 109
TRANSMEM 109
TRANSMEM 175
TRANSMEM 175
TRANSMEM 207
TRANSMEM 276
TRANSMEM 276
TRANSMEM 276
TRANSMEM 276
TRANSMEM 304
SEQUENCE 342
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FltzGerald L.M., Clayton R.A., Gocayne J.D. Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D. Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., "Klenk H.-P., Fraser C.N., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcum Jannaschil.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., G
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Har
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodoys
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.
"Complete genome aequence of the methanogenic archaeon, Mei
                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 431
MEDILINE-96337999; PubMed-8688087;
Bult C.J., White O., Olaen G.J.,
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jannaachli.";
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08EFEC3E2C4955D8 CRC64;
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                                                                                                                                                                                                                                               43067;
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                                             Methanococcus
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Methanococcua
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RESULT 13
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This SWISS-PROT entry la copyright. It is produced through a copyright between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatica Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitics requires a license agreement (See http://www.lab-sib.or send an email to license@isb-sib.ch).
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01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Resact receptor precursor (Guanylate Cyclaae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR;
                                                                                                                                                                                  Singh S., Lowe D.G., Thorpe D.S., Rodriguez H., Kuang W.-J., Dangott L.J., Chinkers M., Goeddel D.V., Garbers D.L.; "Membrane guanylate cyclase is a cell-surface receptor with to protein Kinases.";
Nature 334.708-712(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                    Echinoidea; Eucchinoidea; NCBI_Tax1D=7641;
                                                                                                                                                                                                                                                                                                                             Arbacia punctulata (Punctuate sea urchin) 
Eukaryota; Metazoa; Echinodermata; Eleuth
                                                                                                                                                                                                                                                                                                                                                                                                        CYGR_ARBPU
P11528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as ita content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                  MEDLINE-88318927; PubMed-2901039;
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                                                                                                          FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON FOR 'RESACT' A CHEMOTACTIC PEPTIDE, AND ON VARIOUS AS A RECEPTOR FOR ARRIAL NATRIURETIC PEPTIDE.

CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + dlphose SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through
ween the Swiss Institute of Bioinformatics and the El
European Bioinformatics inatitute. There are no reat
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SIMILARITY:
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MJ0576; -.
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                                                                                                                                                                                                                                                                            AND PARTIAL SEQUENCE.
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POTENTIAL
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632F7671A31DE183 CRC64;
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RESULT 14
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SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D. Alland D., Eisen J
Fleischmann R.D., Alland D., Eisen J
Peterson J., DeBoy R., Dodson R., Gw
ROllonay J.F., Nelaon W.C., Umayam L.
Delcher A., Utterback T., Weidman J.
Biahai W.;
                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
16-OCT-2001 (Rel. 4
Hypothetical 35.4)
RY0493C OR MT0513
                                                                                                                                                  Cole S.T., Broach R., Parkhill J., Garnier T., Churcher C., Ha. Gordon S.V., Eiglmoler K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feitwell T., Gentles S., Hamiln N., Hoirn Hornaby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L. Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Segger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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CARBOHYD
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CARBOHYD
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        iaboratory strains."
Submitted (APR-2001)
-i- SIMILARITY: SOME
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF00211; guanylate_cyc; 1.
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cGMP synthesis;
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NCB1_TaxID-1773;
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                                            Whole genome comparison of Mycobacterium tuberculosis clinical
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S05480; OYURGA.
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40, Last annotation updat
kDa protein Rv0493c.
OR MTCY20G9.19C.
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  to the EMBL/Genbauk/ Dubu
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62.5%;
                  the EMBL/GenBank/DDBJ databases
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                                                                 en J.A., Carpenter I
, Gwinn M.L., Haft [
n L.A., Ermolaeva M.
n J., Khouri H., Gil
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    Phosphorylation; Lyase;

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   EMBL; M31939, AAA26719.1;
PIR; A32260; A32260.
PDB; 184V; 06-JAN-99.
PDB; 188S; 09-FEB-99.
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as ione as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send en email to license@isb-sib.ch).
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"Crystal structure determination of cholesterol oxid
Straptomyces and structural characterization of key
mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces sp.";
J. Bacteriol. 171:596-601(1989).
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MEDLIME-89123081; PubMed-2914858;
Ishizaki T., Hirayama N., Shinkawa
Mucleotide sequence of the gene fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces sp. (strain SA-COO).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
MCBI_TaxID=1931;
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EMBL; AE006952; AAK44736.1; -.
TIGR; MT0513; -.
Tuberculist; Rv0493c; -.
Hypothetical protein; Complete proteome.
SEQUENCE 329 AA; 35427 MW; BE48524750277B56 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         -1- PATHWAY: CHOLESTEROL METAOOLISM.
-1- SUBUNIT: MONOMER.
-1- SUOCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 38:4277-4286(1999).
-!- CATALYTIC ACTIVITY: Cholesterol +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.5 AMGSTROMS), AND MUTAGEMESIS MEDLINE-99211873; PubMed-10194345;
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-!- COFACTOR: FAD
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6; Conservation
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InterPro; IPR00172; GMC_oxred.
InterPro; IPR000172; GMC_oxred.
InterPro; IPR000172; GMC_oxred.
InterPro; IPR000172; GMC_oxred.
InterPro; IPR000172; GMC_oxred_1; 1.
INTERPROSITE; PS00624; GMC_OXRED_2; FALSE_NEG.
Oxidoreductase; Signal; Flavoprotein; FAD;
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PDB; 1CC2; 11-MAR-99.
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PDKRSSWFKNRTEAPLGSF 116
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H->N,Q: REDUCED ACTIVITY.
EF22A1FE5EA68D21 CRC64;
                                                                                                                                CHOLESTEROL OXIDASE
FAD (ADP PART) (POTI
                                                                                                                       PROTON ACCEPTOR.
                                   Mismatches
                                            36;
                                                      1; Length 546;
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Search completed: September 13, 2002, 09:30:44 Job time: 1134 sec

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Perfect score:
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4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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## ALIGNMENTS

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Beat Local Similarity 63.2
Matches 12; Conservative
 Q9M371;
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01-OCT-2000
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09W624;
01-NOV-1999 (TIEMBLIE1. 12,
01-NOV-1999 (TIEMBLIE1. 12,
01-DEC-2001 (TIEMBLIE1. 19,
                                                                                                                                                                                                                             Satake H., Minakata H., Fujlmoto M.;

"Carassius RFamide (C-RF amide).";

Submitted (NOV-1998) to the EMBL/GenBank/DOBJ databases.

EMBL; AB020024; BAA76652.1; -.

SEQUENCE 117 AA; 12879 MW; O5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                Carasslus auratus (Goldf1sh).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopteryg11: Neopteryg11; Teleoste1;
Cypriniformes; Cyprinidae; Carasslus.
NCBI_TaxIO-7957;
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57 PEIDPFWYVGRGVRPIGRF 75
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(TrEMBLrel. 19, Last annotation update)
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63 2%;
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Last sequence update)
Last annotation update)
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Pred. No. 3.3e-06;
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Actinomycetales; Streptomycineae; Stre
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Spermatophyta; Magnoliophyta; Eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
KCBI_TaxID-3702;
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Xylella
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Submitted (JAN-2000) to the
EMBL, AL133959; CAB71097.1;
                               01-OCT-2000 (TrENBLrc1. 15, Created)
01-OCT-2000 (TrEMBLre1. 15, Last sequence update)
01-DEC-2001 (TrEMBLre1. 19, Last annotation updat
HYDROXYBEHSOATE OCTAPRENTLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces aureofaciens CCN3239.";
Submitted (MAY-3001) to the EMBL/GenBank/DDBJ
EMBL, AY033994; AAK61719.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kormanec J., Bistakova J., Novakova R., 
"Cloning and characterization of a new 
Streptomyces aureofaciens CCN3239.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

De Haan M., Maarse A.C., Griveli L.A., M
Mayer K.F.X., Quetler F., Salanoubat M.;
Submitted (HOV-1999) to the ENBL/GenBank
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NCBI_TaxID=1894;
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he EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                    Score 46.5; D
Pred. No. 9.4;
1; Mismatches
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Pred. No. 6.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   3C27E22BE88C2DEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation update)
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                                                                                                                                      ζ
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                                                                                                                                                                                                                                                                                                                                                           Length 420;
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ne cluster
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RESULT OF SERVICE SERV
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RA Alvarenga R., Alves L.N.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.N., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.N., Briones M.R.S.,
RA Bueno M.R.P., Camaryo A.A., Canaryo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.N.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferrerira A.J.S., Ferricira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais N.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Nachado M.A., Madeira A.N.B.N., Madelra H.M.F., Narino C.L.,
RA Marques M.V., Martins E.A.L., Nartins E.M.F., Matsukuma A.Y.,
RA Manck C.F. M., Miracca E.C., Mlyaki C.Y., Nonteiro-Vitorelio C.B.,
RA Monok C.F. M., Miracca E.C., Mlyaki C.Y., Nonteiro-Vitorelio C.B.,
RA Hhani A. Jr., Nobrega F.G., Nunes L.R., Olivelra M.A.,
RA Hhani A. Jr., Nobrega F.G., Nunes L.R., Olivelra M.A.,
RA Quaggio R.B., Reberto P.G., Rodrigues V., de Rosa A.J.M.,
de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Savasaki H.E.,
RA da Silva A.C., R., da Silva B.A., M. Silva F.R., Silva M.A.,
RA da Silva A.C., R., da Silva B.M., Macsima H.S.,
RA Vallada H., Van Sluys M.A., Verjowski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubai J.C.,
RT Tengan M.G., Santelli R., Setubai J.C.,
RA Santeria M.G., Meidanis J., Setubai J.C.,
RA Santeria M.G., Santelli R., Setubai J.C.,
RA Santeria M.G., Santelli R., Setubai J.C.,
RA Santeria M.G., Setubai J.C.,
RA Santeria M.G., Santeria M.G., Santeria M.G., Santeria M.G.,
RA Nelecca M.G., Setubai J.C.,
RA Santeria M.G., Santeria M.G., Santeria M.
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Best Local S
Matches 8
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Q9LGZ0;
Q9LGZ0;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
            STRAIN-CV. NIPPONBARE;
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto
"Oryza sativa nipponbare(GA3) geno
"Oryza sativa nipponbare(GA3) geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
Complete
SEQUEHCE
                                                                                                                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Enspermatophyta; Wagnoliophyta; Liliopsida;
Ehrhartoidese; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AE003860; AAF82881.1; -.
InterPro; IPR000537; UblA.
Pfam; PF01040; UblA; 1.
                                                                                                                                                 SEQUENCE FROM
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                                                                                                                                                                                                         NCBI_TaxID=4530;
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8; Conser
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(JUH-2000) to
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0 (TrEMBLrei.
1 (TrEMBLrei.
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                                                                                                                                                    H. A.
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UBIA; UNKHOWN_1.
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53.38;
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the
EMBL/Gen8ank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
DNDS TO A REGIOH OF THE
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Pred. No. 8.9;
2; Mismatches
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                                                    genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECF3F4716C962B95 CRC64;
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                                                       DNA,
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                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta;
a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ξ
                                                          chromosome
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RESULTATION OF CASE OF
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Best Local S
Matches 7
                                                                                       Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                          investigating bloTogy.",
Science 282:2012-2018(1998).
EMBL, Z68342; CAA92775.1;
InterPro; IPR001656; Cation_chan_non_lig.
InterPro; IPR00152; ChanneI_pore_K.
InterPro; IPR000595; cNMP_binding.
Pfam; PF00027; CNMP_binding; 1.
Pfam; PF00520; lon_trans; I.
SMART; SM00100; CNMP; 1.
                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q20170
Q20170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUHCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIH LYSIHE - AMP + PYROPHOSCHATE + PROTEIH N-UBIQUITYLLYSIHE.
-1- PATHWAY: SECOND STEP IN UBIQUITIN COHOUGATION.
-1- MISCELLANEOUS: A CYSTEIHE RESIDUE IS REQUIRED FOR UDIQUITIN-THIOLESTER FORMATIOH (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING EHZYME FAMILY.
EMBL; AP002481; BAA96583.1; -.
EMBL; P06104; BAYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-HOV-1996 (TREMBLIEL.
01-HOV-1996 (TREMBLIEL.
01-DEC-2001 (TREMBLIEL.
F38E11.7 PROTEIH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUEHCE FROM N.A. MEDLIHE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Hemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F38E11.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00179; UQ_con; 1
SMART; SM00212; UBCc; I.
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matthews P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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747
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DLGVAWWRVRGLRP 82
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POVKPAWY 754
                                           PDIHPAWY 8
                                                                                          Similarity
6; Conser
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                                                                                                                                                                                                     PS00888; CNMP_BINDING_I; UHKHOWH_1.
PS50042; CNMP_BINDING_3; I.
767 AA; 89988 MW; F7ECF69DBBEAACF3
                                                                                     43.7%;
llarity 75.0%;
Conservative
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50.0%;
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                                                                                       Score 45; DB:
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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Last annotation update)
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Pred. No.
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                                                                                                                                   Length 767
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RESULT

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RESULT
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Best Local Simllarity
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01-MAR-2001 (
01-OCT-2001 (
HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                           opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004642; AAG05539.1; -.
InterPro; IPR001589; Actinin_act_bind.
InterPro; IPR000461; Alpha_amylase.
Ffam; PF00128; Alpha_amylase; I.
PROSITE; PS00019; ACTININ_1; UHKNOWH_1.
Hypothetical protein; Complete proteome.
SEQUENCE 664 AA; 76329 MW; 8F59FEED54C308AD CRC64;
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STRAIN-ATCC I5692 / PAO1;

MEDLINE-2043737; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Le Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lin Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Relzer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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                                                                                                                                                               Pseudomonas.
NCBI_TaxID=287:
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                           SEQUENCE TISSUE=BRAIN;
MEDLINE=99097350; PubMed=987
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InterPro; IPR001330; Prenyltrans.
InterPro; IPR003662; sub_transporter.
Pfam; PF00432; prenyltrans; 2.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 284 AA; 32319 MW; 8E0E7BC3711D3815 CRC64;
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Kawarabayasi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
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Mammalia; Eutheria; Primates;
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NCBI_TaxID=53953;
    Zeviani M.;
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EMBL; BC000416; AAH00416.1; --
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SEQUENCE FROM N.A.

Gerbatyu

de Lonlay P., Valnot I., Barrientos A., Gorbatyu

Benayoun E., Chretien D., Kadhom N., Lombes A.,

Niaudet P., Munnich A., Rustin P., Rotig A.;

"Mutations in bcsl. a mitochondrial respiratory

are responsible for the complex III deficiency o

tubulopathy and liver failure.";
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                                                                                                                                                                                                                                                           Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Ricaffente J.Y., Wentland M.A., Lennon G., Gibbs R. "Large-scale concatenation cDNA sequencing."; Genome Res. 7:353-358(1997).
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Andersson B., Wentland M.A., Ricafrente
"A 'double adaptor' method for improved
                              Pseudomonas
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Strausberg R.;
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function of the mitochondrial respiratory chain.";
Dmics 54:494-504(1998).
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01-JUH-2001 (
HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM
STRAIN-ATCC
                                                                                                                                                                                                                                 WEDLIHE-20036896; PubMed-10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D. Dodson R.J., Haft D.H., Gwinn M.L., Helson W.C., Richardson D.L. Moffat K.S., Qin H., Jlang L., Pamphlie W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova R.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Hature 406:959-964(2000).
EMBL; AE004709; AAG06209.1; -.
InterPro; IPR004046; GST_C.
InterPro; IPR004046; GST_H.
Transferase; Complete proteome.
SEQUENCE 220 AA; 24716 MW; 6596183EA6CAA050 CRC64;
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337 PubMed-10984043;

MEDLINE-20437337 PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., La Hickey M.J., Brinkman F.S.L., Hufnagie W.O., Kowalik D.J., La Garber R.L., Golkry L., Tolentino E., Westboock Waddan S., Yu Brody L.L., Coutter S.H., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.,
                                                                                                                 InterProj. IPR003737; DUE158.
InterProj. IPR003737; DUE158.
Pfam; PF02585; DUE158; 1.
Hypothetical protein; Complete
SEQUEHCE 232 AA; 24979 MW;
                                                                                                                                                                               radiodurans Rl.";
Science 286:1571-1577(1999).
EMBL; AE001862; AAF12317.1;
                                                                                                                                                                                                                                                                                                                                                                                             Deinococcus radlodurans.
Bacteria, Thermus/Deinococcus
                                                                                                                                                                                                               "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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PDHRAAWHLLRGVLP
                                               Similarity 46.7
7; Conservative
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9; Conserv
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(TIEMBLIE1. 13, LAST sequence up
(TIEMBLIE1. 17, LAST annotation
L 25.0 KDA PROTEIN.
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64.38;
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                                               Score 43; DB
Pred. Ho. 20;
2; Mismatches
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Pred. No. 19;
1; Mismatches
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A044FA2F38435DA7
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                                                                           Length 232;
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n S., Yuan Y.,
K., Lim R.M.,
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SEQUENCE FROM H.A.

SEQUENCE FROM H.A.

STRAIN-C57BL/6J; TISSUE-EMBRYO:

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MANAGE T., Shinagawa A., Shibata K., Konno H., Matsuda H.A., Ashburner M., Batalov
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Best Local
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InterPro; IPRO04045; GST_N.
Pfam; PF000403; GST_C; I.
Pfam; PF002798; GST_H; I.
Hypothetical protein.
SEQUENCE 309 AA; 35021 MW
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01-JUH-2001
01-DEC-2001
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01-JAN-1998
01-DEC-2001
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01-DEC-2001 (TrEMBLrel.
9130022019RIK PROTEIH.
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Submitted (AUG-2001) to the
EMBL; AF025462; AAB71002.I;
HSSP; P78417; LEEM.
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STRAIN-BRISTOL H2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-JAN-1998 (TYEMBLTel. 05, Last sequence up
01-DEC-2001 (TYEMBLTel. 19, Last annotation
HYPOTHETICAL 35.0 KDA PROTEIN.
                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutherla;
HCBI_TaxID=10090;
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MEDL1HE=99069613; PubMed=9851916;
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Rodentia;
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EMBL/GenBank/DDBJ
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Sciurognathi; Muridae;
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         YOShino M., Itoh M., 1shli
Konno H., Adachi J., Fukuda
Sawa H., Kondo S., Yamanaka
Bono H., Rasukawa T., Salto
M., Batalov S., Casavant T.,
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InterPro; IPR003959; AAA_subfam.
Pfam; PF00004; AAA; 1.
SMART; SK00382; AAA; 1.
ATP-binding.
SEQUENCE 418 AA; 47406 MW; 949
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Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wasner L., Washio T.,
Schai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wiiming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Havashizaki Y.
                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoo; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Eukaryota; Metazoo; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Q19879;
Q1-DDV-1996 (TIEMBLIEL 01,
Q1-DEC-2001 (TIEMBLIEL 19,
Q1-DEC-2001 (TIEMBLIEL 19,
                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
EMBL; 270684; CAA94603.2; -.
SEQUENCE 360 AA; 39234 MW;
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EMBL; AKO12324; BBAB2862.1; -.
MGD; MGI:1914071; 9130022D19R1k.
                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A investigating biology.":
                                                                                                                                                                                                             none;
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53 INPSWFDWRVSVSIDGHLGIWPIG
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                                                                       Score 42.5;
Pred. No. 38;
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Pred. No. 37;
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Search completed:

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Perfect score:
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1: /SIDSI/gcgdats/h
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AAW97236
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# ALIGNMENTS

RESULT AAW31394

06-APR-1998

(first entry)

AAW31394;

AAW31394 stsndard; Peptide;

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Human type G protein-coupled receptor ligsnd frsgmcnt 4.

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18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                     Fujli R.
Kawamata
                                                                                                                                                                G protein-coupled receptor; ligsnd binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
WPI; 1997-363672/33.
N-PSDB; AAV02431.
                                                                                               26-DEC-1996;
                                                                                                              10-JUL-1997.
                                                                                                                            W09724436-A2
                                                                                                                                           Homo sapiens.
                                                                                                                                                         therapeutic agent.
                                           (TAKE ) TAKEDA CHEM IND
                     Fukusumi S,
Y, Kitada C;
                                                          96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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                             Habata Y,
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                             Hinuma
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RESULT
AAM91
XX AAM92
XX AAM92
XX AAM92
XX Rat
KW Rat
KW G px
KW proll
KW acrr
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Matches 16
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                                                                                                                                                                                                                                                                                                                                  Human; oxytocin secretion promoter: G protein-coupled receptor protein: treatment; disease; pain; atonic bleeding: uterine recovery failure; concaesarean section; artificial fertilization; galactostasis; goat; plg; veterinary medicine; mlik production.
           Physiologically-active polypeptide recognized as ilgand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                           Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                Human oxytocln secretion promoting peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10365 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal
                                                                                                                                           (TAKE ) TAKEDA
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Disclosure;

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Matches 16
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The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 1982 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pitultary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta,
                                                                                                                                Disclosure; Page 26; 73pp; Japanese.
                                                                                                                                                                                                                       Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAY49294;
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                                                                                                                                                        studying
                                                                                                                                                                    New monocional antibodies,
                                                                                                                                                                                                                                                (TAKE
                                                                                                                                                                                                                                                                        21-MAY-1998;
                                                                                                                                                                                                                                                                                                   20-MAY-1999;
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                                                                                                                                                                                                                                                ) TAKEDA
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16; Conserv
                                                                                                                                                         diseases related
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Pred. No.
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                                                                                                                                                        In diagnosis, abnormality
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6.3e-10;
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Best Local 9
                                            Matches
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Best Local :
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                                                                                                                            corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysesic or for treating, preventing or amellorating diseases associated with CRH secretion such as hyperaidosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cortlcotrophin releasing hormone; CRH; G protein analgesic; hyperaldosteronism; hypercortisolaemia; hypoa Addison's disease; adrenal gland hyperfunction; obesity.
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                                                                                                                                                                                                                 The present sequence describes a method of controlling the secretion of
                                                                                                                                                                                                                                       Claim 4; Page
                                                                                                                                                                                                                                                           cortlcotropin
                                                                                                                                                                                                                                                                    Use of G
                                                                                                                                                                                                                                                                                                                Kitada
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26-SEP-2000; 2000JP-0297073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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16; Conserv
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Pred. No. 6.3e
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6.3e-10;
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RESULT

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                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
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10-SEP-1999;
15-OCT-1999;
AAW31395;
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                             AAW31395 standard;
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99US-0153406.
99US-0159783.
                            Peptide;
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Pred. No. 6.3e-10;
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                                                                                                                                                                                    Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                    Query Match
Best Local (
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                             AAB10366 standard; peptide;
                                                                                                                                                                                                                                                                Sequence
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N-PSDB; AAV02432.
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modulator; pituitary; central nervous system; pancreas; prophylactic;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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AAB10366:

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RESULT
AAG62535
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DE Huma
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Best Local s
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
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                                                                                                                       Human; corticotrophin releasing hormone; CRH; G protein receptor ligand analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-NDV-2000
                       WD200135984-A1
                                                                           Homo sapiens
                                                                                                                                                                                                                                                                            24-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DINPAWYXXRGIRPVGRF 18
                                                                                                                                                                                                                        CRH releasing
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.98;
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                                                                                                                                                                                                                        related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93; DB:
Pred. No. 6.7e
0; Mismatches
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                                                                                                                                                                                                                        peptide SEQ
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. 6.7e-10;
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Best Local S
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                                                          18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal giand hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NDV-1999;
26-SEP-2000;
                  Fu)11 R,
                                     (TAKE ) TAKEDA CHEM IND
                                                                                                            26-DEC-1996;
                                                                                                                                 10-JUL-1997
                                                                                                                                                     WO9724436-A2
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                             therapeutic
                                                                                                                                                                                                       G protein-coupied receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system: pancress: pro
                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                           06-APR-1998
                                                                                                                                                                                                                                                                                                   AAW31396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence describes a method of controlling the secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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                                                                                                                                                                                                                                     type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                             16; Conserv
        Fukusuml S, xitada C;
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                                                                                                                                                                                                      pitultary;
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                                                                                                                                                                                             agent.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 75; 90pp; Japanese.
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                     protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-0297073
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                                                         96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                            96WD-JP03821
                                                                                                                                                                                                                                                                                                   Peptide;
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                                                                                                                                                                                                      central
                   Habata
                                      GLT
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Pred. No. 6.7e-10;
D; Mismatches 2
                                                                                                                                                                                                                                   receptor ligand fragment
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                                                                                                                                                                                                     nervous system; pancreas; prophylactic;
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                   Hinuma
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                   Новоуа
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                         Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
 proteln-coupled
                  Physiologically-active
                                                        WPI; 2000-452298/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB10367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                           Matsumoto
                                                                                                                             (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                    22-DEC-1999;
                                                                                                                                                                                                                                     06-JUL-2000
                                                                                                                                                                                                                                                                         WO200038704-AL
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          veterinary medicine; milk
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
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)B; AAV02433.
                                                                                                                                                                                                                                                                                                                                                                                                                                oxytocin secretion promoting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; peptide;
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of the G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                         Kitada
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                                                                                                                                                                98JP-0369585
                                                                                                                                                                                                  99WQ-JP07199
-active polypeptide
receptor protein, f
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                                                                                           Hinuma
                                                                                                                                                                                                                                                                                                                                          production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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Pred. Ho. 7e-10;
D; Mismatches
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for promoting secretion (
                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                               failure; co
oxytocin,
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Best Local :
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medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                        analgesic;
Addlson's d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
         disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                  diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's
                                                              The present sequence describes a method of controlling the secretion corticotrophin releasing hormone (CRH), involving the use of a G protreceptor ligand. This can be used to control the secretion of CRH and useful as an analgesic or for treating, preventing or ameliorating
                                                                                                                                                                            Use of G
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
                                                                                                                                      Disclosure;
                                                                                                                                                              corticotropin
                                                                                                                                                                                                                                 Kitada C,
                                                                                                                                                                                                                                                                                       18-NOV-1999;
26-SEP-2000;
                                                                                                                                                                                                                                                                                                                               17-NOV-2000; 2000WO-JP08119
                                                                                                                                                                                                                                                                                                                                                          25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG62536 standard;
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                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conser
                                                                                                                                                              protein receptor ligand or peptide ropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diseases relating to oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                 Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                    Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                      99JP-0327900.
2000JP-0297073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         describes a movel oxytocin secretion-regulating agent a ligand peptide or its salt for the G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                    75; 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                        adrenal gland
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88.9<del>%</del>;
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Pred. No. 7e-J
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     This sequence represents a peptide fragment from a novel human type caligned polypeptide corresponding to main acid residues 23 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, Schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, courosis, asthma, rheumatoid arthrititis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinoccrebeliar degeneration, coppelle of altering the binding activity of the ligand affecting activity of the ligand affecting
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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capable of activation
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DB; AAV02428.
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                                                                                                                                                                                                                                                                             2; Page 184; 258pp;
                                                                                                                                                                                                                                                                                                      peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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"*tada C;
altering
of the G
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ilarity 88.9%;
Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                 The present sequence represents a human type ligand fragment. It

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or piacental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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Pred. No. 1e-09;
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   This is the amino acid sequence of the human pituitary G
CP protein coupled receptor ligand 1992L. A method suitable for
CC commercial high-level production of 1992L comprises expressing
CC the ligand in host cells as a recombinant fusion protein e.g. with
CC been modified to include an N-terminal cysteine residue. The
CC cigand is released from the fusion by cyanylation followed by
CC ammonolysis. 1992L has prolactin secretion-stimulating and (at
C1)4h doses) prolactin secretion-inhibiting properties. It can be
C2 used in the treatment and prevention of various diseases including:
CC seniie dementla, cerebrovascular dementla, and dementia associated
CC vith: genealogical disorders (e.g. Alzheimer's disease, Parkinson's
CC disease, Pick's disease, Huntington's disease), infectious diseases
CC (e.g. Creutzfeldt-Takob's), endocrine or metabolic disease or
CC intoxication by drugs, metal and organic compounds), tumourigenic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
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CC diseases associated with prolactin hypo and hyperseretion
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CC disease associated with prolactin hypo and hyperseretion
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing a 19P2 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 35; S6pp; English.
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proiactin releasing peptide; human; dementia: breast cancer;
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Search completed:
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                                                                                                                    Matches 16;
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Best Local Similarity
                                                                                                                                                                                                        osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 1992 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                                                                                                                                  Sequence
                                                               14 dinpawyasrgirpvgrf 31
                                                                             1 DINPAWYXXRGIRPVGRF
                                                                                                                                                                                    31 AA;
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Perfect score:
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seq length: 2000000000
          protein search, using sw model
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/18a/6B_COMB.pep:*
/cgn2_6/ptodata/2/18a/FCTUS_COMB.pep:*
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US-08-776-971-64
US-09-421-208-48
US-09-105-678A-47
US-08-776-971-66
US-09-105-678A-48
US-09-105-678A-48
US-09-105-678A-48
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-43
US-09-105-678A-44
US-09-105-678A-44
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US-08-776-971-138
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(without alignments)
3.397 Million ceil updates/sec
Sequence 46, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 43, Appl Sequence 43, Appl Sequence 44, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 48, Appl Sequence 49, Appl Sequence 49, Appl Sequence 45, Appl Sequence 45, Appl Sequence 45, Appl Sequence 47, Appl Sequence 48, Appl Sequence 49, Appl Sequence 59, Appl Sequence 50, Appl Sequence 50,
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                       Query Match
Best Local Similarity
Matches 16; Conserv
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Result No.

Conservative

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Mismatches

0,

Gaps

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96.9%;

Score 93; Pred. No. 1

DB 3; 1.3e-09;

Length 20. Indels

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US-09-105-678A-31	US-09-105-678A-8	US-09-105-678A-7	US-09-421-208-42	2	-776	US-08-776-971-10	US-09-105-678A-42	US-09-105-678A-36	US-09-421-208-41	US-09-421-208-35	US-08-776-971-51	US-08-776-971-9	US-09-105-678A-41	US-09-105-678A-35	421	US-09-421-208-34	US-08-776-971-98
Sequence 31, App	Sequence 8, Appl	Sequence 7, Appl	-	Sequence 36, App	52	10,		Sequence 36, App.			51,	9, A	Sequence 41, App	-	-	Sequence 34, App	-

ALIGNMENTS

#### ; MOLECULE TYPE: peptide US-09-105-678A-46 RESULT 1 US-09-105-678A-46 COMPUTER: LIM PC COMPATIBLE COMPUTER: LIM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-POS SOFTWARE: PATENTIA Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PAIOR APPLICATION NUMBER: JP 172118/1997 APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: Conlin, David G. RESERENCE/DOCKET NUMBER: 48466-342 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400 Sequence 46, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION: TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids APPLICANT: Suenaga, Masato APPLICANT: Morlya, Takeo APPLICANT: Morlya, Tokoo APPLICANT: Nishimura, Osamu Tifle Of INVENTION: METHOD OF PI NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk STREET: 130 W CLTY: Boston STATE: MA STRANDEDNESS: TOPOLOGY: 11 TYPE: amino acid COUNTRY: U. Z1P: 02109 ADDRESSEE: 130 Water Street USA linear DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 46 PRODUCING A 19P2 LIGAND

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                                                                      Ouery Match
Best Local s
Matches 16
                                                                                                                                                                                                                                                                                                     NAME: CON111, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-34400
TELEPAX: 617-523-64:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: P 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: P 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: P 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: P 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: P 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                         Local Similarity
                                     1 DINPAWYXXRGIRPVGRF 18
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COMPUTER READABLE FORM:
MEDIUM TYPE: Dlskette
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DINPAWYXXRGIRPVGRF 18
DINPAWYASRGIRPYGRF 20
                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
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Kavamata, Yuja
Hosoya, Masaki
Fujii, Ryo
Fujii, Ryo
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Kitada, Chieko
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                                                                                       96.98;
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a, Yuji
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Pred. No. 1.3e-09;
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                                                                                                          Length 20;
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US-09-105-678A-47; Sequence 47, Ap; Patent No. 6103
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US-09-421-208-46
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Patent No. 6
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Best Local Similarity
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APPLICANT: Suenaga, Massato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                 APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE APPLICATION: ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: 11n
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSEE:
STREET: 13
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
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6258561
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E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
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Pred. No.
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                           COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOETWARE: FESTESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: DS/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
OF TIME OF THE OF TIME OF THE OF
                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOSOYA, MASSÁÍ

FUJII, RYO

FUKUSUMI, ShOJÍ

KItada, Chieko

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinuma, Shuji
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                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/0877697IB
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Kawamata, Yuji
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Pred. NO. 1.3e-09;
0; Mismatches 2;
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-421-208-47
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47, Application US/09421208 Patent No. 6258561
                                                                                                                        PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
ADME: CORIA
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                                                                                                                                                                                                                                                                                                                                              COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
              NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Moriya, Takeo
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CODNTRY: U. ZIP: 02109
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boston
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88.9%;
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Pred. No. 1.3e-09;
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US-09-105-678A-48
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                                                                                                                                    US-09-105-678A-48
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release $1.0, Version $1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-198
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
Matches 16; Conservat
                                                           Matches
                                                                           Best
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                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           TELEPHONE: 617-523-340)
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CUARACTERISTICS:
LENGIN: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Nasato
APPLICANT: MOTIga, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: MIShimuta, Osamu
TITLE OF INVENTION: NETHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                     NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                NOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: linear
                                                                        Local Similarity
                                                                                                                                                                                                TYPE: amino acid
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                            1 DINPAWYXXRGIRPVGRF 18
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48, Application US/09105678A
5, 6103882
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Pred. No. 1.3e-09;
                                                     Score 93; DB 3; Pred. No. 1.4e-09; Wismatches 2;
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RESULT 9 US-09-421-208-48

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; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-08-776-971-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-776-971-66
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                                                                                       Matches 16;
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-9400
TELEFAX: 617-523-6440
INFORMATION FOR SED ID NO: 66:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOTER: IBM COMPACTIBLE
COMPOTER: IBM COMPACTIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 11-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 11-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 11-MAG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 11-MAG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN. DAVId 6.
REGISTRATION NUMBER: 27.036
REGISTRATION NUMBER: 27.036
3 DINPAWYASRGIRPVGRF
                                         1 DINPAWYXXRGIRPVGRF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHWAN, LLF
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, TNEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ninuma, Shuji
Nabata, Yugo
                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                        LENGIN: 22 amino acids
                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawamata,
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                                                                                                            96.98;
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20
                                                                                     Score 93; DB 4;
Pred. NO. 1.4e-09
0; Mlsmatches
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                                                                                                                                 DB 4; Length 22,
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                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                Sequence 9, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Bost Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4
Patent No.
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION CASE-TUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                         TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: MOrlya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Moriya, Takeo
APPLICANT: Tahaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Morlya, Takeo
                                                                                                    CORRESPONDENCE ADDRESS:
                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CONLIN, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 02109
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                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
COUNTRY: USA
ZIP: 02109
                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                            3 DINPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                 1 DINPAWYXXRGIRPVGRF 18
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o. 6258561
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                                                                                                                                                                                                                                                                                                                                                                                                                             ch 96.9%;
1 Similarity 88.9%;
16; Conservative
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                                                                   130 Water Street
                                                                                     DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93; DB 4;
Pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 22;
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APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                    APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA: APPLICATION DATA: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY,AGENT INFORMATION:
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: #loppy dlak

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD OF PRODDCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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CITY: Boston
STATE: MA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
TELEPHONE:
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| 16; Conserv
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Pred. No. 2.1e-09;
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: Sequence 61, Application:
: Patent No. 6228984
: GENERAL INFORMATION:
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Best Local Similarity

Matches 16; Conserv
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SEQUENCE CHARACTERISTICS:
                                                        REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
1NFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                FRICA AFFLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DF 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-BUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/ACENT INFORMATION:
NAME: CON111, DAV1d G.
REGISTRATION NUMBER: 27,026
DEPERDENCY FORCEFOR WITHERE: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 DINPAWYASKGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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Habata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 1BM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 130 Water Street CITY: Boston STATE: MA
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukusumi, Shoji
Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                          ENGTH: 31 amino acids
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Fujii, Ryo
Fukusumi, Shoji
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Kawamata, Yuji
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Pred. No. 2.1e
0; Mismatches
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ches 2;
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; STRANDEDNESS:
; TOPOLOGY: 11r
; MOLECULE TYPE:
US-09-421-208-9
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MOLECULE TYPE: protein
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FRAGMENT TYPE: internal
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-421-208-9
                                                      Query Match
Best Local S
Matches 16
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Patent No. 6258561
GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                                               APPLICATION NDMBER: JP 172118/1997
EILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 517-523-3400
                                                                                                                                                                                                                     TELEFAX: 617-523-6440
1NFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTER1STICS:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, M
APPLICANT: MOTIYA, Tal
APPLICANT: Tanaka, Yol
APPLICANT: Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
14 DINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 DINPAWYASRGIRPYGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                       LENGTH:
                 1 DINPAWYXXRGIRPVGRF 18
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                                                       16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suenaga, Masat
Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                                        31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                               linear
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                                                                                                                                              peptide
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                                                                    96.98;
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                                                      Score 93; DB
Pred. No. 2.le
0; Mismatches
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Pred. No. 2.1e-09;
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                                                                                   DB 4;
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                                                      Gaps
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RESULT

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Patent NO. 610382

GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METNOD DF PRODUCING A
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CU
                                                                                                                                                                                                                                                                                                                                                                                                     9
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; MOLECULE TYPE: peptide
US-09-421-208-43
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US-09-I05-678A-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.9
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                 Sequence 44, Application US/09105678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICATION DATA:

PRIOR APPLICATION UMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
EILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: MOTIYA, Takeo
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
TELEFAX: 617-523-6440
 ADDREST: 1.
STREET: 1.
CITY: Boston
TTE: MA
11SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTN: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FDRM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1. STREET: 1. Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                               14 DINPAWYASRGIRPVGRF 31
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                                                       E: DIKE, BRONSTEIN,
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3I amino acids
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USA
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                                                                       ROBERTS & CUSHMAN, LLP
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                                                                                                                               A 19P2 LIGAND
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                                                                                                                                                                 US-09-105-678A-44
                                                                                                                                                                                                                                                  TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CNARACTERISTICS:
LENGIN: 32 amino acids
                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/105,678A
EFILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 48466-342
REFERENCE/DOCKET NUMBER: 48466-342
TELEPNONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
CURRENT APPLICATION DATA;
                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
14 DINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                       TYPE: amino acid
                      1 DINPAWYXXRGIRPVGRF 18
                                                                       Conservative
                                                                                       96.98;
                                                                       0:
                                                                    Score 93; DB 3; Le
Pred. No. 2.1e-09;
0; Mismatches 2;
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                                                                                                        Length 32;
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec

Gaps

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OM protein &
                                                                                         protein search, using sw model
                                            September 13, 2002, 09:23:59
                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
/ Search time 172.41 Seconds
(Without alignments)
10.589 Million cell updates/
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Title: Perfect score: US-09-446-543A-73\_COPY\_3\_21 96

cell updates/sec

Sequence: 1 DinPawyxxrGIRPVGRFX 19

Scoring table:

Gapop 10.0 , Gapext 0.5 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

Minimum Maximum 88 seq iength: 0
seq length: 2000000000

Post-processing: Ninimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

score and is Ė No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

### SUMMARIES

43	47.9 790 44.8 220 44.8 476	มมมา	N82852 T47959 C83292
444	4.8 476 4.8 719	226	G85480 S61046
42.5 44	ω c	26	T21499
	.е	N	н87660
	. 7	N	AB7664
	2.7 338	N	T20100
41 42	. 7	N	B64395
41 42	.7	N	H64371
41 42	.7	N	AG0502
41 42	. 7	N	A87448
40 41	. 7	N	T35841
40 41.	7	బ	F71015
40 41	٠,	N	T35901
40 41	. 7	N	G82844
40 41	.7	<b></b>	в69009
40 41	.7	N	T00708
40 41	.7	N	AF1174
40 41	1.7 486	N	AG1531
	.7	N	AE0418
39.5 41	<u>;</u> _	N	T49717
	ò	N	D81319
39 40	6	<u>.</u>	NEBP37
39 40	0.6 250	N	G83400

45	4	43	42	<u>4</u>	40	39	38	37	36	35	3	33	32	ω H	30	
38	38	38	30	38.5	38.5	38.5	38.5	38.5	38.5	39	39	39	39	39	39	
39.6	39.6	39.6	39.6	40.1	40.1	40.1	40.1	40.1	40.1	40.6	40.6	40.6	40.6	40.6	40.6	
167	167	158	127	906	906	877	831	374	154	1296	953	936	485	340	256	
N	N	N	N	<b>-</b> -	_	Ц	N	N	N			N			N	
B97575	AB2796	F72725	B83157	LJMSCN	IJHUCN	LJBOCN	S26675	G70947	AH0264	T16859	E82068	C84480	E83663	T20102	E95936	
hypothetlcai prote	acetyltransferase	probable ribosomal	hypothetical prote	N-cadherin precurs	cadherin 2 precurs	N-cadherin precurs	DNA-directed DNA p	hypothetlcai prote	conserved hypothet	hypothetlcai prote	valyl-tRNA synthet	hypothetical prote	glutamyl-tRNA synt	hypothet1cal prote	hypothetical prote	

# ALIGNMENTS

prolactin-releasing peptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

G;Accession: JC7607
R;Yamada, N.; Ozawa, A.; Ishii, S.; Shlbusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001
A;Titie: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; NUID:21092765; PNID:11178959
A;Accession: JC7607

A; Molecule type: DNA A; Residues: 1-83 <YAM>

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release release, and stimulation of ACTN secretion from the pituitary. from rat anterior

C; Genetics:

A; introns: 33/1 A; Gene: PrRP

Оy	Ques Best Nato
35	t Loc thes
DINPAW 	Query Natch Best Locai Sim Natches 16;
1 DINPAWYXXRGIRPVGRF 18                     35 DINPAWYTGRGIRPVGRF 52	Query Natch 95.8%; Score 92; DB 2: Length 83; Best Local Similarity 88.9%; Pred. No. 1.4e-08; Natches 16; Conservative 0; Mismatches 2; Indeis
RF 18	95.8%; 88.9%; 1ve
	Score Pred. 0; Mis
	92; No. smatc
	DB 2: 1.4e-0
	ع; 2;
	2; Len9th 83; 08; 2; Indeis
	0; Gaps
	0;

hydroxybenzoate octaprenyltransferase xF0068 [imported] - Xyiella fastidiosa (strain C;Species: Xylelia fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000 C;Accession: H82852 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Rature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: H82852

Nucleotide Seq

A; Status: preliminary

A;Molecuie type: DNA
A;Residues: 1-333 <SIM>
A;Residues: 1-333 <SIM>
A;Cross-references: GB:AE003860; GB:AE003849; NID:99104830; PIDN:AAF82881.1; GSPDB:GN
A;Cross-references: strain 9a5c
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.N.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

```
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, H.M. F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.V.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za; Reference number: A59328
A; Experimental source: strain PAO1 C; Genetics:
                                                                                                                                                                                                                                                              probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001
C;Accession: C83292
                                                         A; Molecule type: DNA
A; Residues: 1-220 <STO>
                                                                                                                     A;Title: Complete genome se
A;Reference number: A82950;
A;Accession: C83292
                                                                                                                                                                               R:Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                     몽
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A; Residues: 1-790 <DEH>
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A; Accession: T47959
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C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
                                      A; Cross-references: GB: AE004709; GB: AE004091; NID: g9948904; PIDN: AAG06209.1; GSPDB: GN00:
                                                                                                  A; Status: preliminary
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A; Introns: 39/1; (
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50; MUID:20437337
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3; Mismatc
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lger, K.R.; Kas,
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A; Mcalcus, r-v--
A; Molecule type: DNA
A; Residues: 1-476 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB33430.1; PID:gl3359463;
A; Cross-references: strain O157:H7, substrain RIMD 0509952
                                                                                                                      R; Hayashi, T.; Makino, K.; Ohnishi, M.; gasawara, N.; Yasunaga, T.; Kuhara, S.; DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of ent A; Reference number: A99629; MUID:2115623
A; Accession: G90629
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G64720
                                                                                                                                                                                                                                    probable inner membrane transport protein EC30007 [imported] - Escherichia C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: G90629
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F;391-407/Domain:
F;414-430/Domain:
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C;Accession: G64720
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C;Superfamily: plaice glutathione transferase
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A; Residues: 1-476 <BLAT>
                                                                                                       A; Status: preliminary
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Pred. No. 18;
2; Mismatches
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submitted to the Protein A; Reference number: $6770 A; Accession: $67719
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A; Rosidues: 1-492; NY, 494-719 <WEH>
A; Cross-references: EMBL: X68020; NID: 9577609;
A; Note: the nucleotide sequence was submitted
R; Pohl, T.M.
                                                                                                                                                                                  A;Cross-references: EMBL:267750; NID:91061256; PIDN:CAA91579.1; PID:91061272 R;Wehner, E.P.; Rao, E.; Brendel, M. Moi. Gen. Genct. 237, 351-358, 1993 A;Title: Molecular structure and genetic regulation of SFA, a gene responsible A;Reference number: S31138; MUID:93247548
                                                                                                                                                                                                                                                                                                                                                                                       ARP1 protein - yeast (Saccharomyces cerevislae)
N;Alternate names: protein D1478; protein YDL167c
C;Species: Saccharomyces cerevislae
C;Date: 15-Feb-1996 *sequence_revision O1-Mar-1996
C;Accession: S61046; S31139; S67719
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C; Date: 16-Feb-2001
C; Accession: G85480
   A; Molecule type: |
A; Residues: 1-719
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A; Residues: 1-719 < POH>
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Pred. No.
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                         November 1995
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18;
                                                                                                  PIDN:CAA48159.1; PID:g288590 to the EMBL Data Library, Au
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                                                                                                                                                                                                                      a gene responsible for resi
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                                                                                                                                                                                                                                                                                                                                                                                                            29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPDB:GN00145;
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                                                                                                  August 1992
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K.; Apodaca,
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                                                                                                                                 A;Cross-references:
C;Genetics:
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A; Introns: 71/1;
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A;Cross-references: MI
                                                                                                                   A;Gene:
                                                                                                                                                                    A; Molecule type:
A; Residues: 1-433
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                                                                                                                                                                                                  A:Status: preliminary
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Best Local S
Matches 6
                                                 Query Match
Best Local
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Best Local
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hes 9; Conserv
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4 PAWYXXRGIR 13
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R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.T.; Doddon, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; Halte, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Nati. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter Crescentus.
                                                                                                                                                                                                                                                                                                                                            peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus C;Speckes: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: H87660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z19430
A; Accession: T21499
A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: Z19430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F28D1.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21499
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                                                                                                                                                                                                             A; Reference number: A87249; A; Accession: H87660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross·references: EMBL: 270684; PIDN: CAA94603.1; A;Experimental source: clone F28D1
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|INPSWFDWRYSVSIDGHLGIWPIG
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6; Conserv
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6; Conservative
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   Conservative
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                                                                                                                                    GB:AE005673;
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37.5%;
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                   43.8%;
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                                                                                                                                                                                                                                 MUID:21173698;
                                                                                                                                  NID: g13425020; PIDN: AAK25284.1;
Score 42; DB
Pred. No. 24;
2; Mismatches
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Pred. No. 27;
3; Mismatches
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Pred. No. 20;
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CiSpecles: Cablobacter crescentus
C;Date: 20-Apr-2001 #aequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A87664
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, D.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87664
C:Accession: B64395
C:Accession: B64395
R;Bult, C.J.; White, O.; Disen, G.J.; Zhou, L.; Flelschmann, R.D.; Sutton, G.G.; R;Bult, C.I.; Overbeek, R.; Kirkneas, E.F.; Weinstock, K.G.; Merrick, J.M.; Glot rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
                                                                                                                                                                     RESULT
B64395
                                                                                                   malic acid transport protein - Methanococcua jannaachii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_reviaion 13-Sep-1996 #tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Realdues: 1-338 <WIL>
A;Cross-references: EMBL:272505; PIDN:CAA96608.1; GSPDB:GN00023; CESD:C50c10.2
A:Experimental aource: clone C50C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C50C10.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Dct-1999 #sequence_revision 15-Dct-1999 #text_change 15-Oct-1999 C;Accession: T20100
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C:Specles: C:
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A;Reference number: 219224
A;Accession: T20100
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A;Molecule type: DNA
A;Realdues: 1-226 <STD>
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A; Introns: 74/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:C50Cl0.2
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Matches 7
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Best Local S
Matches 7
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nes 7; Conserv
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PAWWEARGVR
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                  42.7%;
hllarity 53.8%;
Conservative
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41.28:
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Pred. No.
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Pred.
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                                                                                                 13-Sep-1996 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                          Length 338;
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A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus A.Reference number: A64300; MUID:98337999

A:Stratus - ----
                                                                                                                                                                                                                                                                  probable amino-acid transport protein STY0006 [imported] - Salmonella enter C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C;Accession: AG0502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Bult, C.J.: White, D.: Olaen, G.J.: Zhou, L.: Fleischmann, R.D.; Sutton, G.G.: Blak R:Relch, C.J.; Dverbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.: Glodek, rson, J.D.; Sadow, P. W.: Hanna, M.C.: Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A:Authora: Kaine, B.P.; Borodovaky, M.; Klenk, H.P.: Fraser, C.M.; Smith, H.D.; Woese A;Tille: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Reference number: A64300; MUID:96337999

A:Accession: H64371
  A; Moiecule type: DNA
A; Residues: 1-476 <PAR>
A; Cross-references: GB: AL513382;
                                                                                                                                                        , S.: Moule, S.: D'Gaora, P.
Nature 413, 848-852, 2001
A; Authora: Parry, C.: Quall. M.:
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A:Molecule type: DNA
A:Residuea: 1-342 <BUL>
                                                                                                                A:Title: Complete genome sequence A;Reference number: AB0502: PMID:1
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th, T.; Connerton, P.; Cronln, A.;
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A:Gene: STY0006
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it is coinforme ute. The as long is removed bent (See b.ch).	Rawamata T., Niah Teleasin releasin (PRL) re h its re pRL. Le PRL)	es; Catarrhini s; Catarrhini 18., Kawamata T., Matsumoto Onda H., Fuji	PRT; 87 uence upda otation up ecursor (F	TRPE_SULSO YG3D_YEAST Y493_MYCTU YNHG_ECOLI YL2_HPY6A YL2_HPY6A ALO_CANAL SDP_EIMBO RA32_SCHPO EPB4_HUMAN SYY_XYLFA TP2M_DICDI ALIGNNENTS
uced through a coilaborati and the EMBL outstation are no restrictions on i its content is in no w asage by and for commerci p://www.lsb-sib.ch/announc p://	Habata Y., Hinuma S., a O., Onda H., ptide (PrrP) and ita se and regulates the or GPR10. May stimulate HYPOTHALAMUS.	<pre>Pertebrata; Euteleostomi; Hominidae; Homo.  'Y., Hosoya M., Fukusumi S., o H., Sekiguchi M., ain.*;</pre>	AA. (te) date) rRP) (Prolactin-releasing peptide PrRP31; Prolactin-	P50386 sulfolobus P53281 saccharomyc Q111158 mycobacter1 P76193 escherichia Q84297 human papil P03106 human papil P03852 candida alb P42789 eimeria bov Q09683 schizoaacch P54760 homo mapien Q9ph12 xyieila fam P90520 dictyosteli

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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fu
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A projactin-releasing peptide in the brain.";
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Projactin-releasing hormone) [Contains: Projactin-releasing peptide PrRP31; Projactin-releasing Projactin-releasing peptide PrRP31; Projactin-releasing Projactin-r
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P81278;
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Eukaryota; Metazoa; Chordata;
Mammaila, Eutheria; Rodentia;
NCBI_TaxID-10116;
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Sekiguchi M., Kitada C.,
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FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May stillactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: Widely expressed, with highest levels 1
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                                                                 DINPAWYXXRGIRPVGRF
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16; Conserv
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                                                                                                             Conservative
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BY SIMILARITY.
PROLACTIN-RELEASING PEPTI
PROLACTIN-RELEASING PEPTI
PROLACTIN-RELEASING PEPTI
AMIDATION (G-53 PROVIDE A
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                                                                                                                                   Score 92;
Pred. No.
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T., Nishimura
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2.1e-09;
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ra О., Onda н
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PRP_BOVIN
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PRP_BOLE
AC 981264
DT 30-MAY
DT 1SSUE
RN SEQUEN
RN HINUMB
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EXL1_HUMAN
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Best Local S
Matches 16
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EMBL; AB015417; BAA29025.1; -
Hormone; Amidation; Signal; C
SIGNAL
PEPTIDE 23 53
PEPTIDE 23 53
PEPTIDE 33 53
NOD_RES 53 53
SEQUENCE 98 AA; 10544 kW;
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P81264;
30-MAY-2000
                                                       EXTLI OR EXTL.

Homo sapiens (Human).

Homo sapiens (Human).

Chordata; Mctazoa; Chordata; Mctazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kurokawa T., Nishimura O., Onda H., Fu
"A prolactin-releasing peptide in the
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98268781; FUDFACE
HINUMA S., Habata Y., Fujii R., Kavamacu ... Se
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kitada C., Masuo Y., Onda H., Fujino M.;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Pr hormone) (Contains: Prolactin-releasing peptide
                                                   Eukaryota; Metazoa;
Memmalia; Eutheria;
NCBI_TaxID-9606;
                                                                                                                               Exostosin-like 1 EXTL1 OR EXTL.
                                                                                                                                                                                                                              EXL1_HUMAN 092935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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Eukaryota; Metazoa;
SEQUENCE FROM N.A MEDLINE-97189339;
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15-JUL-1998 (Rei
16-OCT-2001 (Rei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May stillactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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 PubMed-9037597,
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Cetartiodactyla; Ruminantia;
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98
                                                                                                                                                                     Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92; DB 1;
Pred. No. 3.6e-09;
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                                                                       Craniata; Vertebrata; | Catarrhini; Hominidae;
                                                                                                                                                                                                                                                  PRT;
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minantia; Pecora;
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Sekiguchi M.,
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Anti-oncogene; Multi--
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YAAJ OR BOOO7.
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SEQUENCE FROM N.A.

Wuyts W., Spieker N., Van Roy N., De Paepe A., De Boulle K.,

Willems P.J., Van Nul W., Versteeg R., Speieman F.;

"Refined physical mapping and genomic structure of the EXTL1 gene.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: APPEARS TO DE A TUMOR SUPPRESSOR (BY SIMILARITY).
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SEQUENCE
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"Mutations of the
Chinese.";
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SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
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## AF08363; AAD02840.1;
## AF08363; AAD02840.1;
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## AF083625; AAD02840.1;
## AF083627; AAD02840.1;
## AF083628; AAD02840.1;
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## AF083631; AAD02840.1;

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8; Conservative
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subdivision;
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gene for EXTL, a third member
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EMBL; AE000111; AAC73118.1; -.
ECOGENE; EG11555; yas_J
InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR001463; Na_ala_symp.
InterPro; IPR00145; Na_Ala_symp.
Pfam; PF01235; Na_Ala_symp; 1.
PROSITE; PS00873; NA_ALANINE_SYMP; 1.
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Symport; Comp
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STRAIN-K12 / MG1655;
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"Systematic sequencing of the Escherichia
the 0-2.4 min region.";
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MEDLINE-97426617; PubMed-9278503;
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SWART; SM00547: ZnF_RBE; 2.
PROSITE: PS00030: RRW_RNP_1: FALSE_NEG.
PROSITE: PS00030: RRM_RNP_1: FALSE_NEG.
PROSITE: PS01358: ZF_RANBP2_1; 2.
PROSITE: PS0199: ZF_RANBP2_2: 2.
Nuclear protein; Zinc-finger; RNA-binding:
                                                                                                                                                                                                                                                                                          ZN_FING
                                                                                  STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Wehnor E.P., Rao E., Brendel M.;

*Molecular structure and genetic regulation of SFA, a gene responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product. *;

**Rol. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
     Probable
                                                        Q9FBM3:
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR000504; RRM.
InterPro: IPR001876; znf-Ram
Pfam; PF00076; rrm; l.
Pfam; PF00641; zf-RamBP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P04170; 6RXN.
SGD: S0002326; NRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; x68020; CAA48159.1: -.
EMBL; z67750; CAA91579.1: -.
EMBL; z74215; CAA98741.1: -.
PIR; S31139; S31139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93247548; PubMed-8483449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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NRP1 OR ARP1 OR
                                                                   EX7L_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1995) to
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                                                                                                                                    244
                                                                                                                                                            5 AWYXXRG1RPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: CONVAINS 2 RANBP2-TYPE ZINC FINGERS.
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                   SWFTOYGVRPVG
                                                                                                                                                                                                                                                                                        protein;
226
355
581
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6; Conserv
  001 (Rel. 40, Last sequence update)
001 (Rel. 40, Last annotation updat
exodeoxyribOnuclease VII large sub
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Pred. No. 7.9;
3; Mismatches
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ADA9BC09FD582669 CRC64:
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RESULT 6
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AC 058172;
DT 01-NOV-1997
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FltzGerrald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.l., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fibhrmann J.L., Nguyen D., Stott J.L., Geoghagen N.S.M., Weidman J.F., Fibhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                               STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O. Olsen G.J., Zhou L.,
Sutton G.G., Blake J.A., FitzGerald L.M.,
                                                                                                                                                                                               NCB1_Tax1D=2190;
                                                                                                                                                                                                              Methanococcus
                                                                                                                                                                                                                              Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                           01-NOV-1997
16-OCT-2001
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SEQUENCE 402 AA; 43882 MW: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: 1PR003753: Exonuc_VII_L.
InterPro: 1PR00309; tRNA-synt_2.
Pfam: PF02601; Exonuc_VII_L; 1.
Pfam: PF01336; tRNA_ant1; 1.
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Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-A3(2):
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Exonuclease VII large subunit).
XSEA OR SCK7.29c.
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               Methanococcus
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CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield 5'-phosphomononucleotides.

SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatles and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE XSEA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PEWYAPRGQLSLRAAEIKPVG
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                                                                                                                                                                                                                                               jannaschii.
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Pred. No.
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Matches 8
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weldman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Keiley J.M., Peterson J.D., Sadow P.W., Henna M.C.,

Cotton M.D., Roberts K.M., Nurst M.A., Kaine B.P., Borodovsky M.,

Klank N.-P., Fraser C.M., Smith N.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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TIGR; MJ0762;
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Science 273:1058-1073(1996).
-!- SUBCELLULAR LOCATION: In
      This
                                                                                           Science 273:1058-1073(1996).
-!- SUBCELLULAR LOCATION: in-
-!- SIMILARITY: STRONG, TO M
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jannaschil.";
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SIMILARITY: STRONG, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                   PERMEASE (MAEL).
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53.3%;
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Last annotation updat
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TO M.JANNASCHII MJ0576 AND T
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1; Mismatches
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Matches 8
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21-JUL-1986
21-JUL-1986
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SEDUENCE
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                                                                DNA to the beginning of gene 4.";

J. MOL. BLOL. 148:303-330(1981).

J. HOL. BLOL. 148:303-330(1981).

J. FUNCTION: ENDODEOXYRIBONUCLEASE I, WHICH IS EXPRESSED IN THE LATE STAGE, IS RECESSARY FOR T7 GENETIC RECOMBINATION AND THE BREAKDOWN OF NOST DNA. IN THE EARLY STAGE OF INFECTION, T7 DNA REPLICATES AS A LINEAR MONOMER. 1N THE LATE STAGE, THE T7 DNA REPLICATES YIA LINEAR CONCATEMERS SEVERAL GENOMES IN LENGTN. THE GENE 3 PRODUCT NAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS.

-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphooligonuclectide end-products.
                                                                                                                                                                       Dunn J.J., Studier F.W.,

"Nucleotide sequence from the genetic
"Nucleotide sequence from the genetic
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         This SWISS-PROT entry is copyright. It is produced through a copyred the Swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                           Bacterlophage T7.
Viruses; dsDNA viruses,
T7-like phages.
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the Euro
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Nypothetical
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                                                                                                                                                                                                             MEDLINE-82078034;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      J. Moi. Biol.
[2]
                                                                                                                                                                                                                                                           Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage T7 DNA and
iocations of T7 genetic elements.";
                                                                                                                                                                                                                                                                                               MEDLINE-83241725; PubMed-6864790
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
lifted and this statement is not removed. Usage by and for com
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(Rel. 01, Last sequence update)
(Rel. 32, Last annotation update)
bonuclease I (EC 3.1.21.2) (Endonuclease).
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166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                               PubMed-7310871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
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53.3%;
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5 POTENTIAL.
6 POTENTIAL.
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                                                                                                                      EMBL; AP001507; BAB03828.1; ...
InterPro; IPR000924; tRNA-synt_lc.
InterPro; IPR001112; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the alkaliphilic bacterium Bacillus Inalodurana and genomic sequence comparison with Bacillus subtility Nucleic Acids Res. 28:4317-4331(2000).

-1- CATALYTIC ACTIVITY: ATP + L-9litamate + tRNA(Glu) = AMP + diphosphate + L-glutamyl-tRNA(Glu).
                                                                                                                                                                                                                                                                                                                                                                                                                    Takami H., Nakasone K., Takab
Fuji F., Nirama C., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; V01127; CAA24345.1;
EMBL; V01146; CAA24402.1;
PIR; A00785; NEBP37.
PIR; S42301; S42301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GluRS).
GLTX DR BH0109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Nuclease: Endonuclease.
SEQUENCE 149 AA; 17172 พพ; D092AA28E3743BCl CRC64;
                                                                      Aminoacyl-tRNA synthetase;
                                                                                                 Pfam; PF00749; tRNA-synt_lc; 1
PRINTS; PR00987; TRNASYNTHGLU.

    -1- SUBCELLULAR LOCATION: Cytoplasmic.
    -1- SIMILARITY: BELDNGS TD CLASS-I AMINDACYL-TRNA SYNTHETASE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                       Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus
NCBI_TaxID-86665;
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Bacteria; Firmicutes;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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57.1%;
tive .
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Last annotation update)
ase (EC 6.1.1.17) (Glutan
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us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group;
     3
                                                                    Protein blosynthesis; Ligase; ATP-binding;
"KMSKS" REGIDN.
ATP (BY SIMILARITY).
; 7D34A862918F57B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                ki Y., Maeno G., Sasaki R., Masui
Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB
Pred. No. 8.4;
                                            "NIGN" REGIDN
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Query Match

40.6%;

Score

39:

DB 1;

Length 485

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RESULT 12

SYV_VIBCH

ID SYL_VIBCH

O9KP73;

AC 09KP73;

DT 16-OCT-2001 (Rei. 40, L)

DA CLEATA SYNTHELSE (REI. 10, L)

RA CLIS DR VC2503.

RA SALDERS TORM N.A.

RA CLII S.R. Nelson K.E.,

RA G111 S.R. Nelson R.J. Nelson K.E.,

RA G111 S.R. Nelson R.J. Nelson R.

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Matches
                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-EL TDR N16961 / SERDTYPE D1;
MEDLIND-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwlnn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gili S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermonlaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR002300; tRNA-Synt_1a.
Interpro; IPR001412; tRNA-Synt_I.
Interpro; IPR0012303; tRNA-Synt_val.
Pfam; PF00133; tRNA-Synt_1; 1.
PRINTS; PR00986; TRNASYNTNVAL.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004320; AAF95645.1; -. NSSP; P96142; IGAX. TIGR; VC2503; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria: Proteobacteria:
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                           Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen vibrlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
                                               4 PAWYXXRGIRPVGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + L-valy1-tRNA(Val).
SUBUNIT: MONDMER (BY SIMILARITY).
SUBCELULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TD CLASS-I AMINDACYL-TRNA SYNTNETASE FAMILY.
PAWYDEQGNVFVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAKGIKPVVRF
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7; Conserv
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Last annotation update)
(BC 5.1.1.9) (Valine--tRNA ligase) (ValRS).
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                                                                                               Score 39; DB
Pred. No. 51;
1; Mismatches
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P (BY SIMILARITY).
D93471A33CF4F69C
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                                                                                                                                               Length 953;
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THE RESERVE TO THE PROPERTY OF THE PROPERTY OF
RESULT 14
CAD2_BOVIN
ID CAD2_B
AC P19534
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01-APR-1993 (Rel
15-DEC-1998 (Rel
DNA polymerase I
POLA OR POL
                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00868; DNAPOLI.
SWART; SW00475; 51EXOC; 1.
SWART; SW00278; HhH1; 1.
SWART; SW00279; HhH2; 1.
SWART; SW00485; POLAC; 1.
SWART; SW00485; POLAC; 1.
SWART; SW00485; POLY POLY PROSITE; PS00447; DNA POLY MERASE_A; 1.
PROSITE; PS00447; DNA-POLY MERASE_A; 1.
Transferase; DNA-directed DNA POlymerase; DNA replication; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THEFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ACM B-1257;
STRAIN-ACM B-1257;
MEDLINE-93087201; PubMed-1454544;
MEDLINE-93087201; Vakhitov V.A.;
Akhmetzjanov A.A., Vakhitov V.A.;
  CAD2_BDVIN
P19534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from Thermus flavus.";
Nucleic Acids Res. 20:5839-5839(1992).
-!- CATALYTIC ACTIVITY: N deoxynucleos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermus aquaticus (subsp. flavus).
Bacteria; Thermus/Deinococcus group; Thermus group; Thermus
                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                    DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                 162
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SINILARITY: BELONGS TO
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$26675; $26675.
; P19821; ITAQ.
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                                                                                                                                                          INPAW-YXXRGIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01367; 5_3_exonuclease; 1.
PF02739; 5_3_exonuc_N; 1.
PF00476; DNA_pol_A; 1.
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                                                                                                                                                                                                                Similarity 57.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ); IPR002421; 5_3_exonuclease.

); IPR002298; DNA_polI.

); IPR001098; DNA_pol_A.

); IPR001513; Exo_N_I.

); IPR003583; HHIL1.

); IPR003584; HHIL2.

); IPR001532; XPG_I.
                                                                                                                                                                                                                                                                                                                           409
831 /
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                      STANDARD,
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. 25, Last sequence
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, thormostable (EC 2
                                                                                                                                                                                                                                                                                                                       93783 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                Score 38.5; [Pred. No. 55; ]
                                                                                                                                                                                                                   <u>-</u>-
                                                                                                                                                                                                                                                                                                                           POLYMERASE (BY SIMILARITY).
; 96F93CEFA3CA536D CRC64;
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                      PRT;
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2.7.7.7) (TFL polymerase 1).
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EMBO J. 9:2701-2708(1990).

-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS. THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROCENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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01-FEB-1991 (Rel. I7, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neural-cadherin precursor (N-cadherin) (Cadherin-2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002126; Cadherin.
InterPro; IPR00233; Cadherin_C_term.
Pfam; PF00028; cadherin; 5.
Pfam; PF01049; Cadherin_C_term; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
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Mammalia; Eutheria;
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-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- SINILARITY: CONTAINS 5 CADHERIN DOMAINS.
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                   40.1%;
50.0%;
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Score 38.5; D
Pred. No. 58;
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ID CADZ_HUMAN STAN
AC P19022; 014923;
DT 01.NOV-1990 (Rei. 1
DT 01-0CT-1996 (Rei. 3
DT 16-OCT-2001 (Rei. 4
EMBL: X57548; CAA40773.1: -
EMBL: X54315; CAA38213.1: -
EMBL: S42303; AAB22364.1: -
EMBL: M34064; AAA03236.1: -
EMBL: 227420; CAA81799.1: -
PIR; A38870; IJHUCN.
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Wallis J.A., Fox N. Walsh F.S.;
"Structure of the human N-cadherin gene: YAC analysis and fine chromosomai mapping to 18q11.2.";
Genomics 22:172-179(1994).
-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
-1- FUNCTION: CADHERINS ARE CALCIUM THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF NETEROCENEOUS CELL TYPES. N-CADHERIN MAY BE INVDLVED 1
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MEDLINE-90347462: PubMed-2384753:
Walah F.S. Barton C.H., Putt W..
Spurr N.. Goodfellow P.N.:
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MEDLINE=91016946; PubMed=2216790;
Reid R.A., Hemperly J.J.;
*Human N-cadherin: nucleotide and deduced Nucleic Acids Res. 18:5896-5896(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-1996 (Rei. 34. Last sequence update)
16-OCT-2001 (Rei. 40. Last annotation update)
Neural-cadherin precursor (N-cadherin) (Cadherin-2).
CDN2 DR CDNN OR NCAD.
Nome sariose (N-cadherin)
                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                               modified and this statement
                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-cadherin gene maps to human chromosome E-cadherin gene.";
J. Neurochem. 55:805-812(1990).
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Salomon D. Ayaion O., Patei-King R., Hynes
"Extrajunctional distribution of N-cadherin
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Mammaiia; Eutheria; Primates;
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 5 CADNERIN DOMAINS.
                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collable en the Swiss Institute of Bioinformatics and the EMBL outset European Bioinformatics institute. There are no restrictions by non-profit institutions as long as its content is in field and this statement is not removed. Usage by and for confided and this statement is not removed.
                          P15116; iNCJ
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Catarrhini; Hominidae;
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019879 caenorhabdi
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Best Local Similarity
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Q9w624;
01-NOV-1999 (TremBirel. 1
01-NOV-1999 (TremBirel. 1
01-DEC-2001 (TremBirel. 1
C-RF AMIDE.
       Q93LZ7
Q93LZ7;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carasalus.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Satake H., Minakata H., Fujimoto M.;
"Caraasiua RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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58 EIDPFWYYGRGYRPIGRF 75
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Created)
Last sequence update)
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Pred. No. 2.8a-05;
4; Mismatches 3; Indels
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RA Barros M.H., Bonaccorsi E.D., Bordin S., Boylista C.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F., Costa M.C.R., Costa-Net. C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Forro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nontelro-Vitorello C.B.,
RA Moliveira M.C. de oliveira R.R., Oliveira M.A.,
RA de Oliveira M.C. de oliveira R.A., Onontelro-Vitorello C.B.,
RA Quaggio R.B., Roberto P.G., Rodríques V., de Rosa A.J.M.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA de Sulva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA de Sulva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Aimeida S., Vettore A.L.,
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RT The genome sequence of the plant pathogen Xylella fastidicas ".
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                       The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AE003860: AAF82881.1; -.
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"Cioning and characterization of a new polyketide gene of

Streptomyces aureofaciens CCM3239.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases

EMBL, AY033994; AAK61719.1:
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STRAIN-CCM3239;
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AUR2B.
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Alvaren9a R., Alves L.M.C., Araya J.E., Baia G.S., Ba
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NYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01040; UbiA; : PROSITE; PS00943; UBIC Complete proteome. SEQUENCE 333 AA; 3:
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SMART; SM00212: UBCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                         "Oryza sativa ni
cione:P0702F03."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta;
Ehrhartoldeae; Oryzeae; Oryza,
NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Eukaryota; VIridiplantae;
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01-OCT-2000
                                                                                                                              1 DINPAWYXXRGIRP
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                                                                                                                                                                                                     PS50127; UBIQUITIN_CONJUGAT_2;
Ubiquitin conjugation.
E 540 AA: 60487 MW: 5DELFF4EE
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8: Conser
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 (TrEMBLrel. 15, Created)
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(TrEMBLrel. 19, Last annotation
187.4 KDA PROTEIN.
                                                                                                                                                    Conservative
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ipponbare(GA3) genomic
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yta, Lillopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                          THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
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3; Mismatches
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COVALENT ATTACHMENT OF UBIQ
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09Y276;
01-NOV-1999
de Lonlay P., Valnot I., Barrientos A., Gorbatyu
Benayoun E., Chretien D., Kadhom N., Lombes A.,
Niaudet P., Munnich A., Rustin P., Rotig A.;
"Mutations in bcgl, a mitochondrial respiratory
are responsible for the complex III deficiency o
                                                                                                                                                                                                                                    Yu W. Andersson B., Rorley K.C., Muzny D.M., Ricafrente J.Y., Wentland M.A., Lennon G., Gi "Large-scale concatenation cDNA sequencing."; Genome Res. 7:353-358(1997).
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL132959; CAB71097.1; -,
Hypothetical protein.
SEQUENCE 790 AA; 87376 MH; B222724B75690F3
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Mayer K.F.X., Quetier F.,
Submitted (NOV-1999) to t
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                                                                                                                                     SEQUENCE FROM N.A.
de Lonlay P., Valnot I.,
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97264341; PubMed-9110174;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               construction.";
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Andersson B., Wentland M.A., Ricafrente
"A 'double adaptor' method for improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification and characterization of human cDNAs pET112, SCO1, COX15, and COX11, five genes involved and function of the mitochondrial respiratory chain. Genomics 54:494-504(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petruzzella V ,
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Catarrhini; Hominidae;
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16;
                                                                                              Gorbatyuk M.,
mbes A., Ogier
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shotgun library
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 Gibbs R.A.;

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Matches 7
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X Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener A. Hickey M.J., Brinkman F.S.L., Hufnagle R.O., Kowalik D.J., Lagro A. Hickey M.J., Brinkman F.S.L., Hufnagle R.O., Kowalik D.J., Lagro A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.Y.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Mature 406:959-964(2000).

MR EMBL, AE004709; AAG06209.1; -.

R Interpro; IPR004046; GST_C.

RR Interpro; IPR004045; GST_N.

RR Transferase; Complete proteome.
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EMBL; AF038195; AAB97365.1; ...
EMBL; AF346835; AAK29417.1; ...
EMBL; BC000416; AAH00416.1; ...
EMBL; BC007500; AAH07500.1; ...
InterPro; IPR00393; AAA.
InterPro; IPR003939; AAA.
SMARY; SM00382; AAA; 1.
SMARY; SM00382; AAA; 1.
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Submitted (F
[5]
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Q91022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created 01-MAR-2001 (TrEMBLrel. 16, Last se 01-DEC-2001 (TrEMBLrel. 19, Last an PROBABLE GLUTATHIONE S-TRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-
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Strausberg R.;
Submitted (MAY-2001)
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Submitted (NOV-2000)
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(FEB-2001) to the EMBL
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                                                              Score 43; DB
Pred. No. 13;
1; Mismatches
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RA AZZAWA K., IZAWA M., NIShi K., KIYOSWA H., KONDO S., YAMBADKA I.

RA AZZAWA K., IZAWA M., NIShi K., KIYOSWA H., KONDO S., YAMBADKA I.

RA AZZAWA K., IZAWA M., NIShi K., KIYOSWA H., KONDO S., YAMBADKA I.

RA KAGOTA K., MALEJUDA H.A., ASHDUTNEY M., BATALOV S., CASAVANT T.,

RA KAGOTA K., MALEJUDA H.A., ASHDUTNEY M., BATALOV S., CASAVANT T.,

RA FLEISCHMANN W., GABSTETLAND Y., NIKAJOO I., PESOIC G., QUACKENDUSH J.,

RA KUCHL P., LEWIS S., MATAUO Y., NIKAJOO I., PESOIC G., QUACKENDUSH J.,

RA KUCHL P., LEWIS S., MATAUO Y., NIKAJOO I., PESOIC G., QUACKENDUSH J.,

RA SCHITHI L.M., STAUDHI F., SZUNLI R., TOMITA M., RASHOT T.,

RA SAKAI K., OKIGO T., FUTUNO M., AONO H., BALDATEILI R., BATSH G.,

RA SAKAI K., OKIGO T., FUTUNO M., AONO H., BALDATEILI R., BATSH G.,

RA BIOMSTEIN M.J., BULL C., FIETCHER C., FUJITA M., GARIDOIDI M., F.,

RA BOOMSTEIN M.J., BULL C., FIETCHER C., FUJITA M., GARIDOIDI M.,

RA LYONS P., MATCHIONI L., MASHIMA J., MAZZARELLI J., MOMBAETTS P.,

RA LYONS P., MATCHIONI L., MASHIMA J., MAZZARELLI J., SAKAMOTO N.,

RA LYONS P., MATCHIONI L., MASHIMA J., MAZZARELI J., SAKAMOTO N.,

RA AUGUNT P., RIUT G., FIETCHER C., WHITTING L.,

RA WYNSHAW-BOTIS A., YOSHIDA K., HASEGAWA Y., KAWAJI H., KOHTSUKI S.,

RA HAYASHAICAKI Y., STONCH R.,

RA HAYASHAICAKI Y.,

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Best Local
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9130022019Rik.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Morazoa; Chordata; C
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019879;
01-NOV-1996 (Tremetrel. 0
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F28D1.8 PROTEIN.
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SMART; SM00382; AAA; 1
ATP-binding.
SEQUENCE 418 AA; 47
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        Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
NCBI_TaxIO-6239;
[1]
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Nature 409:685-690(2001).
EMBL; AKO1234; BAB2862.1; -.
MGO; MGI:1914071; 9130022019Rik.
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NCBI_TaxIO=10090;
                                                                                                                                                                      Caenorhabditis elegans.
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                                                                                       Nematoda; Chromadorea; rinae; Caenorhabditis.
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Q99ZA9;
01-JUN-2001
01-JUN-2001
                                                O9A382 PRELIMINARY; PRT; 433 AA.
09A382;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-DEC-2001 (TrEMBLrel. 17, Last sequence update)
01-OEC-2001 (TrEMBLrel. 19, Last annotation update)
PEPTIOOGLYCAN-BINDING PROTEIN, PUTATIVE.
                                                                                                                                                                                                                                                                                                          Complete
SEQUENCE
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OLTD OR SPY1309.
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Science 282:2012-2018(1998).
EMBL; Z70684; CAA94603.2; -.
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Baynes C.;
Caulobacter.
             Bactería;
                          Caulobacter crescentus
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Bacteria; Firmicutes; B
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           alpha subdivision; Caulobacter group;
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01-JAN-1998
01-JAN-1998
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SEQUENCE FROM
STRAIN-ATCC 19
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                    Dekkers L.C., van der Bij A.J., Mulders H.M., Phoelich C.C., Wentwoord A.R., Glandorf D.C.M., Wijffelman C.A., Lugtenberg D.J.J. Wentwoord h.R., Glandorf D.C.M., Wijffelman C.A., Lugtenberg D.J.J. Role of the O-antigen of lipopolysaccharide, and possible roles of growth rate and NADN:ubiquinone oxidoreductase (nuo) in competitive comato root-tip colonization by Pseudomonas fluorescens wCS365.*; Noi. Plant Microbe Interact. 11:763-771(1998).
                                                                                                                                                                                                                                                                                                       STRAIN-WCS365;
MEDLINE-98340543: PubMed-9675892;
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STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698: PubMed-11259647;
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CC3322; -.
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Pred. No. 12;
3; Mismatches
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C STRAIN-ATCC 19089 / CB15;

X MEDILINE-21173698: PubMed=11259647;

X Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Neison K.E.

A Nierman W.C., Feldblyum T.V., Laub M.T., Ohta N., Maddock J.R.,

A Potocka I., Neison W.C., Newton A., Stephens C., Phadke N.D., Eiy

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.N.,

Kolonay J.F., Smit J., Craven M.B., Khouri N., Shetty J., Berry K

Kolonay J.F., Smit J., Craven M.B., Khouri N., Shetty J., Berry K

Utterback T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.":

"Troc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NYPOTNETICAL 31.4 KDA PROTEIN (SIMILAR TO NYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96925
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                                                                                                                                    Nypothetical protein.
SEQUENCE 280 AA; 31429 MW;
                                                                                                                                                                                                                                                                             TISSUE-COLON ADENOCARCINOMA:
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2001) to
                                                                                                                                                                                                                                                                                                                                                                            Strausberg
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-BONE MARROW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nomo saplens (Numan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     096925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nypothetical protein; Complete SEQUENCE 226 AA; 25010 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=69394:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
: PROTEIN CC3347.
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY:
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Primates:
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41.2%;
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                   Score 41; DB
Pred. No. 38;
1; Mlsmatches
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Pred. No.
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CD9C0AAAC38B26CD CRC64;
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ock J.R.,
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M., White
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Q9NVR5
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DT 01-CCT
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Search completed: September 13, 2002, 09:29:19 Job time: 1064 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NVR5 PRELIMINARY; PRT; 328 AA.
Q9NVR5;
Q9NVR5;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2010 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2010 (TrEMBLrel. 17, Last annotation update)
CDNA FL110563 FIS, CIONE NTZRP2002769.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NAEMMBAILA; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SUBJURNA T., Ota T., Hayashi K., Suglyama T., Otsuki T., Hara H.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujli A., Hara H.,

Tanase T., Nomura Y., Toglya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK001425; BAA91684.1;

EMBL; AK001425; BAA91684.1;

SEQUENCE 328 AA; 36943 MW; 67875CE2A89AF663 CRC64;
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|:|| || |
42 DINPLWYKLR 51
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB acq
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Perfect score:
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1: /SIDS1/gcgdata/hold-geneseq/geneaeqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneaeqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneaeqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneaeqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/hold-geneseq/geneaeqp-emb1/AA1984.DAT:*

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10: /SIDS1/gcgdata/hold-geneaeq/geneaeqp-emb1/AA1989.DAT:*

11: /SIDS1/gcgdata/hold-geneaeq/geneaeqp-emb1/AA1999.DAT:*

12: /SIDS1/gcgdata/hold-geneaeq/geneaeqp-emb1/AA1999.DAT:*

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length: 2000000000
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Match
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Gapop 10.0 ,
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AABW97236
AABW97236
AAAY49294
AAAG62534
AAAB90992
AAB10366
AAG62535
AAB103667
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Human type G prote
Human type 11gand
Human oxytocin sec
19P2 11gand peptid
Human CRH releasin
Prolactin releasin
Human cype G prote
Human oxytocin sec
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AAB46954	ADDOOR	AAB90994	AAG62527	AAG62519	AAY49302	AAY49301	AAB10358	AAB10350	AAW95175	AAW95191	AAW97234	AAW97232	AAW31374	AAW31387	AAG62530	AAB10361	AAW97226	AAW31390	AAG62533	AAB10364	AAW31393	AAG62532	AAB10363	AAW31392	AAB90995	AAB90991	AAG62531	929	AAB10362	AAW87615	AAW97235	139	AAG62536
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### ALIGNMENTS

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AAW31394
ID AAW3
XX AAW3
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Kawamata Y,
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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   WPI; 1997-363672/33.
N-PSDB; AAV02431.
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Y, Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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ARBSULT

AAAWA

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KW Rat

KW Proid

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                                          Fuj11 R,
                                                                                                                      (TAKE ) TAKEDA CHEM
                                                                                                                                                                                                       23-JUN-1997;
                                                                                                                                                                                                                                                                                        22-JUN-1998;
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                                          Hinuma
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                                          Kawamata
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Pred. No. 9.9e
0; Mismatches
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                                          Matsumoto
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9.9e-09;
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is used in the course of the invention. The specification describes
an agent for modulating prolactin secretion which comprises a
ligand polypeptide or a sait, for a 6 protein coupled receptor (GPCR)
protein. The agents for promoting prolactin secretion can be used for
treating or preventing hypocovarianism. They can by used for promoting
syndrome, euthyroid or hypometabolism. They can by used for promoting
lactation in a domestic mammal and as an aphrodisiac. The agents for
inhibiting prolactin secretion can be used for treating or preventing
plutitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
The inhibitory agents can also be used for treating or preventing
chorres acromedaling hydatid mode, irruption mode, abortion, unthrifty fetus,
shours lacecharametabolism abortion mode, abortion, unthrifty fetus,
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Best Local :
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physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                                                                                                                                                                                                                                                                        Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretion or placental function, e.g. for treating menopaus syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                              (TAKE ) TAKEDA
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Matches 15
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1982 11gand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosassy can also be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                                                                                                          Disclosure; Page 26; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                        New monocional antibodies, studying diseases related
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumoto H,
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/ mechanism; (
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Pred. No.
0; Mismatc
                                                                                                                                                                                                                                                                                                        useful in diagnosis,
o ligand abnormality
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vous system; pancreat
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                                                                                                                       The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysis or for trasting, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; corticotrophin releasing hormone; CRH; G analgesic; hyperaldosteronism; hypercortisolaem; Addison's disease; adrenai gland hyperfunction;
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                                                                                             Sequence
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                                                                                                                                                                                                                                                      Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
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26-SEP-2000;
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                                                                                                                   Invention
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                       1 INPAWYXXRGIRPVGRF 17
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15; Conserv
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15; Conservative
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                                            Conservative
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2000JP-0297073
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hypercortisolaemia; hypoadrenocorticism:
hyperfunction; obesitυ
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9.9e-09;
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10-SEP-1999;
15-OCT-1999;
AAW31395;
                            AAW31395 standard; Peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
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                                                                                                                                                            Confervative
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9905-0153406.
9905-0159783.
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                                                                                                                                                                          96.7%;
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Pred. No. 9.9e-09;
Pred. matches 2;
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                                             AAB10366 standard; peptide;
                                                                                                                                                                                                                                                                    Sequence
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N-PSDB; AAV02432.
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15-MAR-1996;
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                                                                                                                                                          1 INPAWYXXRGIRPVGRF 17
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                                                                                                                                           2; Page 186; 258pp; English.
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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Matches 15
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                                                              Human; corticotrophin releasing hormone; CRH; G protein receptor ligand analgesic; hyperaldosteronism; hypercortisolsemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting aecretion of oxytocin, as drugs for diaeaaes relating to oxytocin secretion and in veterinary
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                                                                                                                     Human
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                                       Homo sapiena
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15; Conservative
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                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                     96.7%;
88.2%;
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                                                                                                                   related
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                                                                                                                                                                                                                                                                                                                                     Score 87:
Pred. No.
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                                                                                                                  peptide SEQ
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Best Local
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                                                                                                                                    18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, hair alsease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the invention.
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26-SEP-2000:
                     Kawamata
                                           Fujii R,
                                                                                       (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                      26-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic agent.
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modulator: pituitary; central nervous ayatem: pancreas; pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW31396 standard;
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15; Conserv
                     Fukusumi S,
Y, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (flrat entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-coupled receptor ligand fragment
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                                                                                                                                  96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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88.2%;
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                                           Habata
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Pred. No. le-C
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous ayatem: pancreas; prophylactic;
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                                           HLnuma
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                                         Hosoya
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc ligand polypeptide corresponding to amino acid residues 34 to 55 of the csequence represented in AAW31390 and is used in an assay to monitor cligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitsry function modulator, a central nervous system modulator or a psncreatic function modulator. This ligand could have specific applications as a syndrome, containing this specific applications as a syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, crawing growth hormone secretory disease, hyper-and polyphsgia, crawing growth hormone secretory disease, hyper-and polyphsgia, crawing growth hormone secretory disease, hyper-and polyphsgia, crawing syndrome, neurosis, asthms, rhemmatoid arthritis, spinal injury, crassiant brain ischaemia, spilapsy, amylotrophic lateral sclerosis, active myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic demustitis, osteoporosis snd/or coligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local S
Matches 15
  Physiologically-active protein-coupied receptor
                                            WPI; 2000-452298/39
                                                                                                                                                                                                                                                                                      treatment; disesse; psin; atonic bleeding; uterine recovery failure; c caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancress and pituitary gland
                                                                        Matsumoto H,
                                                                                                                                                            22-DEC-1999;
                                                                                                                                                                                        06-JUL-2000
                                                                                                                                                                                                                     WO200038704-A1
                                                                                                                                                                                                                                                 HOMO
                                                                                                                                                                                                                                                                          veterinsry medicine;
                                                                                                                                                                                                                                                                                                                                              Human oxytocin secretion promoting peptide SEO
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)B; AAV02433.
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                                                                                                                                                                                                                                                                                                                     oxytocin
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                                                                                                    TAKEDA CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                        Kitada
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                                                                                                                                98JP-0369585.
                                                                                                                                                            99WO-JP07199
 receptor protein, 1
                                                                                                                                                                                                                                                                                                                     secretion promoter; G
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                                                                                                    LTD.
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    for
 recognized as ligand by for promoting secretion (
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2;
promoting
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34 to 55 of
 of oxytocin,
                                                                                                                                                                                                                                                                                                       cor protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel oxytocin secretion-regulating sgent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for smellorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and sfter expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostssis and is also sppiicsble in veterinsry medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
          corticotrophin relessing hormone (CRH), invoiving the use of a G prot receptor ligand. This can be used to control the secretion of CRH and useful as an snaigesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addisor disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrensi gland hypofunction and obesity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                Humsn; corticotrophin releasing hormone; CRH; analgesic; hyperaldosteronism; hypercortisolae Addison's disesse; adrenal giand hyperfunction
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                                                                                                                                                                  Use of G protein receptor ligand or peptide for corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                             18-NOV-1999;
26-SEP-2000;
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                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                      Kitada C,
                                                                                                                                                                                                                                                                                                                                      17-NOV-2000; 2000WO-JP08119
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                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       releasing
                                                                                                                                                                                                                                      Matsumoto
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                                                                                                                                        Page
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                                                                                                                                                                                                                                                                                             99JP-0327900.
2000JP-0297073.
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                                                                                                                                        75;
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                                                                                                                                     90pp;
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88.2%;
                                                                                                           describes a method of controlling the secretion of
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                                                                                                                                        Japanese
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used
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hypercortisolaemia; hypoadrenocorticism;
nd hyperfunction; obesity.
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                                                                               of a G protein
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peptide

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RESULT
AAW31391
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This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic Syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth bormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperpolactinaemia, diabetes, cancer, pancrestitis, renai disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinai injury, translent brain lschaemia, spihepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebeilar degeneration, CC bone fracture, traums, atopic dermatitis, osteoprosis and/or colloqualectia. Assays can also be developed to screen compounds which are CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                          Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor; ilgand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                           1997-363672/33
DB; AAV02428.
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                                                                                                                                                                                                                                                                                                               2; Page 184; 258pp; English.
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Y, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreas; prophylactic;
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RESULT 14
AAW97235
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Best Local Similarity
Watches 15; Conserve
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           The present sequence represents a human type ligand fragment. It

CC is used in the course of the invention. The specification describes

cC an agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a salt, for a G protein-coupied receptor (GPCR)

CC protein. The agenta for promoting prolactin secretion can be used for

CC treating or preventing hypocvarianism, genecyat cacogenesis, menopausal

CC syndrome, euchyroid or hypometabolism. They can by used for promoting

CC lactation in a domestic mammal and as an aphrodisiac. The agents for

CC inhibiting prolactin secretion can be used for treating or preventing

CC pituitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease,

CC prolactinoma, infertility, impotence, amenoribea, galactorrhea,

CC prolactinoma, chiarl-Frommel syndrome, Argonz-dei Castilo syndrome,

CC prolactinoma syndrome, lymphoma, Sheehan syndrome or dyszoospermia.

CC represe-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.

CC modulating placental function can be used for treating or preventing

CC choriocarcinoma, hydatid mode, irruption mode, abortion, unthrifty fetus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat type ligand; modulation; projectin accretion; gonecyst cacogenesia; gonecyst-cacogenesia; gonecyst-cacogenesia; menopausal syndrome; euthyrold; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disease; projectinome; infertifity; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; rorbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mode; truption mole; abortion; unthrifty fetus; abortmai aaccharometabolism;
                                                                                                                                                                                                                                                                                                                                                            Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hlnuma S,
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88.2%;
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Pred. No. 1.6e-08;
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RESULT 15
AAW87615
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QX
CC This is the amino acid sequence of the human pituitary G
CC protein-coupled receptor ligand 1921. A method suitable for
CC commercial high-level production of 1921 comprises expressing
CC the ligand in host cells as a recombinant fusion protein e.g. with
CC human basic fibroblast growth factor (see AAV83796-97) that has
CC been modified to include an N-terminal cysteine residue. The
CC ligand is released from the fusion by cyanylation followed by
CC ammonolysis. 1992 has prolactin secretion-stimulating and (at
CC high doses) prolactin secretion-inhibiting properties. It can be
CC used in the treatment and prevention of various diseases including:
CC with: genealogical disorders (e.g. Alzhamer's disease, Parkinson's
CC disease, Pick's disease, Huntington's disease, infectious diseases
CC (e.g. Creutzfeidt-Jakob's), endocrine or metabolic disease or
CC toxicosis (o.g. hypothyroidism, vitamin 812 deficiency, alcoholism,
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
CC subarachnoidal heamorrhage, and other types of dementia, depression,
CC diseases associated with prolactin hypo and hypersecretion
CC consciousness, It is also useful for prevention and treatment of
CC consciousness, infertility, impotence and autoimmune disease
CC (hypersective ty, including; hyperprolactineemia, pituitary adenoma,
CC breast cancer, infertility, impotence and autoimmune disease
CC (hypersectively, including; hyperprolactineemia, pituitary adenoma,
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing a 1972 pituitary G protein receptor ligand of a fusion protein, useful for preventing and treating breast cancor, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-047884/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moriya T, Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1992 ligand; G protein coupled receptor; pituitary;
prolactin releasing peptide; human; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 35; 56pp; English.
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88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suenaga M,
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Pred. No. 1.6e-08;
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Best Local Similarity
                                                                                                                                                                                          osteoporosis, menopausal syndrome and renal failure (hyposecration disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                                                                                                                      Sequence
                                                           15
                                                                     1 INPAWYXXRGIRPVGRF 17
                                                           inpawyasrgirpvgrf
                                                                                                                                                                       31 AA;
                                                                                                           Conservative
           September 13,
                                                                                                                       96.78;
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           2002, 09:18:35
                                                                                                         Score 87; DB pred. No. 1.6e 0; Mismatches
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                                                                                                                       DB 20;
1.6e-08;
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Minimum DB :
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Maximum Match 10
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Perfect score:
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seq length: 2000000000
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          No. is the number of resuits predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,
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Match
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/1aa/5B_COMB,pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB,pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB,pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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          200077
    US-09-105-678A-46
US-09-421-208-47
US-09-105-678A-47
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-48
US-09-105-678A-48
US-09-105-678A-49
US-09-105-678A-43
US-09-105-678A-34
US-09-105-678A-34
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US-09-105-678A-34
US-09-105-678A-34
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US-09-105-678A-34
US-09-105-678A-34
US-08-776-971-50
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  sequence
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e 446, Apple 6 47, Apple 6 47, Apple 6 47, Apple 6 48, Apple 6 48, Apple 6 48, Apple 6 48, Apple 6 43, Apple 6 43, Apple 6 43, Apple 6 44, Apple 6 44,
                      Query Match
Best Local Similarity
Matches 15; Conserv
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Result

Conservative

0

Score 87; DB Pred. No, 1,2e 0; Mismatches

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Gaps

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Length 20; Indels

96.7%;

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-105	105	US-09-105-678A-7	421	US-09-421-208-36	US-08-776-971-52	US-08-776-971-10	US-09-105-678A-42	US-09-105-678A-36	US-09-421-208-41	US-09-421-208-35	US-08-776-971-51	US-08-776-971-9	US-09-105-678A-41	US-09-105-678A-35	US-09-421-208-40	US-09-421-208-34	-776
Sequence 31, Appl	Sequence 8, Appli	Sequence 7, Appli	Sequence 42, Appl	Sequence 36, Appl	Sequence 52, Appl		Sequence 42, Appl	Sequence 36, Appl	-	Sequence 35, Appl		Sequence 9, Appli	Sequence 41, Appl	Sequence 35, Appl	Sequence 40, Appl	•	Sequence 98, Appl

ALIGNMENTS

#### TOPOLOGY: iinear TOPOLECULE TYPE: peptide US-09-105-678A-46 US-09-105-678A-46 Patent No. 6103882 GENERAL INFORMATION: Sequence 46, TELEFAX: 617-523-6440 INFORMATION FOR SEQ 1D NO: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Release #1.0, Version #1.30 SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400 TELEFAX: 617-523-6440 APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: CONLIN, DAVID G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342 APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-UN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JF 172118/1997 APPLICANT: Suenaga, Masato APPLICANT: Moriya, Takeo APPLICANT: Tanaka, Yoko APPLICANT: Nishimura, Osamu TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: CURRENT APPLICATION DATA: STREET: 130 W CITY: Boston STATE: MA COUNTRY: U.ZIP, 02109 ADDRESSEE: Application DS/09105678A 6103882 130 Water Street USA DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 엵 PRODUCING A 19P2 LIGAND

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                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-64
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Best Local S
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GENERAL INFORMATION:
                                                                         Matches
                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/776,9718

FILING DATE: 06-Feb-1997

CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: UP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: UP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: UP 8/5419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: UP 8/211805

FILING DATE: 13-MG-1996

APPLICATION NUMBER: UP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: UP 8/246573
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les 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinuma,
                   INPAWYXXRGIRPVGRF 17
INPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INPAWYASRGIRPVGRF 20
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                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 Water Street
                                                                                                                                                                                                                                           TOPOLOGY: 1inear
                                                                                                                                                                                                                                                                                                   LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08776971B
                                                                       Conservative
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Kitada, Chieko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryo
Shoji
                                                                                           96.7%;
88.2%;
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                                                                                           Score 87; DB 4;
Pred. No. 1.2e-08
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                                                                         Mismatches
                                                                                                                                                                                        64 :
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                                                                                                        Length 20;
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US-09-421-208-46
                                                                                                                                                                                                       US-09-105-678A-47
                                                                                                                                                                                                                         RESULT
                                                                                                                                                     Sequence 47, application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
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Patent No. 62
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osa
APPLICANT: Nishimura, Osa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                               APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METNOD OF PRODDCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-JDN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CNARACTERISTICS:
LENGTN: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/105,678 FILING DATE: 26-JDN-1998 APPLICATION NUMBER: JP 172118/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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   STREET:
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                                                                                                                                                                                                                                                                                            1 INPAWYXXRGIRPVGRF 17
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130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
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                                                                                                                                                                                                                                                                                                                                                           96.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65, Application US/0877697IB Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local !
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
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les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I INPAWYXXRGIRPVGRF 17
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                 COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                               COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                               Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INPAWYASRGIRPVGRF 20
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                                                                                                                                                                                                                                                         STATE: MA
                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                             STREET: 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numa, Shuji
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Pred. No. 1.3e
0; Mismatches
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-65
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
RESISTRATION NUMBER: 27,026
RESISTRATION NUMBER: 27,026
RESISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      COUNTRY: USA
2IP: 02109
2IP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Massato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Ogamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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NAME: CONIIn, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Application US/09421208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
FILING DATE: 15-MAR-1996
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 21 amino acids
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88.2%;
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Pred. No. 1.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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; MOLECULE TYPE: peptide
US-09-421-208-47
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US-09-105-678A-48
                                                                 Query Match 96.7
Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
                                                                                                                                                          MOLECULE TYPE: peptide -09-105-678A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: ULIVA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CONTRACT OF TOWN NUMBER: US/09/105,678A
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                             TOPOLOGY: 11
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ZIP: 02109
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   4 INPAWYASRGIRPVGRF 20
                         1 INPAWYXXRGIRPVGRF 17
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                                                                                                                                                                                                                                                22 amino acids
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                                                                                     96.7%;
88.2%;
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88.2%;
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                                                                 Score 87; DB 3; Pred. No. 1.4e-08; 2;
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Pred. No. I.3e-08;
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                                                                                                     Length 22;
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RESULT 9
US-09-421-208-48
                                                                                                                                                                                                                             ; MOLECULE TYPE: protein
; PRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID
US-08-776-971-66
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                                                                                                                                        Matches
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CNARACTERISTICS:
                                                                                     I INPAWYXXRGIRPVGRF 17
                                                                   4 INPAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSED FOR WINDOWS VERSION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400 TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2'
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ZIP: 02109
COMPUTER READABLE FORM:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPQLOGY: linear
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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STATE: MA
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Kitada, Chieko
OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
R OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                    LENGTN: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
                                                                                                                                        Conservative
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88.2%;
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Pred. No. I.4e-08;
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Best Local :
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Patent No.
                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440 INFORMATION FOR SEQ 10 NO: SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING OATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIA RELEASE #1.0, Version #I.30
CURRENT APPLICATION OATA:
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                                                                                                            APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yakeo
APPLICANT: Tanaka, Yosamu
TITLE OF INVENTION: METNOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: .
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APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                              CORRESPONDENCE ADDRESS:
                                                 STREET:
CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            Match 96.7%;
Local Similarity 88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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COUNTRY: USA
ZIP: 02109
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                                  STATE:
                                                                               ADDRESSEE:
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o. 6258561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 amino acids
                                                            130 Water Street
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                                                                               OIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 87;
Pred. No.
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; MOLECULE TYPE:
US-09-105-678A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 172118/1997
APPLIAGATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
TELEPAN: 617-523-6440
INFORMATION FOR SEQ IO NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMPUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                   FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAY1d G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #I.0, Version #I.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CNARACTERISTICS:
LENGTN: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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15 INPAWYASRGIRPVGRF 31
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 02109
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nes 15; Conser
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                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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130 Water Street
                                                                                                                                                                                                                                                                                                                                           USA
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Pred. No. 2e-06;
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TOPOLOGY: Inear
MOLECULE TYPE: peptide
US-09-105-678A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-776-971-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.2
Matches 15; conservative
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Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CNARACTERISTICS:
                                                   INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MUG-1996
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CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CDSHMAN, LLP
                                                                                    TELEFAX: 617-523-6440
                                                                                                                                                      APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                       CDRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUKUSUM1, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
Nabata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: MA
                                  ENGTN: 31 amino acids
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Fujii, Ryo
Fukusumi, Shoji
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Pred. No. 2e-08;
0; Mismatches
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ
DS-08-776-971-61
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                                                                                                                                  US-09-421-208-9
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Best Local S
                                                          Matches
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                                                                                    Query Match
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIn, David G.
REGISTRATION NUMBER: 27,026
REGERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
                                                                                                                                                                                                                 TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suenaga, Ma
APPLICANT: MOTIYA, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CORRENT APPLICATION DATA:
                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1
                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
15 INPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CODNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                      Local
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                          1 INPAWYXXRGIRPVGRF 17
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Moriya, Takeo
Tanaka, Yoko
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                                                                                                                                                             linear
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                                                                    96.7%;
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88.2%;
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                                                       Score 87; DB 4;
Pred. No. 2e-08;
0; Mismatches
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Pred. No. 2e-08;
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                                                                                    Length 31;
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RESULT

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US-09-421-208-43; Sequence 43, Appl.; Patent No. 625856;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                               문
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US-09-105-678A-44
                                                                                                                                                                                                                       Sequence 44, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN, DAVId G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 48466-342

TELEPHONE: 617-523-3400

TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: DIKE, BRONSTEIN, ROBERTS & COSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109
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                                       CITY:
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COUNTRY:
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                                                   130 Water Street
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                                                                       DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.7%;
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Pred. No. 2e-0
0; Mismatches
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2e-08;
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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                                                                                                                                                             Query Match
Best Local Similarity 88.7
Matches I5; Conservative
                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/105,678A
ETLING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ETLING DATE: 27-UN-1997
APPLICATION NUMBER: JP 172118/1997
ETLING DATE: 27-UN-1997
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,0
                                                                                          96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27,026
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                                                                                                                                                                   0
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Pred. No. 2e-08;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Comp Compugen Ltd

OM protein · protein search, using sw modei

Run on September 13, 2002, 09:23:59 ; Search time 172.41 Seconds
(without alignments)
10.032 Million cell updates/

celi updates/sec

Title: Perfect score: US-09-446-543A-73\_COPY\_4\_21 90

Sequence: 1 INPAWYXXRGIRPVGRFX 18

Scoring table: BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283138

283138 seqs, 96089334 residues

Minimum

Maximum BQ BG seq seq length: 0 iength: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* pirl: pir2: pir3: pir4:

pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

#### SUMMARIES

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	ر د	42.2	42.2	42.2	42.2	42.2	42.2	42.2	42.8	42.8	42.8	42.8	42.8	42.8	43.3	43.3	
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#### ALIGNMENTS

RESULT

prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607

R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMIO:11178959
A;Contents: Spleen
A;Accession: JC7607

A; Molecule type: DNA A; Residues: 1-83 < YAM>

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.

C; Genetics:

A; Gene: PrRP A; Introns: 33/1

Ş 밁 Query Match Best Local Similarity Matches 36 INPAWYTGRGIRPVGRF 52 1 INPAWYXXRGIRPVGRF 17 Conservative 95.6%; 0 Score 86; DB 2; Pred. No. 8.2e-08; 0; Mismatches 2 Ν Length 83; Indels 0 Gaps 0

RESULT N

hydroxybenzoate octaprenyltransferase XF0068 [Imported] - Xylelia fastidiosa (strain C;Species: Xylelia fastidiosa (c;Species: Xylelia fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000 C;Accession: H82852
R:anonymous, The Xylelia fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylelia fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Rote: for a complete list of authors see reference number A59328 below A;Accession: H82852
A;Accession: H82852
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 (SIMP)
A;Cross-references: GB:AE003860; GB:AE003849; NIO:g9104830; PIDN:AAF82881.1; GSPDB:GN
A;Cross-references: GB:AE003860; GB:AE003849; NIO:g9104830; PIDN:AAF82881.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

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R;Stover, C.K.; Pham, X.Q.; E;
adman, S.; Yuan, Y.; 8rody, L.
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome seque
A;Reference number: A82950; M.
A;Accession: C83292
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A. M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F. A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Qliveira, M.A.; de Oliveira, M.C.; de Oliveira; R.C.; Palmieri, D.F. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelii, R.V.; Savasak A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, R.G.; Santelii, R.V.; Savasak A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, R.F.; Van Silvai, A.M.; Silva Jr., W.A.; da Silvai, A.R.; Reference number: A59328
A.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-790 <DBH>
A;Cross-references: EMBL:AL132959
A;Experimental source: cultivar Columbia;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: 224480
A;Accession: T47959
A;Station: T47959
                                                                                                                                                                                                                                                                         probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Daecies: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: C83292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F15G16.60 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) C; Species: Arabidopsis thaliana (Mouse-ear cress) C; Date: 20-Apr-2000 *tequence_revision 20-Apr-2000 *tec; Accession: T47959
A/Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GN00:
A/Experimental source: strain PAO1
C;Genetics:
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C;Superfamily: 4-hydroxybenzoate
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A; Hote: F15G16
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8; Conscrv
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50; MUID:20437337
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L.L.; Coulter, S.N.; Folger, K.R.; Kas,
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Pred. No.
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Pred. No. 2
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January 2000
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Larbig,
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K.; Lin,
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hypothetical protein F28D1.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21499
R:Baynes, C.
Submitted to the EMBL Data Library, April 1996
A:Accession: T21499
A:Accession: T21499
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T21499
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A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pohi, T.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; R;Wehner, E.P.; R&o, E.; Brendel, M. Mol. Gen. Genet. 237, 351-358, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARP1 protein - yeast (Saccharomyces N;Alternate names: protein D1478; pr C;Species: Saccharomyces cerevisiae C;Date: 15-Peb-1996 #sequence_revisic: C;Accession: S61046; S31139; S67719
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C;Superfamily: plaice glutathione transferase
A; Moiecule type: DNA
A; Residues: 1-443 <W
                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-719 < POW>
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A; Accession: S31139
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A;Reference number: $61010
A;Accession: $61046
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A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: S67719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the Protein Sequence Database, July 1996
A;Reference number: S67708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-492,'N',494-719 <WEH>
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A; Residues: 1-719 < POH>
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hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
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S31139; S67719
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Pred. No. 20;
3; Mismatches
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Pred. No. 6.1;
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peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
R;Mierman, W.C.: Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, J.
B.; Laub, M.T.: DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.: Haft, D.H.; Kolon
n, J.; Ermolaeva, M.: White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87660
A,Scaus preliminary
A;Molecule type: DNA
A;Residues: 1-433 STO>
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A;Experimental source: clone F28D1
C;Genetics:
A;Gene: CESP:F28D1.8
A;Map position: 4
A;Introns: 71/1; 103/3; 162/3; 215/2; 360/2
                                                                                                                                                                                                                                                                      R.Nierman, W.C.: Feldblyum. T.V.: Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, J. B.; Laub, M.T.: DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.: Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein CC3347 [imported] - Caulobacter crescentus C:Species: Caulobacter crescentus C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change C:Accession: A87664
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C;Genetics:
A;Gene: CC3347
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A87664
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A: Gene: CC3322
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A, Residues: 1-226 <5'
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INPAWYXXRGIRPVGRF 17
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6; Conserv
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7; Conser
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                                                                                                                                                                            GB: AE005673;
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                                                       45.6%;
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                                    Score 41; DB Pred. No. 14; 3: Mismatches
                                                                                                                                                                          NID:gl3425049; PIDN:AAK25309.1; GSPDB:GN00148
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hypothetical protein C50C10.2 - Gaenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T20100 R;McMurray, A.
malic acid transport protein homolog - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: l3-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Ju1-2000 C;Accession: N64371 C;Accession: N64371 R;Bult, C.J.: White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, O; Reich, C.1.: Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Gene
A; Kap
                                                                                                                                           RESULT
N64371
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A; A; Authors: Kaine, B.P.; Borodovsky, M.; Klonk, H.P.; Fraser, C.M.; Smith, H.O.; Woess A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannas
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A; Residues: 1-342 <BUL>
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C:Date: 13 Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: B64395
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A; Introns: 74/3; 144/3;
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A; Residues: 1-338 <WIL>
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125 VNPDWRSGRALRDVFOF
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Similarity 53.8%;
7; Conservative
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8; Conserv
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53.38;
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L.; Fleischmann, R.D.; ; Weinstock, K.G.; Merr

J.M.:

G: Blak

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probable inner membrane transport protein ECs0007 [imported] - Escherichia coli C;Specles: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: G90629
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G90629
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R;Blattcer, F.R.; Plunkett 111, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile; R; Rose, D.J.; Mau, B.; Shso, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Rtie: The complete genome sequence of Escherichia coli K-12.
A;Recession: G64720
R;Hayashl, T.; Mskino, K.; Dhalshl, gasswara, N.; Yasunaga, T.; Kuhsra, DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;91-107/Domain: transmembrane #status predicted <TM3>
F;142-158/Domain: transmembrane #status predicted <TM3}
F;178-194/Domain: transmembrane #status predicted <TM3
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C;Superfamlly: sodlum-dopendent
C;Keywords: amino acid transport
F;10-26/Domain: transmembrane #s
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A;Authora: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frsser, A;Tille: Complete genome sequence of the methanogenic archaeca; Reference number: A64300; MUID:96337999
A;Accession: H64371
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A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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t; transmembrane protein
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M.; Shinagawa, H.
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C;Accession: G85480
R;Perna, N.T.; Piunkett III, G.; Burlsnd, V.; Mau, B.; Glasiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalsnta, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                        C; Species: Escherichia coll
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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C; Superfamliy:
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A; Residues: 1-476 <HAY>
A; Cross references: GB: BA000007; P1DN: BAB33430.1;
A; Cross references: strain O157:H7, substrain
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 C; Superfamily:
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S.; MOULE, S.; D'GAOYA, P.

Nature 413, 848-852, 2001

A;Authora: Parry, C.; Quail, M.; Rutherford, K.;

A;Title: Complete 'genome sequence of s multiple complete 'genome' sequence of s multiple complete 'genome' AB0502; PMID:11677608
A;Molecule type: DNA A;Restdues: 1-476 <PAR>
A;Restdues: 1-476 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01159.1; PID:g16501289; GSPDB:GN00176 C;Genetics:
                                                                                                                                                                                                                                                                                  probable amino-acid transport protein STY0006 [imported] - Salmo C;Specles: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #aequence_revision 09-Nov-2001 #text_change C;Accession: AG0502
                                                                                                                                                                                                                                           R;Parkhlil, J.; Dougan, G.; James, th, T.; Connerton, P.; Cronin, A.;
                                                                                     A; Status: preliminary
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Score 41; Pred. No.

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Length 476;

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A.Gene: STY0006
C:Superfamily: sodium-dependent D-alanine/glycine transport protein

QUETY MICH
Bett Local Similarity 66.7%; Pred. No. 29;
MICHAS 6: Conservative 1: Mismatches 2: Indels 0; Gaps 0;
Oy 3 PAWYXRGI 11
Db 129 PAWYXRGI 137

Search completed: September 13, 2002, 09:23:59
Job time: 774 sec
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

September 13, 2002, 09:30:45; Search time 80.21 Seconds (without alignments) 8.689 Milion cell updates/sec

Titie: Perfect score: Sequence: US-09-446-543A-73\_COPY\_4\_21 90 1 1NPAWYXXRGIRPVGREX 18

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 rcsidues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Q84297 human papil	w			P44408 haemophilus		escheric	limulus	P35360 11mulus po1			71			drosophila	Q9yf98 aeropyrum p		mus n	homo		P30313 thermus agu				escherichi	methanococ	3		sacch		bos tau	P81278 rattus norv	P81277 homo sapien	Description	

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	1 VI2_HPY6B P03106 1 SYV_XYLEA P095h12 1 BRR2_YEAST 932639 1 YHNT_ECOL1 P37622 1 RK16_SPTOG P06510 1 LYTB_AQUAE 055518 1 CYCR_CHRVI 936516 1 CYCR_CHRVI P36516 1 TK103_YEAST 936516 1 TRU03_YEAST P3050707 1 GP72_CAMFA P07097 1 GP72_HUMAN 05nym4
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VL2_HPV6B SYV_XYLFA BRY2_YEAST YHNT_ECOL1 RX16_SPIOG LYTB_AQUAE Y528_SYNY3 CYCR_CHRVI RM03_YEAST TH1L_GOORA GP72_CANFA GP72_HUMAN	P03102 995102 P32639 P37622 P06510 O675218 082947 P36516 P36516 P076916 P076916 P076916 P079m4

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SIGNAL
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the Euro
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Hinuma S., Nabata Y., Fujil R., Kawamata Y., Hosoya M.,
Kitada C., Masuo Y., Asano T., Matsumoto N., Sekiguchi I
Kutokawa T., Nishimura O., Onda H., Fujino M.;
*A prolactin-releasing peptide in the brain.";
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRRP_RAT P81278;
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Sekiguchi M., Kitada C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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Mammaiia; Eutheria; Rodentia;
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                                                                                                                                           PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                           "Tissue distribution of prolactin-releasing peptide
                                                                                                                                                                                                                                                                                                                                                                                                       Sumino Y., Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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TISSUE SPECIFICITY: Widely expressed, with highest levels
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                                                                                                                                                                                                                                                                                                         medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Extended the Swiss Institute. There are no restrict by non-profit institutions as long as its content field and this statement is not removed. Usage by and the swiss statement is not removed.
                      INPAWYXXRGIRPVGRF
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                                                                                                                                                                                        AB015418; BAA29026.1;
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an cmail to license@isb-sib.ch).
                                                                     Similarity
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BY SIMILARITY.
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Pred.
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Pred. No.
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Sciurognathi; Muridae;
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ed. No. le-08;
Mismatches
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T., Nishimura
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tent is in
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EXL1_HUMAN
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P81264:
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30-MAY-2000 (Rel. 39, I
01-MAR-2002 (Rel. 41, I
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Hormone; Amidation; Signal; C
SIGNAL 23 53
PEPTIDE 23 53
PEPTIDE 33 53
MOD_RES 53 53
SEQUENCE 98 AA; 10544 MW;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
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Kitada C., Masuo Y., Asano T., Matsumoto N., S
Kurokawa T., Nishimura O., Onda N., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PTRP)
hormone) [Contains: Prolactin-releasing pepti
SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
                                                                                                                                                                                      Exostosin-like l (Exostosin-L) (Multiple exostosis-like EXTL1 OR EXTL.
                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, 15-JUL-1998 (Rel. 36, 16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate actotrophs directly to secrete RL. lactotrophs directly to secrete RL. TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                          sapiens
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Cetartiodactyla; Ruminantia;
                                                                                                        Primates;
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Last annotation updat
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PROLACTIN-RELEASING PEPTIDE PA
AMIDATION (G-54 PROVIDE AMIDE
08AC35A13B0FA908 CRC64;
                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhinl; Hominidae; Homo.
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Sekiguchi M.,
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RESULT 5
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Anti-oncogene; Nultiaring TRANSNEW
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SEQUENCE
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                                                                    NRP1_YEAST STANDARD; PRT; 719 AA P32770; 012228; 01-00T-193 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
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EMBL;
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ENBC;
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Wayts W., Spieker N., Van Roy N., De Paepe A., De Boulle K.,
Willems P.J., Van Hul W., Versteeg R., Speleman F.;
Willems P.J., Van Hul W., Versteeg R., Speleman F.;
"Refined physical mapping and genomic structure of the EXTL1 gene.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submltted [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles regulares a license agreement (See or send an email to license@isb-sib.ch).
                                    Asparagine-rich protein (ARP protein).
NRP1 OR ARP1 OR ARP OR YDL167C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reticulum (By similarity).
-!- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
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  Eukaryota;
                Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                       405
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3; AF083633; AAD02840.1;
3; AF083623; AAD02840.1;
3; AF083625; AAD02840.1;
3; AF083625; AAD02840.1;
3; AF083625; AAD02840.1;
3; AF083626; AAD02840.1;
3; AF083628; AAD02840.1;
3; AF083639; AAD02840.1;
3; AF083639; AAD02840.1;
3; AF083639; AAD02840.1;
3; AF083639; AAD02840.1;
3; AF083631; AAD02840.1;
4; AF083631; AAD02840.1
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  Fungi;
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  Ascomycota;
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SIGNAL-ANCHOR (TYPE-Il NEMBRANE PROTEIN)
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55E006A8762E5633 CRC64;
Saccharomycotina;
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                                                                      update)
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Pfam; PF0007641; zf-RanBP; 2.

Pfam; SM00360; RRM; 1.

SMART; SM00367; ZnF_RBZ; 2.

PROSITE; PS50102; RRM; 1.

PROSITE; PS003030; RRM_RNP_1; FALSE_NEG.

PROSITE; PS01358; ZF_RANBP2_1; 2.

PROSITE; PS01359; ZF_RANBP2_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X68020; CAA48159.1; -.
EMBL; Z67750; CAA91579.1; -.
EMBL; Z74215; CAA98741.1; -.
PIR; S31139; S31139.
HSSP; P04170; 6RXN
                                                                                                                                                                                                               L_STRCO
                                                                                                                       Q9FBM3;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
SEQUENCE
                                                        16-OCT-2001 (Rei. 40, Created)
16-OCT-2001 (Rei. 40, Last sequence update)
16-OCT-2001 (Rei. 40, Last annotation updatc)
Probable excdeoxyribonuclease VII large subunit
(Exonuclease VII large subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Noiecular structure and genetic regulation of SFA, a responsible for resistance to formaldehyde in Saccharc cerevisiae, and characterization of its protein production. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
[1]
                                           XSEA OR SCK7.29c
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SGD; S0002326; NRP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AH22
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Znf-RanBP.
Actinobacteria; Actinobacteridae;
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RANBP2-TYPE
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Pred.
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I -> N (IN REF. 1).
; ADA9BC09FD582669 CRC64;
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RESULT 7
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058172;
01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                     Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Wainstock K.G., Werrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weldman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
          -!- SUBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nypothetical MJ0762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                Cotton M.D., Roberts K.M., Nurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith N.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanocotjannaschii."
                                                                                                                                                                                                                                                                                                STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR003709; tRNA-synt_2.
Pfam; PF02601; Exonuc_VII_L; I.
Pfam; PF01336; tRNA_anti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
11 FDNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA IN ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARLIY).
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCB1_TaxID-2190;
                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Methanococcales; Mcthanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus jannaschii.
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Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-A3(2);
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NCBI_TaxlD-1902;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PAWYXXRG-----IRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY). CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to or 3'- to 5'-direction to yield 5'-phosphomononucleotides.
SUBUNIT: NETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS
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       SUBCELLULAR LOCATION:
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nilarity 42.9%;
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Pred. No. 4.6;
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Science 273:1058-1073(1996).
Science 273:1058-1073(1996).
Integral membrane protein
-!- SUBCELLULAR LOCATION: Integral membrane protein
                                                                                                                                      Bult C.J., White O., Olsen G.J., Zhou L., Flelschmann R.D., Sutton G.G., Blake J.A., FlzGcraid L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Welnstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weldman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
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MEDILNE-96337999; PubMed-86868087;
Bult C.J., White O., Olsen G.J., Zhou L.,
Sutton G.G., Biake J.A., FitzGeraid L.M.,
                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota;
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the European Bioinformatics institute. The
use by non-profit institutions as Iong
modified and this statement is not removed.
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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nn email to license@isb-sib.ch).
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MEDIAINE=97456617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A.,

Riley M., Collado-Vides J., Glasner J.D., Ro

Gregor J., Davis N.W., Kirkpatrick H.A., Goo
                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         Science
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"Systematic sequencing of the Escherichia coli genome: analysis the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
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NCBI_TaxID=562;
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01-JUL-1993 (Rel. 26, Last sequence u.
16-OCT 2001 (Rel. 40, Last annotation
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or send an email t
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license@1sb-sib.ch).
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632F7671A31DE183 CRC64;
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                                                     (See http://www.isb-sib
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Best Local :
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21-JUL-1986
01-NOV-1995
                                                                                               Dunn J.J., Studier F.W.;

"Nucleotide sequence from the genetic left end of bacteriophage T7

DNA to the beginning of gene 4.";

J. Moi. Biol. 148:303-330(1981).

-I- FUNCTION: ENDODBOXYRIBONUCLEASE I, WHICH IS EXPRESSED IN THE LATE
STACE, IS NECESSARY FOR T7 GENETIC RECOMBINATION AND TWE BREAKDOWN
OF HOST DNA. IN THE EARLY STACE OF INFECTION, T7 DNA REPLICATES AS
A LINEAR MONOMER. IN THE LATE STAGE, THE T7 DNA REPLICATES VIA
LINEAR CONCATEMERS SEVERAL GENOMES IN LENGTH. THE GENE 3 PRODUCT
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TRANSMEM
          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics institute. There are no restue by non-profit institutions as long as its content
                                                                                                                                                                                                                                     Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage T7 locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                            Bacteriophage T7.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     _BPT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECOGENE; EG11555; YaaJ.
                                                                                                                                                                                                      MEDLINE=82078034; PubMed=7310871;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE-83241725; PubMed-6864790;
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InterPro; IPR001463; Na_ala_symp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 PAWYMARGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PAWYXXRGI 11
                                                                            HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                               phosphooligonucleotide end-products.
                                                                                                                                                                                                                                                                                                                                                                                                                                         BPT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conserv
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476
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(Rel. 01, Last sequence update)
(Rel. 32, Last annotation update)
bonuclease I (BC 3.1.21.2) (Endonuclease)
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RESULT 11
SYE_BACHD
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Best Local S
Matches 8
     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28.4317-4331(2000).

-I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) - AMP +
diphosphate + L-glutamyl-tRNA(Glu).
-I- SUBUCLIULAR LOCATION: Cytoplasmic.
-I- SUBCELULAR LOCATION: Cytoplasmic.
-I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sa
Fuji F., Hirama C., Makamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYE_BACHD
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EMBL; V01146; CAA24402.1; -.
PIR; A00785; NEBP37.
PIR; S42301; S42301.
Hydrolase; Nuclease; Endonuclease.
Hydrolase; Nuclease; Endonuclease.
SEQUENCE 149 AA; 17172 MW; D092AA28E3743BC1 CRC64;
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                 InterPro; IPR000924; tRNA-synt_Ic.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP001507; BAB03828.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus halodurans.
Bacteria, Firmicutes, Bacillus/Clostridium
                                                                               SEQUENCE
                                                                                                              BINDING
                                                                                                                                                                                        Complete
                                                                                                                                                                                                                                                                  Pfam; PF00749; tRNA-synt_1c; i
PRINTS; PR00987; TRNASYNTHGLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=86665;
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an email to
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1-tRNA synthetase; Protein biosynthesis; Ligase;
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license@isb-sib.ch).
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                                                                             "KMSKS" REGION.
ATP (BY SIMILARITY).
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., Kuhara S.,
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Matches
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HSSP; P96142; IGAX.
TIGR; VC2503; -.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR002412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val.
Pfam; PF00133; tRNA-synt_l; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
Valy1-trna synthetase (
VALS OR VC2503.
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SEQUENCE
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Q9KP73;
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SITE
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MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Nickey E.K., Peterson J.D., Umayam L.A.,
Colli S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gili S.R., Nelson K.E., Read T.D., Tettelin H., Dragol I., Sellerg P.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellerg P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
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436
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                                             3 PAWYXXRGIRPVGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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+ L-valy1-trna(Val).
SUBUNIT: MONOMER (BY SIMILARITY).
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PAWYDEQGNVFVGR
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7; Conserva
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557
953
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57.18;
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Last annotation update)
(EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
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                                                                                                                       Score 39;
Pred. No.
                                                                                                                                                                                                                         "KMSKS" REGION.
ATP (BY SIMILARITY).
4; D93471A33CF4F69C CRC64;
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Mismatches
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37;
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RESULT 14
CAD2_BOVIN
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Bost Local S
Matches 8
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Pfam; PF00476; DNA_POL_A; 1.
PRINTS; PR00868; DNAPOLI.
SMART; SM00475; 53EXDc; 1.
SMART; SM00279; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
SMART; SM00485; XPGN; 1.
SMART; SM00485; XPGN; 1.
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Pfam; PF01367; 5_
Pfam; PF02739; 5_
Pfam; PF00476; DN
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DPO1_THEFL
P30313;
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CAD2_BDVIN
P19534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 20:5839-5839(1992)
-i- CATALYTIC ACTIVITY: N deoxynucleo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ACM B-1257;
MEDLINE-93087201; PubMed-1454544;
Akhmetzjanov A.A., Vakhitov V.A.;
"Molecular cloning and nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus (subsp. flavus).
Bacteria; Thermus/Deinococcus grov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                 DNA-binding.
                                                                                                                                                                                                             Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
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                                                                      162
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SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
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$26675; $26675.
; P19821; 1TAQ.
                                                                    ITPAWLYEKYGLRP
                                                                                 INPAW-YXXRGIRP
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                                                                                                                Similarity 57.8
8; Conservative
                                                                                                                                                                                                                                                                                                                                          ); IPR002421; 5_3_exonuclease.
); IPR002298; DNA_poil.
); IPR001098; DNA_poil.
); IPR001513; Exo_N_I.
); IPR003583; NHH_1.
); IPR003584; NHH_2.
); IPR001532; XPG_I.
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           STANOARD;
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                                                                                                                                                                                                                                                                                                                                _3_exonuclease;
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25, Last sequence update)
37, Last annotation update)
thermostable (EC 2.7.7.7) (TFL polymerase 1).
                                                                                                                                                                                                                         DNA_POLYMERASE_A;
                                                                                                                                                                            93783 MW;
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                                                                                                                           42.8%;
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Pred. No. 39;
L; Mismatches
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                                                                                                                                                                          POLYMERASE (BY SIMILARITY). 96F93CEFA3CA536D CRC64;
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           PRT:
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Matches
              Query Match
Best Locai
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InterPro; IPR000233; Cadherin_C.
Pfam; PF00028; Cadherin; 5.
Pfam; PF01049; Cadherin_C_term;
PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-90360979; PubMed-2390969;
LLAW C.W., Cannon C., Power M.D., K
LLAW C.W., Cannon C., Power M.D., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991
01-FEB-1991
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILLAW C.W., Cannon C., Power M.D., Kiboneka P.K., Rubin L.L.;

"Identification and cioning of two species of cadherins in bovine
endothelial cells.";

EMBO J. 9:2701-2708(1990).

-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
-1- THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF NETEROCENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I

NEURONAL RECOGNITION MECHANISM.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Ch
Mammalla; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                              SEQUENCE
                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                        PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P15116; 1NCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
[1]
 Local Similarity
hes 9; Conserv
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(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
erin precursor (N-cadherin) (Cadherin-2) (Fragment).
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131
131
131
131
  Conservative
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                                                          130
695
695
717
238
363
363
468
574
685
685
373
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5244
685
5243
96845
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              42.8%;
                                                                                                                                                                                                                                                                                                                                                                                               Cadherin_C_term
                                                                                                                                                                                                                                                                                                                                                                       C_term;
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                                                                                                                                                          CYTOPLASMIC CADHERIN 1. CADHERIN 2. CADHERIN 3. CADHERIN 4. CADHERIN 5. SER-RICH.
 9
                                                                        N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
              Pred.
                        Score 38.5;
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-LINKED (GLCNAC.
441B829ED871A249
  Mismatches
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GGLCNAC...
GGLCNAC...
GGLCNAC...
              42
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                         1;
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                        Length 877;
 Indels
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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P19022; Q14923;
O1-NOV-1990 (Rel. 16, Created)
O1-OCT-1996 (Rel. 34, Last sequence updat
16-OCT-2001 (Rel. 40, Last annotation upd
Neural-cadherin precursor (N-cadherin) (C
CDH2 OR CDHN OR NCAD.
Homo sapiens (Ruman).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-20 FROM N.A.

SEQUENCE OF 1-20 FROM N.A.

MEDILINE-95048366; PubMed=7959764;

WAILIS J.A., FOX M., WAISH F.S.;

"Structure of the human N-cadherin gene: YAC analysis and fine chromosomal mapping to 18q11.2.";

Genomics 22:172-179(1994)

-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-1- FUNCTION: CADHERINS ARE CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I NEURONNAL RECOGNITION MECHANISM.
                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *N-cadherin gene maps to human chromosome 18 and is not linked to the E-cadherin gene.";
J. Neurochem. 55:805-812(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 160-906 FROM N.A. MEDLINE-90347462; PUMMED-2384753; Walsh F.S., Barton C.H., Putt W., Spurr N., Goodfellow P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92363956; PubMed-1500442; Salomon D., Ayalon O., Patel-King *Extrajunctional distribution of vendothelial cells.";
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*Human N-cadherin: nucleotide and deduced
Nucleic Acids Res. 18:5896-5896(1990). •
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Mammalia; Eutheria; Primates;
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MIM; 114020
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SL; X54315; CAA38213.1; -.

$42303; AA822854.1; -.

SL; M34064; AAA03236.1; -.

SL; Z27420; CAA81799.1; -.

R; A36870; IJHUCN.
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                                                 P15116; INCJ
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IPR002126; Cadherin
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O9w624 carassius a
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O9y276 homo sapien
Q91022 pseudomonas
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Q19879 caenorhabdi
Q99z89 streptococc
O9a382 caulobacter
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Q1-NOV-1999 (TrEMBLrel. 1
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C-RF AMIDE.
 01-DEC-2001
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                                                                                                                                                                                                    Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
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SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                     Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygil; Neopterygil; Teleostel;
Cypriniformes; Cyprinidae; Carassius.
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RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira N.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manchado M.A., Natracca E.C., Miyaki C.Y., Monteiro-vitorelio C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
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RA Machado R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Pelxoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Souza N.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A.,
RA da Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
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01-OCT-2000 (TremBLrel.
01-DEC-2001 (TremBLrel.
                    "The genome sequence of the plant
Nature 406:151-159(2000).
EMBL; AE003860; AAF82881.1; -.
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submitted (JAN-2000) to the EMEL; AL132959; CAB71097.1; -.
Nypothetical protein.
SEQUENCE 790 AA; 87376 MW;
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PROSITE; PS00943; UBIA; UNKNOWN_1.
Complete proteome.
SEQUENCE 333 AA; 37931 MW; ECF
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots: Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                       MEDLINE-99097350; PubMed-9878253;
Petruzzella V., Tiranti V., Ferna
Zeviani M.;
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                                                                                            TISSUE-BRAIN;
                                                                                                            SEQUENCE FROM N.A.
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Mayer K.F.X., Quetier F.,
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NCBI_TaxID=287;
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01-MAR-2001
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"Mutations in bosl, a mitochondrial respiratory chain assembly are responsible for the complex III deficiency of patients with tubulopathy and liver failure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and function of the mitochondrial respiratory chain.";
Genomics 54:494-504(1998).
[2]
                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria,
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annotation update)
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mbes A., Ogier de Baulny
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C STRAIN-ATCC 15592 / PAOI;

K KEDLINE-20437337; PubMed-10984043;

RX KEDLINE-20437337; PubMed-10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Rowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAOI, an

Opportunistic pathogen.";

RI Nature 406:959-964(2000).

DR EMBL; AE004709, AAG06209.1; -.

DR InterPro; IPR004046; GST_C.

DR InterPro; IPR004045; GST_N.

KW Transferase; Complete proteome.

SQ SEQUENCE 220 AA; 24716 MW; 6596183EA6CAA050 CRC64;
                                                                                                                                                                                                           RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Aizawa K., Izawa M., Nishi K., Klyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Klyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Watsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Schriml K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Hysniki H., Sato K., Kangali M., Kararelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Haysnika P., A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Haysnika P., A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 9
                                   Nature 409:685-690(2001).
EMBL; AK012324; BAB28162.1; -.
MGD; MG1:1914071; 9130022019Rlk.
InterPro; IPR003593; AAA.
InterPro; IPR003595; AAA subfam.
Pfam; PF00004; AAA; 1.
SMART; SM00382; AAA; 1.
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01-DEC-2001 (TREMBLRel. 1
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STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K.
  ATP-binding.
SEQUENCE 418
                                                                                                                                                                              "Functional annotation of a
                                                                                                                                                                                                   Hayashizaki Y
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Mammalla; Eutheria;
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  94905BA9B097F0DE CRC64;
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Proc. Nat
EMBL/ AE(
Complete
                  STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;

MEDLINE-21192684; PubNed-11296296;

Ferretti J.J., McShan W.N., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL, AE006570; AAK34153.1; -.
                                                                                                                                                                                                                                                          Streptococcus.
NCBI_TaxID=1314;
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Streptococcus pyogene.
Bacteria; Flrmicutes;
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01-DEC-2001 (TIEMBLIE1, 19,
01-DEC-2001 (TIEMBLIE1, 19,
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Rhabditidae; Peloderinae; Caer
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Pred. No. 19;
3; Nismatches
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Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E
DeBoy R.T., Dodaon R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khourl H., Shetty J., Berry
Utterback T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., Wh
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.N.,
Complete genome sequence of Caulobacter Creacentus.";
Proc. Natl. Acad., Sci. U.Y., A., 98:4136-4141(2001).
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SEQUENCE FROM N.A. STRAIN-WCS365; MEDLINE-98340543;
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RA NIerman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Potocka I. Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Kolonay J.F., Smil J., Craven M.B., Khouri N., Shetty J., Berry K.,

RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shaplro L., Fraser C.M.;

"Complate genome sequence of Caulobacter crescentus.";

L Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

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EMBL: Y14569; CAN74900.1: -.

InterPro; IPR001135: Complex1_49Kd.
Pfam; PF00346: complex1_49Kd. 1.
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Q9A7W7
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Matches 7
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Science 282:2012-2018(1998).
EMBL; 272505: CAA96608.1; -.
InterPro; IPR003839: DUF215.
Pfam; PF02688; DUF215; 1.
SEQUENCE 338 AA: 39053 MW;
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01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                  Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K. Eisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Schens C., Phadke N.D., E. DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Barry Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus.":

Proc. Natl. Acad. Scl. U.S.A. 98:4136-4141(2001).
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Q9A7W7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / C815;
MEDLINE-21173698; PubMed-11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa; Nemato
Rhabditldae; Peloderinae;
                                                                                                                                                                                                      TIGR; CC1602; -.
Hypothetical protein; Complete
SEQUENCE 545 AA; 60175 MW:
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MEDLINE=99069613; PubMed=9851916;
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242
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                                           3 PAWYXXRGIRPVGRF 17
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1: Mismatches
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ed. No. 55;
Mismatches
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RESULT

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Search completed: September 13, 2002, 09:29:20 Job time: 1065 sec
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RA Addams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Kli P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barndon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Abril J.F., Aqbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballcw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkwa D., Botchan H.R., Bouck J., Brokstein P., Brottler P.,
RA Borkwa D., Botchan H.R., Bouck J., Brokstein P., Brottler P.,
RA Borkwa D., Botchan H.R., Bouck J., Brokstein P., Brottler P.,
RA Borkwa D., Botchan H.R., Bouck J., Brokstein P., Brottler P.,
RA Gebalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Ling Y., Lin X.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Mennison J.A., Ketchum K.A.,
RA Harls N., Waltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Melson D.R., Nelson K.A., Havon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Stapleton M., Stupaki M.P., Saith T.,
RA Melson D.R., Welson K.A., Walners R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Slapson M., Skupski M.P., Saith T.,
RA Harls R., Renington K.B., Walter R., Venter E., Wang A.H., Wang X.,
RA Harls R., Roding F.M., Zhou X., Shue S., Yao Q.A.,
RY J., Xong F.M., Shortley R., Walter R., Shend A.H., Wang X.,
RA Harls R., Shortley R., Walter R., Shen
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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Q1-MAY-2000 (TrEMBLrel 13, C
Q1-MAY-2000 (TrEMBLrel 13, I
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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54.58;
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Last sequence update)
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1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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4.724 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPAWYXXRGIRPVGRFX 17
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   AAB10365
AAY49294
AAG62539
AAB31395
AAB10366
AAG62535
AAW31396
AAW31396
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AAW97236
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Human type G prote
Human type 11gand
Human oxytocin sec
19P2 11gand peptid
Human CRN releasin
Prolactin releasin
Human type G prote
Human oxytocin sec
Human oxytocin sec
Human oxytocin sec
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AAB46954	AAB90996	AAB90994	AAG62527	AAG62519	AAY49302	AAY49301	AABI0358	AABI0350	AAW95175	AAW95191	AAW97234	AAW97232	AAW31374	AAW3I367	AAG62530	AAB10361	AAW97226	AAW31390	AAG62533	AAB10364	AAW31393	AAG62532	AABI0363	AAW31392	AAB90995	AAB90991	AAG62531	AAY49291	AAB10362	AAW87615	AAW97235	139	AAG62536	
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## ALIGNMENTS

AAW31394 RESULT

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AAW3I394 standard;

Peptide;

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06-APR-1998 AAW3I394;

(flrst entry)

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18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
WPI; 1997-363672/33.
N-PSDB; AAV0243I.
                        Fujii R, Fukusumi S,
Kawamata Y, Kitada C;
                                                                                                                                                                                                              Human type G protein-coupled receptor llgand fragment 4.
                                                 (TAKE ) TAKEDA CHEM IND LTD
                                                                                                            26-DEC-1996;
                                                                                                                             10-JUL-1997.
                                                                                                                                             W09724436-A2
                                                                                                                                                             Nomo sapiens.
                                                                                                                                                                              therapeutic agent.
                                                                                                                                                                                       modulator;
                                                                                                                                                                                    protein-coupled receptor; ligand binding; pharmaceutical;
pdulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                 96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
                                                                                                            96WO-JP0382I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                 Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhes; galactorrhea; acromegaly; Chiari-Frommel syndrome; Augonz-del Castilo syndrome; forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; lruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
              Fujli R,
                                             (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                       WO9858962-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human type 11gand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97236 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                  22-JUN-1998;
                                                                                                                                                      30-DEC-1998.
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligand peptide for G protein-coupled receptor - acts function in the central nervous system, pancreas and
                                                                               23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 87.
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                                                                                                                                                                                                                                                            lipldmetabollsm;
              Hinuma
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                                                                               97JP-0165437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.5%;
87.5%;
              Kawamata Y,
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Pred. No. 3.6e-08;
0; Mlsmatches 2;
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              Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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RESULT
AAB10365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of as drugs for diseases relating to oxytocin secretion and in wedicine
                                                                                                                                                                                                                                                                                                                                                   Human; oxytocln secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterlne recovery fallure; co-caesarean section; artificial fertilization; galactostasia; goat; pig; veterinary medicine; milk production.
                                                                                                                                                (TAKE ) TAKEDA
                                                                                                                                                                                                                                                                                      WO20003B704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human oxytocin secretion promoting peptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 - NOV - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB10365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB10365 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secretion or placental function, e.g. for treating menopaus syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                     25-DEC-1998;
                                                                                                                                                                                                                    22-DEC-1999;
                                                                                                                                                                                                                                                     06-JUL-2000
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of G protein-coupled receptor ilgands retion or placental function, e.g. for
                                                                                   2000-452298/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                  Kitada
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                                                                                                                                                   CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
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87.5%;
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                                                                                                                  Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83; DB 20; Le
pred. No. 3.6e-08;
rematches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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for treating menopausa
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                                 of oxytocin,
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and in veterinary

Disclosure; Page

63,

72pp; Japanese

This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion

В Ş

S

20

Query Match Best.Local S Matches 14

Local Similarity 87.

96.5%;

Score Pred.

No.

DB 21; I 3.6e-08; thes 2; w

Length 20,

Indels

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Gaps

0

Mismatches

1 NPAWYXXRGIRPVGRF 16

Sequence

20

RESULT

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AAY49294;

22-FEB-2000

(first cntry)

19P2 ligand peptide fragment.

AAY49294 standard;

peptide;

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The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ilyand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                        Disclosure; Page
                                                                                                                                                New monoclonal antibodies, studying diseases related
                                                                                                                                                                                                           Matsumoto H,
                                                                                                                                                                                                                                                                                    20-MAY-1999;
                                                                                                                                                                                                                                                                                                            25-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory
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                                                                                                                                                                                                                                                                                  99WO-JP02650
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                       26; 73pp; Japanese.
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y mechanism; c
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                                                                                                                                                useful in diagnosis,
to ligand abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; diagnosis; proiactin
central nervous system
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Best Local S
Matches 14
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                                                     Query Match
Best Local :
                                                                                                                       The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                              Claim 4; Page 75; 90pp; Japanese.
                                                                                                                                                                                                                                                 Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG62534 standard;
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                       Kitada
                                                                                                                                                                                                                                                                                                                                               18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             analgesic; hyperalo
Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CRH releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
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                      1 NPAWYXXRGIRPVGRF 16
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npawyasrgirpvgrf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corticotrophin releasing hormone; CRH; G protein receptor ligand; sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
                                                     Similarity
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87.5%;
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hyperfunction; obe
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3.6e-08;
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                                           AAW31395
                                                          RESULT
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                                                                                                                                                                Matches
                                                                                                                                                                           Query Match
Best Local Similarity
AAW31395;
                          AAW31395 standard; Peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection; endogenous therapeutic peptide; peptidase; conjugation; biood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure: Page 244:
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10-SEP-1999:
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99US-0153406.
99US-0159783.
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                                                                                                                                                            Score 83; DB 22; 1
Pred. No. 3.6e-08;
D; M1smatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to albumin prevents length of in vivo activity
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RESULT
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AC AAB1
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                                                                                                                                                                                                                                                                  This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 54 of the Sequence represented in AN#31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, province in according the protein partitity, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC acute myocardial infarction, infertility, spinocerebeilar degeneration. CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC cligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                      Matches
                AAB10366
                                            AAB10366 standard: peptide:
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 186; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligand peptide for G protein-coupied receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-363672/33.
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12-AUG-1996;
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modulator; pituitary: centrai nervous system: pancreas: prophylactic;
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28-DEC-1995;
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                                                                                                                                                                                     Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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Pred. No. 3.8e-08;
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                                                                                                                                                                                     Mismatches
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Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                   which contains a ligand peptide or its salt for the G protein coupled receptor protein. It is useful in the form of drugs for ameliocating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physiologically active polypeptide recognized as ligand by G protein coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cocaesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                     AAG62535 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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                                                                 analgesic; hyperai
Addison's disease;
                                                                                                                    Human CRH releasing
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                                                                                                                                                                             AAG62535;
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel oxytocin secretion-regulating agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD.
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                                       domo sapiens.
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5 NPAWY8Srgirpvgrf 20
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                                                              corticotrophin releasing hormone; CRH; G protein receptor ligand; sic; hyperaidosteronism; hypercortisolaemia; hypoadrenocorticism; n's disease; adrenal gland hyperfunction; obesity.
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                                                                                                                                                (first
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                                                                                                                                                                                                     peptide;
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87.5%;
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                                                                                                                    related peptide SEQ
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Pred. No. 3.8e
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cches 2;
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Best Local (
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                                                              28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                  G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                    AAW31396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
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                    Fujii R,
                                       (TAKE ) TAKEDA
                                                                                              18-SEP-1996;
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                                                                                                                                         10-JUL-1997
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                                                                                                                                                                                   Homo sapiens
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          Fukusumi S,
Y, Kitada C;
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                                                                                                                                                                                                        agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                      (first entry)
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95JP-0343371.
96JP-0059419.
96JP-0211805.
                                        CHEM IND LTD
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87,5%;
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                 Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; G caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand peptide for G protein-coupied receptor - acts by modulating function in the central nervous system, pancreas and pituitary glam
  protein-coupled
               Physiologically-active
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                                          WPI; 2000-452298/39.
                                                                                            (TAKE ) TAKEDA
                                                                                                                                                 22-DEC-1999;
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                                                                                                                                                                                                    WO200038704-AL
                                                                                                                                                                                                                                HOMO
                                                                                                                                                                                                                                                      veterinary medicine;
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                                                                                                                                                                                                                                                                                                                                                                                                   standard; peptide;
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-active polypeptide
reccptor protein, f
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                                                                                             LTD.
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                                                                                                                                                                                                                                                       production.
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Pred. No. 3.9e
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for promoting secretion (
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3.9e-08;
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 oxytocin,
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The present sequence describes a method of controlling the secretion corticotrophin releasing hormone (CRH), involving the use of a G protreceptor ligand. This can be used to control the secretion of CRH and useful as an analysesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisoisemia, secondary or chronic hyposadrencorticism, Addison disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            analgesic;
Addison's d
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medicine
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26-SEP-2000; 2000JP-0297073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                          corticotropin
                                                                                                                                                                                                                                              Kitada C,
                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND
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h contains a ligand peptide or its salt for the G protein-c
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14; Conser
                                                                                                                                                                       protein receptor ligand or peptide ropin releasing hormone secretion -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease;
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                                                                                                                                                                                                                                               Matsumoto
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                                                                                                                                              Page 75;
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CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the CC Bequence represented in ARW31390 and is used in an assay to monitor CC ligand binding to the G protein coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia. CC hyperpiplademia, hypercholesterolacmia, hypercidaemia, disease, cancer, pancreatitis, renal disease, phyperpolactinaemia, disease, cancer, pancreatitis, renal disease, cute myocardial infarction, infertiity, spinocerebellar degeneration, cc bone fracture, trauma, atopic dermatitis, osteoporosis and/or capable of aitering the binding activity of the ligand affecting cc activation of the G protein-coupled receptor protein.
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12-AUG-1996;
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N-PSDB; AAV02428.
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odulator; pituitary; centrai nervous system; pancreas; pro
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                                                                                                                                                                                                                                                                                                       peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary giand
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                              258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                   Habata
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Pred. No. 3.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor ligand fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                 Hinuma
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3.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreas; prophylactic;
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RESULT 1
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         The present sequence represents a human type igand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a g protein-coupied receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, robbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing characteristics and account of the contraceptives. The agents for modulating placental function can be used for treating or preventing characteristics.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; contraceptive; placental function; choriocarcinoma; hydatid mole; lruption mole; bobrtion; unthrifty fetus; abnormai saccharometabolism; abnormai lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                    Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 159; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 menopausal syndrome; euthyroid; hypometabollsm; lactation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulation; prolactin secretion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 83; DB
Pred. No. 5.7e
0; Mismatches
abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y, Matsumoto H;
11p1dmetabo11sm
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5.7e-08;
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               unthrifty fetus
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This is the amino acid sequence of the human pituitary GC protein-coupled receptor ligand 1992L. A method suitable for commercial high-level production of 1992L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with location basic fibroblast growth factor (see AAV83796-97) that has composite the ligand is released from the fusion by cyanylation followed by camaonolysis. 1992L has prolactin secretion-stimulating and (at high doses) protactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including: eachle dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease, infectious diseases (e.g. treutzfeldt-Jakob's), endocrine or metabolic disease or toxicosis (e.g. brain tumour), traumatic diseases (e.g. chronic consciousness (e.g. brain tumour), traumatic diseases (e.g. chronic consciousness. It is also useful for prevention and treatment of disease associated with prolactin hypo and hypersecretion disease of consciousness. It is also useful for prevention and treatment of consciousness. Infertility, impotence and autoimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Bost Local Similarity
Matches 14; Conser
                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 35; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing a 19P2 pituitary G protein receptor ligand -
of a fusion protein, useful for preventing and treating
breast cancer, renal failure and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19P2 ligand; G protein coupled receptor; pituitary; projectin releasing peptide; human; demontia; breast cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-D47884/D5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTIYA T, Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAKE ) TAKEDA CHEM IND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83; [
Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                by cleavage dementia,
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                                                  Query Match
Best Local Similarity
Matches 14; Conser
                                                                                                                                      osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 192 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                                                                 Sequence
     16
               1 NPAWYXXRGIRPVGRF 16
npawyasrgirpvgrf 31
                                                                                                                31 AA;
                                                     Conservative
                                                                96.5%;
                                                                 Score 83;
Pred. No.
                                                    Mismatches
                                                              DB 20;
5.7e-08;
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                                                                          Length 31;
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Search completed: Job time: 500 sec

September 13,

2002, 09:18:35

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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        Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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6: /cgn2_6/ptodata/2,
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Match
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/cgn2_6/ptodata/2/las/5B_COMB.pep:*
/cgn2_6/ptodata/2/las/6B_COMB.pep:*
/cgn2_6/ptodata/2/las/6B_COMB.pep:*
/cgn2_6/ptodata/2/las/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/las/PCTUS_COMB.pep:*
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        US-09-105-679A-46
US-09-176-971-64
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-48
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-43
US-08-776-971-138
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(without alignments)
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6 48. Applies 43. Applies 61. Applies 61. Applies 62. Applies 43. Applies 44. Applies 44. Applies 45. Applies 46. 
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95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3	95.3
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Sequence 31, Appl	Sequence 8, Appll	Sequence 7, Appl1	Sequence 42, Appl	Sequence 36, Appl	Sequence 52, Appl		Sequence 42, Appl	Sequence 36, Appl	Sequence 41, Appl		Sequence 51, Appl	>	•	•	Sequence 40, Appl	Sequence 34, Appl	Sequence 98, Appl

AL IGNMENTS

#### Sequence 46, Application US/09105678 Patent No. 6103882 GENERAL INFORMATION: APPLICANT: Suenaga, Masato APPLICANT: Moriya, Takeo APPLICANT: Tanaka, Yoko APPLICANT: Nishimura, Osamu TITLE OF INVENTION: METHOD OF PR NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ; TYPE: amino acid ; STRANDEDNESS: ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-105-678A-46 RESULT 1 US-09-105-678A-46 NAME: CONIIN, David G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-6400 TELEPAX: 617-523-6400 INFORMATION FOR SEO ID NO: 46: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids STREET: 130 W CITY: Boston STATE: MA APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 COUNTRY: ADDRESSEE: 02109 R PT H: 20 amino acids amino acid Application US/09105678A 130 Water Street DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP PRODUCING A 19P2 LIGAND

Query Match Best Local Similarity

96.5%; 87.5%;

Score 83; [ Pred. No. 3

DB 3; 3.1e-08;

Length 20:

Matches

14;

Conservative

0

Mlsmatches

0

Gaps

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                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: US-08-776-971-64
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GENERAL INFORMATION:
                                                                         Matches
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NDMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
                                                                                          Local Similarity
                                  1 NPAWYXXRGIRPVGRF 16
5 NPAWYASRGIRPVGRF 20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                       LENGTN: 20 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <0nknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08776971B
                                                                     Conservative
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Kawamata, Yuji
Nosoya, Masaki
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Fujli, Shoji
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Kitada, Chieko
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                                                                                    96.5%;
                                                                     Score 83; DB 4; Length 20,
Pred. No. 3.Ie-08;
0; Mismatches 2; Indels
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                                                                                                          Length 20;
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PRIOR APPLICATION NUMBER: US 09/10-,...
APPLICATION NUMBER: US 09/10-,...
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPRONE: 617-523-3400
TELEPRONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTN: 20 amino acids
LENGTN: 20 amino acids
                                                                                                                                                                                                                                                                                                                                      밁
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; MOLECULE TYPE:
US-09-421-208-46
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US-09-421-208-46
                                                                                                                                                                                                                                                       US-09-105-678A-47
                                                                                                                                                                                                                 Patent No.
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                                                                                                                                                                                                                                     Sequence 47,
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                          GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimuta, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TIPLE OF INVENTION: MENOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421, 208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/421, 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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5. 6258561
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Boston
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                        130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                96.5%;
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Pred. No. 3.Ie-08;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998

PRIOR APPLICATION NUMBER: JUN-1998

PRIOR APPLICATION NUMBER: JUN-1997

FILING DATE: 27-JUN-1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: CON1In, DAVId G.
REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 48466-342

TELECOMMUNICATION:
TELEPHONE: 617-523-3400

INFORMATION: FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-776-971-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scquence 65, Application Patent No. 6228984
GENERAL INFORMATION:
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Best Local :
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LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 87.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                             COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: F8stSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitado, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                          ClTY: Boston
                                                                                                                                                                                                                                                                              STREET: 130 Water Street
                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08776971B
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Kawamata, Yuji
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Pred. No.
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                                                                                                                                                                                                                        COUNTRY: USA
COUNTRY: USA
2.TP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release $1.0, Version $1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/09421208 Patent No. 6258561
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Best Local Similarity
                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 65:
NAME: CON11n, Dav1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 NPAWYASRGIRPVGRF 20
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
MATION FOR SEQ ID NO. 67
                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Conlin, David G. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morlya, Takeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suenaga,
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87.5%;
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Pred. No. 3.
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                                                                                                                      ; MOLECULE TYPE: peptide US-09-105-678A-48
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1-ENGTH: 21 amino acids
                                                                  Query Match
Best Local :
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Best Local Similarity
                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/09105678A Patent No. 6103882
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                                                                                                                                                                                    TELEFAX: 617-523-6440
TELEFAX: 617-523-6440
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 1992 LIGAND
NDMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                     NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                  Local Similarity 87.
                                                                                                                                                STRANDEDNESS
TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DIKE, .....
PURPLY: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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              NPAWYXXRGIRPVGRF 16
NPAWYASRGIRPVGRF 20
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                                                                96.5%;
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Pred. No. 3.3e
0; Mismatches
                                                 Score 83; DB 3; Le
Pred. No. 3.5e-08;
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3.3e-08
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                                                                            Length 22;
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                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ US-08-776-971-66
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Sequence 66, Application US/0877697IB
Patent No. 6228984
GENERAL INFORMATION:
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                                                                                       Query Match
Best Local Similarity
                                                                       Matches
                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                     1 NPAWYXXRGIRPVGRF 16
5 NPAWYASRGIRPYGRF 20
                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUKUSUML, Shoji

Kitada, Chicko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
                                                                       i4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 7/343371
FILLING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILLING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILLING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILLING DATE: 18-SEP-1996
                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                               LENGTH: 22 amino acids
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                                                                                       96.5%;
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                                                                     Score 83; DB 4;
Pred. No. 3.5e-08,
0; Mismatches
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                                                                                                      DB 4; Length 22;
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RESULT 9 US-09-421-208-48

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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.5
                                                                                                                                                                                                                                       Sequence 9, Application US/09105678A Patent No. 6103882
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/105, FILING OATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118, FILING DATE: 27-JUN-1997
AFTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48461
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                         APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 12M PC COMPATIBLE PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION OATA:
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MEDIUM TYPE: Fioppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Toko
APPLICANT: Nishimura, Osamu
TITLE OF INVERTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
COUNTRY: USA
ZIP: 02109
                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                     STATE:
                                                                                 ADDRESSEE:
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o. 6258561
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                                                Boston
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                                                                130 Water Street
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                                                                                   DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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N-1998
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Pred. No. 3.5e
0; Mismatches
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APPLICATION NUMBER: US/09/105,678A
ETILING DATE: 26-UUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
APTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION : 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-JUN-1998
PRIOR APPLICATION DAWA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY, AGENT INFORMATION:
NAME: CON111, DAVID GREENERSTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEOTIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Massto
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino aclds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 W
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 NPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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87.5%;
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Pred. No. 5.1e-08;
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INFORMATION FOR SEQ ID NO: SEQUENCE CNARACTERISTICS: LENGTN: 31 amino acids

amino acid

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US-08-776-971-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                      TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                            APPLICATION NUMBER: JP 8/246573
FILING DATE: I8-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON111, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 NPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION; <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ninuma, Shuji
                                                                                                                                                                                                                                                             OR APPLICATION NUMBER: PCT/JP96/03821
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
STRANUEDNESS: single
                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY; USA
                                     LENGTN, 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08776971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamata, Yuji
Nosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.5%;
87,5%;
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Pred. No. 5.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.1e-08;
2;
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RESULT

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FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID
US-08-776-971-61
                                                                                                                                    ; MOLECULE TYPE; US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Suenaga, Mai
APPLICANT: Moriya, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Applic
Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                            Matches
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                             TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTON NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
16 NPAWYASRGIRPVGRF 3I
                                                                                                                                                                  STRANDEDNESS
TOPOLOGY: 1
                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 NPAWYASRGIRPVGRF 31
                                                                         Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NPAWYXXRGIRPVGRF 16
                           1 NPAWYXXRGIRPVGRF 16
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                                                                         Similarity
                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 Water Street
                                                                                                                                                                                                                31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moriya, Takeo
Tanaka, Yoko
Nishimura, Osamu
                                                          Conservative
                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHOD OF PRODUCING A 19P2 LIGAND 52
                                                                       96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/09/421,208
                                                         pred. No. 5.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                         48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 83; DB 4;
Pred. No. 5.1e-08;
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                                                                         le-08;
                                                                                       Length 3I;
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                                                         Gaps
                                                         0;
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RESULT 15
US-09-105-678A-44
; Sequence 44, Application US/09105678A
: Patent No. 6103882
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-421-208-43; Sequence 43; Appli; Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
REGISTRATION NUMBER: 27,026
REFERENCE/OCCKET NUMBER: 48466-342
TELEPHONE: 617-523-4400
TELEPHONE: 617-523-4400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CMARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suenaga, Masato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                             APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                ADDRESSEE:
STREET: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02I09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                      16 NPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
COUNTRY:
                                    CITY:
                                                                                                                                                                                                                                                                                                                                                                            I NPAWYXXRGIRPVGRF 16
                                 Boston
               ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 Water Street
                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83; DB
Pred. No. 5.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
5.1e-08;
2;
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TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                       Ouery Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-JUN-1998
PRIOR APPLICATION DAWA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY, AGENT INFORMATION:
NAME: CON110, David G.
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
ZIP: 02109
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                             STRANDEDNESS:
16 NPAWYASRGIRPVGRF 31
                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/105,678A
                      1 NPAWYXXRGIRPVGRF 16
                                                                           Conservative
                                                                                            96.5%;
                                                                           0
                                                                       Score 83; DB 3;
Pred. No. 5.3e-08;
0; Mismatches 2
                                                                                                              Length 32;
                                                                       0,
                                                                       Gaps
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 13, 2002, 09:23:59 ; Search time 172.41 Seconds
(without alignments)
9.475 Million cell updates/sec

Sequence: Title: Perfect score: US-09-446-543A-73\_CQPY\_5\_21 86 1 NPAWYXXRGIRPVGRFX 17

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB Maximum DB

seg length: 0 seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR\_71:\* p1r1:\*
p1r2:\*
p1r3:\*
p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	u	4	ئما	2	1		Result No.
38	38.5	38.5	38.5	38.5	39	39	39	39	39	39	40	40	40	40	40	40	41	41	41	41	41	41	42	43	43	44	46	82		Score
44.2	44.8	44.8	44.8	44.8	45.3	٠	45.3	٠	•		46.5		46.5		46.5		47.7	47.7	47.7	47.7	47.7	47.7	48.8	9	50.0	51.2	53.5	Ġ	٠	Query Match I
127	906	906					485				965				324					476					220			83		Length DB
2 138:	1 19										2 AE				2 T3							-			2 C8:				:	B ID
B83157	IJMSCN	IJHUCN	IJBOCN	T21499	E82068	C84480	E83663	0102	E95936	NEBP37	AE0418	AG1531	AF1174	G82844	T35901	T35841	A87448	AG0502	G85480	G90629	G64720	T20100	Н87660	1046	C83292	H82852	T47959	:7607		
9	precur			hypothetical prote	valy1-tRNA synthet	hypothetical prote	glutamyl-tRNA synt		hypothetical prote	endodeoxyribonucle	ഥ		lysine-specific pe	cystelne synthase	probable araC fami	probable membrane	conserved hypothet	probable amino-aci	lnner membrane tra	probable inner mem	probable amino aci	hypothetical prote	peptidoglycan-blnd	ARP1 protein - yea	probable glutathio	hydroxybenzoate oc	hypothetical prote	prolactin-releasin		Description

	valine tRNA synthe	E86124	N	951	44.2	38	5
	valine tRNA synthe	C91283	N	951	44.2	38	44
	valinetRNA ligas	SYECVE	μ	951	44.2	38	43
	valyl-tRNA synthet	G83167	N	950	44.2	38	42
	acetate kinase - D	B75254	N	398	44.2	38	<u>4</u> 1
	oxldoreductase alp	T35179	N	359	44.2	86	40
	malic acid transpo	H64371	N	347	44.2	38	39
	malic acid transpo	B64395	N	342	44.2	38	38
	hypothetical prote	H72646	N	238	44.2	38	37
4.	_	A87664	N	226	44.2	86	36
	hypothetical prote	D87357	N	194	44.2	38	35
	50s ribosomal prot	D97897	N	178	44.2	. 38	34
	ribosomal protein	D95026	N	178	44.2	38	33
	hypothetical prote	в97575	N	167	44.2	38	32
	acetyltransferase	<b>АВ2796</b>	N	167	44.2	38	31
	probable rlbosomal	F72725	N	158	44.2	38	30
•							

## ALIGNMENTS

prolactin-releasing peptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shlbusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem, Blophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Accession: JC7607

A; Molecule type: DNA A; Residues: 1-83 < YAM>

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.

C;Genetics: A;Gene: PrRP

A; Introns: 33/1

в <b>3</b>	Que Bes Mat
1 NPAWYXXRGIRPVGRF 16 	Query Match 95.3%; Score 82; DB 2; Length 83; Best Local Similarity 87.5%; Pred. No. 2.6e-07; Matches 14; Conservative 0; Mismatches 2; Indels
PVGRI 	ty ervat
52	95.3%; 87.5%; :1ve
	Score Pred. 0; Mis
	82; No.
	DB 2; 2.6e-07 hes
	Len ; 2;
	gth 83; Indels
	0;
	0; Gaps 0;
	0;

hypothetical protein F15G15.50 - Arabidopsis thaliana C/Speckes: Arabidopsis thaliana (mouse-ear cress) C/Deckes: Arabidopsis thaliana (mouse-ear cress) C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000 C/Accession: T47959

R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Q submitted to the Protein Sequence Database, January 2000 A;Reference number: 224480 A;Accession: T47959

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-790 <DEH>

A; Cross-references: EMBL: AL132959
A; Experimental source: cultivar C
C; Genetics: Columbia; BAC clone F15G16

698/3; 773/2

A; Map position: 3 A; Introns: 39/1; 678/2; A; Note: F15G16.60

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```
A. Experimental source: strain 9a5c

R. Simpson, A. J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Uueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, i as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A. Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.E.; Kuramae, E.E.; Lalgi Chado, M.A.; Madeira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lalgi Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.F. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasai A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.N.; Silva Jr., W.A.; da Silvai, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almelda, S.; Vettore, A.L.; A.S.; M.S.; M.A.; Werjovski-Almelda, S.; Vettore, A.L.; A.S.; M.S.; M.S.; Werjovski-Almelda, S.; Vettore, A.L.; M.S.; M.S.; Werjovski-Almelda, S.; W
        A;Molecule type: DNA
A;Residues: I-220 <STO>
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GN00:
A;Experimental source: strain PAO1
C;Genetles:
                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A; Residues: I-333 <SIM>
A; Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN00:
                                                                                                                                                                  A;Title: Complete genome se
A;Reference number: A82950;
A;Accession: C83292
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C; Superfamily;
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R;anonymous, The XyIella fastidiosa Consortlum
Nature 406, 151-157, 2000
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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                                                                                                                                            A;Status: prellminary
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                                                                                                                                                                                                                                                                                                                                                                                                                 probable glutathione S-transferase PA2821 [Imported] - Pseudomonas aeruginosa (strain
C;Species: Pseudomonas aeruginosa
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;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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50; MUID:20437337
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Pred. No. 5;
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R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, N.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Praser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: H87660
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                                                                                                                                                                                                                  peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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C; Accession: S61046;
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C;Superfamily: plaice glutathlone transferase
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A; Residues: 1-719 < POW>
A; Cross-references: EMBI
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A; Residues: 1-719 < POH>
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ce: strain S288C
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A;Reference number: A64720; WUID:97426617

A;Accession: G64720

A;Status: nucleic acid sequence not shown; translation not show A;Status: nucleic acid sequence not shown; translation not show A;Status: nucleic acid sequence not shown; translation not show A;Status: nucleic acid sequence not shown; translation not show A;Status: nucleic type: DNA

A;Status: nucleic acid sequence not shown; translation not show A;Status: nucleic transport provides: acid translation x-12, substrain MG1655

C;Genetics:
A;Gene: yaaJ

C;Suporfamily: sodium-dependent D-alanine/glycine transport pro
C;Keywords: amino acid transport; transmembrane predicted <TM1>
F;10-26/Domain: transmembrane #status predicted <TM2>
F;142-158/Domain: transmembrane #status predicted <TM3>
F;178-194/Domain: transmembrane #status predicted <TM4>
F;208-274/Domain: transmembrane #status predicted <TM4>
F;208-274/Domain: transmembrane #status predicted <TM4>
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R;Blattner, F.R.; Plunkett I:
A.; Rose, D.J.; Mau, B.; Sh
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                              probable amino scid transport protein yaaJ, sodium-dependent -
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C50C10.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C;Accession: T20100

R:MCMUrray, A.
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A;Molecule type: DNA
A;Residues: 1-433 <STO>
A;Cross-references: GB:AE005673; NID:gl3425020; PIDN:AAK25284.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                A; Title: The complete genome sequence of Escherichia A; Reference number: A64720; MUID: 97426617
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A;Gene: CC3322
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A; Introns: 74/3; 144/3;
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  transmembrane
transmembrane
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Pred. No.
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Matches Query Match Best Local

Similarity 6; Conserv

Conservative

47.78; 66.78;

Score 41; DB Pred. No. 23; l; Mismatches

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F;303-319/Domain: 1
F;349-365/Domain: 1
F;391-407/Domain: 1
F;414-430/Domain: 1
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Gla iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimaianta Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A·Reference number: A99629; MUID:21156231; PMID:11258796
                                           A;Cross-references: GB:AE005174; NID:g12512682; PIDN:AAG54307.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
                                                                           A; Molecule type: DNA
A; Residues: 1-476 <STQ>
                                                                                                                                                                                                                      inner membrane transport protein [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli C;Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change 14-Sep-2001
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C; Superfamily:
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   C;Superfamily:
                 A;Gene: yaaJ
                                C; Genetics:
                                                                                                       A; Status: preliminary
                                                                                                                     A; Accession: G85480
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sodium-dependent D-alanine/glycine
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Masunaga, T.; Kuhara, S.;
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J.; Davis, N.W.; Lim, A.; Dimaianta, E.;
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Pred. No. 23;
1; Mismatches
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Shiba, T.;
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Potamousis,
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probable membrane protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999
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T35841
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A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87448
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C;Superfamily: hypothetical protein u1937b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecuie type: DNA
A; Residues: 1-545 <STO>
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A; Residues: 1-476 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , S.; Moule, S.; O'Gaora, Nature 413, 848-852, 2001 A; Authors: Parry, C.; Qua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Parkhill, J.; Dougan, G.; James,
th, T.; Connerton, P.; Cronin, A.;
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7; Conservative
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genome sequence of a multiple
r: AB0502; PMID:11677608
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                                                                                                                                                                                                                                                                                               Score 41;
Pred. No.
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Davis, P.; Davies, R.M.; Dowd, L.;
                                                                                                                                                                                                                                                                           ore 41; DB ed. No. 26; Mismatches
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A;Cross-references: GB:AE003866; GB:AE003849; NID:g9104906; PlDN:AAF82941.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Relnasch, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Aivarenga, R.
Briomes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E: Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; France, S.C.; Franco, M.C.; Fr
                                                                                                                                                                                                                                                                                                                                                                                                               cysteine synthase XF0128 [imported] - Xylelia fastidlosa (strain 9a5c)
C;Species: Xylelia fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-390 <SIM>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                             C:Accession: 682844 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
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of authors see

reference number A59328 below

pathogen

Xyleila

fastldiosa.

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C; Accessic
R; Harris,
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R; Saunders, D.C.; Harris, D.;
submitted to the EMBL Data Lil
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T35901
                                                                                                                                                                                                                                                                               A; Reference number: Z21593
A; Accession: T35901
                                                                                                                                                                                                                                                                                                                                                                  probable araC family transcription regulator - Streptomyces coelicoior
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: ALO31260; A; Experimental source: strain A3(2)
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A; Residues: 1-184 <HAR>
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A; Accession: T35841
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                                                                                                                                                          A; Gene:
                                                                                                                                                                                                           A; Cross-references:
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211 PAWYRALGDPVVGR
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                               2 PAWYXXRGIRPVGR 15
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brary, January 1998
                                                                  Score 40; DB Pred. No. 24; 0; Mismatches
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Pred. No. 14;
l; Mismatches
                                                                                                                                                                                                         PIDN: CAA22785.1;
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                                                                                                    Length 324;
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajlma, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madelra, A.M.B.N.; Madelra, H.M.F.; Marino, C.L.; Marques, M.Y.; Martins, F.A.; Menthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyakl, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santeill, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira, A.R. Silva Jr., W.A.; da Silvaira, A.R. Silvaira, A.M.; Silvaira, A.M.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A; Reference number: A59328
A; Contents: annotation
C; Genetics: annotation
C; denetics: annotation
A; Sene: XF0128

Ouery Match
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
UNAMYXRGI 10
Indb 354 SPAWYAAHGI 363

Soarch completed: September 13, 2002, 09:24:00

Job time: 775 sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:30:45; Search time 80.21 Seconds (without alignments) 8.206 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_5\_21 86 1 NPAWYXXRGIRPVGRFX 17

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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			P48369 aeromonas s	09pfd6 xylella fas	Q09683 schizosacch	P23182 citrobacter	P42789 eimeria bov	O9hmn5 halobacter1		P32925 geotrichum			

# ALIGNMENTS

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between the Swiss Institute of Bioinformatics the European Bioinformatics Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as impossible and this statement is not removed. Use entitles requires a license agreement (See http or send an email to license(sbr sib.ch).  EMBL; AB015419; BAA29027.1;  MIM; 602663;  NOTHORNOR AMIDATION; Signal. SIGNAL 1 22 BPSTIDE 23 SIGNAL 1 53 BPSTIDE 23 SEPTIDE 23 SECOUENCE 87 AA; 9639 MW; 229A2F3F50CF9818 C	TISSUE SPECIFICITY.  PubMed=10498338,  Fujil R., Fukusumi S., Hosoya M., Kawamata Y., N  Sekiguchi M., Kitada C., Kurokawa T., Nishimura (  Sumino Y., Fujino M.,  "Tissue distribution of prolactin-releasing pept  "Ceceptor.",  receptor.",  Regul. Pept. 83:1-10(1999).  -!- FUNCTION: Stimulates prolactin (PRL) release  expression of prolactin through its receptor  lactotrophs directly to secrete PRL.  11STUE SPECIFICITY: MEDULIA OBLONGATA AND HY  -!- TISSUE SPECIFICITY: MEDULIA OBLONGATA AND HY		STANDAR (Rel. 39, (Rel. 39, (Rel. 41, Relasing pe eleasing pe eptide prap
s Copyright. It is partitute of Bioinformatics The stitute. The stitutes as long ment is not removed. anse agreement (See anse@isb-sib.ch).  7.1;  1.1. BY SIMILARITY. PROLACTIN-RELE PROLACTIN-RELE AMIDATION (G-5 amid-sight).	HOSOYA M., KAWAMAT, NIS, KUTOKAWA T., NIS  Prolactin-releasi 199).  S prolactin (PRL) S prolactin (PRL) S prolactin (PRL) OSECTED PRL MEDUILA OBIGNMATA	pubMed=9607765; Pight R., Kawamata Y., Fujii R., Kawamata Y., Asano T., Matsumoto Linura O., Onda H., Fujil sing peptide in the br 5(1998).	(D) PRT; 87 AA Created) Last sequence update) Last annotation update) ptide precursor (PRRF rolactin-releasin9 pep
the Swiss institute of Bolonformatics and the E bean Bioinformatics Institute. There are no rest non-profit institutions as long as its content and this statement is not removed. Usage by an requires a license agreement (See http://www.isb- in email to license@isb-sib.ch).  1 22 Amidation, Signal. 2 2 BY SIMILARITY. 3 3 4 53 34 PROLACTIN-RELEASING PEPTIDE P 53 53 PROLACTIN-RELEASING PEPTIDE P 53 53 AMIDATION (G-54 PROVIDE AMIDE 87 AA; 9639 MW; 229A2F3F5OCF9818 CRC64;	UE SPECIFICITY.  ided=10498338;  i. R., Fukusumi S., Hosoya M., Kawamata Y., Nabata Y., Ninu guchi M., Kitada C., Kurokawa T., Nishimura O., Onda N., no Y., Fujino M., sue distribution of prolactin-releasing peptide (PrRP) and ptor.";  il. Pept. 83:1-10(1999).  il. Pept. 83:1-10(1999).  il. Pept. 83:1-10(1999) its receptor GPR10. May st expression of prolactin through its receptor GPR10. May st lactotrophs directly to secrete PRL.  TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.	brata; inidae; insoya Hosoya Sekiguc;	de (P
It is produced through a collaboration informatics and the ENBL outstation te. There are no restrictions on its iong as its content is in no way removed. Usage by and for commercial it (See http://www.isb-sib.ch/announce/.ch).  ILARITY.  ILARITY.  ILARITY.  ILARITY.  ILARITY.  ILARITY.  ILORGE PEPTIDE PRRP20.  ION (G-54 PROVIDE AMIDE CROUP).  3F50CF9818 CRC54;	bata Y., Ninuma S., ), Onda N., de (PrRP) and its and regulates the GPR10. May stimulate OTHALAMUS.	Euteleostomi;; Homo.  Homo.  M., Fukusumi S.,  chi M.,	PrRP31; Prolactin-
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PTRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PTRP31; Prolactin-releasing peptide PTRP31; Prolactin-releasing peptide PTRP31; Prolactin-releasing
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Sekiguchi M., Kitada C., Kurokawa
Sumino Y., Fujino M.,
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Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiquchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
Kurokawa T., Pieleasing peptide in the brain.";
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Mammalia; Eutheria; Rodentia;
                                                                                                       SEQUENCE
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TISSUE SPECIFICITY: Widely expressed, with highest levels in
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                     NPAWYXXRGIRPVGRF 16
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             NPAWYTGRGIRPVGRF
                                                                                                                                                                  AB015418; BAA29026.1;
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an email to license@isb-sib.ch).
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BY SIMILARITY.
PROLACTIM-RELEASING PEPTIDE PRRP21.
PROLACTIM-RELEASING PEPTIDE PRRP20.
AMIDATIOM (G-53 PROVIDE AMIDE GROUP
DOC75A264EEE4F29 CRC64;
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Pred. No. 1.8e
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Sciurognathi; Muridae;
                                                    Mismatches
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T., Mishimura
                                                 2.7e-08;
2.7e-2;
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P81264;
30-MAY-2000
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Sigmal
PEPTIDE
PEPTIDE
MOD_RES
SEQUEMCE
                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBi_TaxID=9606;
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Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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Bos taurus (Bovine).
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30-MAY-2000 (Rel.
01-MAR-2002 (Rel.
SEQUENCE FROM N.A
MEDLINE-97189339;
                                                              Homo sapiena
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Tissue-Brain;
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 PubMed=9037597
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Exostosin-like 1 (Exostosin-L) (Multiple exostosis-like protein).
EXTL. OR EXTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatica Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license sgreenest (See http://www.lab-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kitada C., Masuo Y., Asano T., Mataumoto H., S
Kurokawa T., Nishimura O., Onda H., Fujino M.;
*A prolactin-releasing peptide in the brain.";
Mature 393:272-276(1998).
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TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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Metazos; Chordata; C
Metazos; Primates; (
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Cetartiodactyla; Ruminantia; Pecora;
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Pred. No. 3.le
0; Mismatches
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PROLACTIN-RELEASING PEPT
AMIDATION (G-54 PROVIDE .
08AC35A13B0FA908 CRC64;
                     Craniata; Vertebrata;
Catarrhini; Hominidae;
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                       Hominidae;
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Sekiguchi M.,
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                                           Euteieostomi
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SEQUENCE
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                          NRP1_YEAST STANDARD; PRT; 7; 7932770; Q12228; 01-CCT-193 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence upon 1-MAR-2002 (Rel. 41, Last annotation upon 1-MAR-2002 (Rel. 41) (ARP protein). NRP1 OR ARP1 OR ARP OR YDL167C.
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EMBL;
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WHYTE W., Spleker N., Van Roy H., De Paepe A., De Boulle K.,
Willems P.J., Van Hul W., Versteeg R., Speleman F.;
Willems P.J., Van Hul W., Versteeg R., Speleman F.;
"Refined physical mapping and genomic structure of the EXTLl gene.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: APPEARS TO BE A TOMOR SUPPRESSOR (BY SIMILARITY).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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-i- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Xu L., Deng H.X.,
"Mutations of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M.; "Identification and localization of the gene for EXTL, a of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004263; Exostosin.
Pfam, PF03016; Exostosin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Type II membrane
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L; AF083634; AAD02840.1; JOINED.

L; AF083624; AAD02840.1; JOINED.

L; AF083625; AAD02840.1; JOINED.

L; AF083627; AAD02840.1; JOINED.

L; AF083628; AAD02840.1; JOINED.

L; AF083628; AAD02840.1; JOINED.

L; AF083629; AAD02840.1; JOINED.

L; AF083629; AAD02840.1; JOINED.

L; AF083621; AAD02840.1; JOINED.

L; AF083631; AAD02840.1; JOINED.

L; AF083631; AAD02840.1; JOINED.

L; AF153980; AAF73172.1; JOINED.

L; AF153980; AAF73172.1; JOINED.
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Multigene family; Transmembrane; Signal-anchor.

Multigene family; Transmembrane; Signal-anchor.

O 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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53.3%;
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Pred. No. 2.1;
2; Mismatches
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N-LINKED (GLCNAC. .
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hereditary
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Saccharomycetes;
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OS Strept
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SGD; S0002326; NRP1.
InterPro; IPR000504; RRM.
InterPro; IPR001876; Znf-RanB
Pfam; PF00076; rrm; 1.
Pfam; PF000761; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00367; ZnF_RBZ; 2.
                                                                 16-0CT-2001
16-0CT-2001
16-0CT-2001
                                                                                                                                                                                                                                                                                                              DOMAIN
CONFLICT
SEQUENCE
                                       16-OCT-200I (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyribonuclease VII large subunit
(Exonuclease VII large subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS50102; RRM; 1
PROSITE: PS00030; RRM_RNP_1; F/
PROSITE: PS01358; ZF_RANBP2_1;
PROSITE: PS50199; ZF_RANBP2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular structure and genetic regulation of SFA, a gene responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product."; Mol. Gen. Genet. 237:351-358(1993).
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EMBL; Z67750; CAA91579.1;
EMBL; Z74215; CAA98741.1;
EMBL; S31139; S31139.
                         (Exonuclease VII XSEA OR SCK7.29c.
                                                                                                          Q9ЕВМЗ;
                                                                                                                       EX7L_STRCO
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-1- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.
-1- SIMILARITY: COHTAINS 1 RNA RECOGNITION MOTIF (RRM).
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NCBI_TexID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                               Nuclear
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  Firmicutes;
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  Actinobacteria; Actinobacteridae;
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Pred. No. 3
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RNA-BINDING (RRM).
RANBP2-TYPE 1.
RANBP2-TYPE 2.
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[2]
SEQUENCE FROM N.A.
STERIN-K12 / MG1655;
STERIN-K12 / MG1655;
NEDLINE-97426617; PubMed-9278503;
NEDLINE-97426617; PubMed-9278503;
Blattncr F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattncr F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Giasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Giasner J.D., Rode D.J.,
                                                                                                                               Yura T., Mori H., Nagai H., Nagata T., Ish
Isono K., Nizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia
the O-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                      p30143;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-t-FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA IN

ACID-INSOLUBLE OLIGONUCLEDTIDES, WHICH ARE THEN DEGRADED INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
                                                                                                                                                                                                MEDLINE-92334977;
                                                                                                                                                                                                                                                                                                                   Putative transporter YAAJ OR B0007.
                                                                                                                                                                                                                                SEQUENCE FRON N.A.
                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                      Escherichla coii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a iicense agreement (See http://www.isb-s1b
or send an email to iicense@isb-sib.ch).
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                                                                                                                                                                                                                                                         NCBI_TaxID=562;
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NCBI_TaxID=1902;
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SIMILARITY: BELONGS TO
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9; Conser
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402 AA; 43882 MW; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harris
                                                                                                                            region.";
Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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TO THE XSEA FAMILY
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Pred. No. 2.9;
1; Mismatches
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T7-like phages.
NCBI_Tax1D-10760;
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P00641;
21-JUL-1986
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Hypothetical I
Symport; Comp
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the Euro
                                                                                     Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                               Bacteriophage T7.
Viruses; dsDNA viruses,
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21-JUL-1986 (Rel.
01-NOV-1995 (Rel.
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InterPro; IPR001463; Na_ala_symp.
Pfam; PF01235; Na_Ala_symp; 1.
PRINTS; PR00175; NAALASNPORT.
PROSITE; PS00873; NA_ALANINE_SYMP
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EMBL; AE000111; AAC73118.1; -.
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                Dunn J.J.,
                               SEQUENCE FRON N.A.
NEDLINE-82078034; PubMed-7310871;
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MEDLINE=83241725; PubMed=6864790;
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e complete genome sequence of Escherichia
ence 277:1453-1474(1997).
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Last annotation updat
1 (EC 3.1.21.2) (Endo
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 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W.
                                                                                                                                                                                                                                                     RNA stage;
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Pred. No.
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genet1c
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bacteriophage
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RESULT 9
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Best Local S
Matches 8
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Q9KGF6;
                                                                                                                                                                                                             STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Naeno G., Sa
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V01127; CAN24345.1; -. EMBL; V01146; CAN24402.1; -. PIR; A00785; NEBP37. PIR; S42301; S42301.
                                                                                                                                                                                                                                                                   SEQUENCE FRON N.A
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                                                                                                                                                                                                                                                                                          NCBI_TaxID-86665;
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16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                       GluRS)
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FUNCTION: ENDODEDXYRIBDIUGCLEASE I, WNICN IS EXPRESSED IN THE LATE STAGE, IS NECESSARY FOR T7 GENETIC RECOMBINATION AND THE BREAKDOWN OF HOST DNA. IN THE EARLY STAGE OF INFECTION, T7 DNA REPLICATES AS A LINEAR MONOMER. IN THE LATE STAGE, THE T7 DNA REPLICATES VIA LINEAR CONCATENERS SEVERAL GENORIS IN LENGTH. THE GENE 3 PRODUCT HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS. CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-phosphooligonucleotide end-products.
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclease; Endonuclease
149 AA; 17172 MW; DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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57.18;
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us group; Bacillus.
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330(1981).
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              moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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3.8;
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., Kuhara S.,
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RESULT 10
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Best Local S
Matches 7
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Q9KP73;
16-OCT-2001
InterPro; IRR002300; tRNA-synt_la.
InterPro; IRR001412; tRNA-synt_I.
InterPro; IRR002303; tRNA-synt_val.
Pfam; pF00133; tRNA-synt_i; l.
PRINTS; PR00986; TRNASYNTNVAL.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                   This SWISS-PRDT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as iong as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-EL TOR N16961 / SERDTYPE D1;

NEDLINE-20406833; DUBMEd-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn N.L.,

Dodson R.J., Naft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva N.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.

MCDOnald L., Utterback T., Fleischmann R.D., Nierman W.C., White D.,

Salberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000924; tRNA-Synt_IC.
InterPro; IPR001412; tRNA-Synt_I.
Pfam; PF00749; tRNA-Synt_G; 1.
PRINTS; PR00987; TRNASYNTHGLU.
PROSITE; PS00178; AA_IRNA_LIGASE_I; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                 EMBL; AE004320; AAF95645.1; -.
NSSP; P96142; 1GAX.
TIGR; VC2503; -
                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: ATP + L-valine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Valy1-tRNA synthetase VALS DR VC2503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last squence up
16-OCT-2001 (Rel. 40, Last annotation
Valy1-trna synthetase (EC 6.1.1.9) (Va
                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Cytopiasmic.
-1- SIMILARITY: BELDINGS TD CLASS-I AMINDACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                             Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEDUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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255
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Pred.
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ATP (BY SINILARITY).
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(Valine--tRNA ligase) (ValRS).
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Complete proteome.
SITE 52
SITE 54 58
BINDING 557 557
SEQUENCE 953 AA; 108170 h
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Eukaryota; Metazoa; C
Nammaila; Eutheria; C
Bovidae; Bovinae; Bos
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01-FEB-I991
I6-OCT-2001
 DOMAIN
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DOMAIN
DOMAIN
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PIR; S11693; IJBOCN.
HSSP; P15116; INCI.
InterPro; IPR002126; Cadherin.
InterPro; IPR000233; Cadherin_C_term.
                                                                                       PROPEP
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NEDLINE-90360979;
Liaw C.W., Cannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAD2_BOVIN
PI9534;
                                                                                                                                         PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_2; 5.
                                                                                                                                                                                                                Pfam; PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                 modified and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEDLINE=90360979; PubNed=2390969;
Liaw C.W., Cannon C., Power N.D.,
"Identification and cloning of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neural-cadherin
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SUBCELLULAR LOCATION: Type I membrane protein.
SINILARITY: CONTAINS 5 CADHERIN DOMAINS.
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J. 9:2701-2708(1990).

FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

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TNEY PREFERENTIALLY INTERACT WITH THE TO THE TOTAL TH
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an email to license@isb-sib.ch).
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SEQUENCE OF 1-20 FRON N.A.

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MEDLINE-95048366; PubMed=7959764;

Wallis J.A., FOX M., Walsh F.S.;

"Structure of the human N-cadherin gene: YAC analysis and fine chromosomal mapping to 18q11.2.";

Genomics 22:172-179(1994).

-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADNESION PROTEINS.

TNEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A NOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE MANNER IN CONTRIBUTE TO THE
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CDN2 OR CDNN OR NCAD.

Homo sapiens (Numan).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Eutheria; Primates; Catarrhini: Hominical Collinatoria; Eutheria; Eut
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MEDLINE=90347462; Pubmed=2384753;
Walsh F.S., Barton C.N., Putt W.,
Spurr N., Goodfellow P.N.;
"N-cadherin gene maps to human ch
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NEDLINE-91076946; PubNed-2216790;
Reid R.A., Hemperly J.J.;
"Human N-cadherin: nucleotide and
                                                                                                                                                                                                                                              E-cadherin gene.";
J. Neurochem. 55:805-812(1990).
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                                      (Rel. 14, Created)
(Rel. 14, Last sequence
                                                                                                                                                                                                                                         Conservative
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                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                   CADHERIN.
                                                                                                                                                                                                                                                     44.88;
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CADHERIN 4.
CADHERIN 5.
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CADHERIN
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POTENTIAL.
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1 -> L (IN REF. 4).

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29;
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MEDLINE-95191680; PubMed-7885471;
Shapiro L., Fannon A.M., Kwong P.D., Thompson A., Gruebel G., Legrand J.-F., Als-Nielsen J., Colman Hendrickson W.A.;
"Structural basis of cell-cell adhesion by cadher: Nature 374:327-337(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
Tamura K.
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SEQUENCE FROM N.A.
MEDLINE-89346748; PubMed=2762814;
Miyatani S., Shimamura K., Hatta M.,
Miyatani S., Shimamura K., Takeichi M.;
EMBL;
                                                                                                                    between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as ional
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa;
Mammaiia; Eutheria;
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Neural-cadherin precursor (N-cadherin) (Cadherin-2).
CDH2.
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricted the companion of the companion o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reaction.";
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Tamura K., Shan W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A comprehensive survey of the cadherins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6; TISSUE-Testis;
MEDLINE-97033837; PubMed-8879495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci.
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                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS: CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
NEURONAL RECCONITION MECHANISM.
SUBCELLOLAR LOCATION: Type I membrane protein.
DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES OF TESTICULAR
DEVELOPMENT WITH HIGHEST LEVELS FOUND IN TESTES OF 21-DAY-OLD
                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS
M31131; AAA37353.1; -. AB008811; BAA23549.1; -. S45011; AAB23356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.B., Blaschuk O.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reprod.
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cadherin: role in selective ceil-ceil adhesion.";
245:631-635(1989).
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.S., Hendrickson
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89:8443-8447(1992).
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en J., Colman
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                                                                                                                                                 (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colman D.R.,
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N-cadherin
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PDB; 1NCH; 10-JUL-95.
PDB; 1NCJ; 10-MC-95.
PDB; 1NCJ; 18-MAR-99.
MGD; MGI: 88355; Cdh2.
InterPro; 1PR0002126; Cadherin.
InterPro; 1PR000233; Cadherin_C_term.
Pfam; PF01049; Cadherin_C_term.
Pfam; PF01049; Cadherin_C_term; 1.
PRINTS: PR00205; CADHERIN.
SMART; SM00112; CA; 5.
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16-OCT-2001 (Rel. 40, Creat
16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Neural-cadherin precursor (
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Eukaryota; Mettazos; Chordata;
Mammalia; Eutharia; Rodentia;
NCBI_TaxID=10116;
                                                                                            SEQUENCE PROM N.A. AND TISSUE SPECIFICITY.
STRAIN-SPRAGUE-DAWLEY TISSUE-TESTIS;
MEDILINE-98187820; PubMed-9528971;
Chung S.S. MO N.Y., Silvestrini B., Lee W.
                                                      cloning
                                                                                                                                                                                                                                                                                                                                                                                                          CAD2_RAT
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SEQUENCE
                                      Endocrinology
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                                 testicular N-cadherin: its co
ing and regulation.";
crinology 139:1853-1862(1998).
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1; 3D-structure.
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16 AA; 99761 MW,
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Similarity 50.0%;
9; Conservative
FROM
N.A
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Last annotation ursor (N-cadherin)
                                                                                                                                                                                                                                                                                                                                                                Created)
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CADHERIN 2.

CADHERIN 3.

CADHERIN 4.

CADHERIN 4.

CADHERIN 5.

SER-RICON (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Pred. No. 29;
0; Mismatches
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                          PRT:
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                                                                       i B., Lee W.M., Cheng C.Y.;
complementary deoxyribonucleic
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Pfam; PF01049; Cadherin_C_term;
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PROSITE; PS00232; CADHERIN_1; 3
PROSITE; PS50268; CADHERIN_2; 5
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"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";

ONA Res. 6:83-101(1999).
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"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76562.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                         Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Cranlata;
Actinopterygli; Neopterygli; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID=7957;
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Submitted (JAN-2000) to the
EMBL; AL132959; CAB71097.1;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spermatophyta; Magnollophyta; eddlcotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabldopsis.
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RA Garnler M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranae E.E., Laigret F., Lambals M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitoreilo C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Consa M.E., Foreira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Kodrigues V. de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Santeili R.V., Savasaki H.E.,
de Rosas V.E. Jr., de Salva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Souza A.P., Teronzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Valiada N., Van Silvs M.A., Verjovski-Almeida S., vettore A.L.,
RA Valiada N., Zatz M., Meidanis J., Setubai J.C.,
RTHE Genome sequence of the plant pathogen Xyleila fastidlosa.",
RTL Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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Q9Y276;
01-NOV-1999
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SEQUENCE
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01-DEC-2001 (TrEMBLIGH.
H-BCS1 (BCS1 (YEAST HOMO
BCS1 OR BCS1L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acenclo M., Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Burno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutlinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Faccincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
                                                                                                                                             Homo saplens (Human).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutherla; Prlmates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000537; UblA. Pfam; PF01040; UblA; 1.
   "Identification and PET112, SCO1, COX15,
                                               MEDLINE-99097350; PubMed-9878253; Petruzzella V., Tirantl V., Ferna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                    Zeviani M.;
                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_TaxID=2371;
                                                                                                                             NCBI_TaxID=9606;
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333 AA;
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 characterization, and COX11, five
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Pred. No. 7.3;
1; Mismatches
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Catarrhini; Hominldae;
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of human cDNAs
genes involved
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Best Local Similarity
Matches 7; Conser
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EMBL; AF026849; AAD08538.1; --
EMBL; AF0368195; AAB97365.1; --
EMBL; AF03468195; AAK29417.1; --
EMBL; BC000416; AAH00416.1; --
EMBL; BC0007500; AAH07500.1; --
INTCIPTO; 1PR003593; AAA_Subfam.
Pfam; PF00004; AAA; 1.
SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
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091022;
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01-MAR-2001
01-MAR-2001
01-DEC-2001
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"Mutations in bosi, a mitochondrial respiratory chain assembly gene, are responsible for the complex III deficiency of patients with tubulopathy and liver failure.";
    Pseudomonas.
NCBI_TaxID=287;
[1]
                                                                       Pseudomonas aeruginosa.
Bacteria; Proteobacterla;
                                                                                                                                                PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00382; AAA; 1.
ATP-binding; Hypothetical protein.
SEQUENCE 419 AA; 47534 MW; 7F0F98BA62F2CBB8 CRC64;
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Strausberg R.;
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Genomics 54:494-504(1998).
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RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 1592 / PAOI;

RX MEDLINE-20437337; PubMed=10984043;

RX MEDLINE-20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallk D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larblg K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen l.T.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen l.T.,

RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAOI, an

Opportunistic pathogen.",

RI Nature 406:959-964(2000).

RR InterPro; IPR004046; GST_C.

DR InterPro; IPR004045; GST_N.

KW Transferase; Complete proteome.

SQ SEQUENCE 220 AA; 24716 MW; 65961B3EA6CAA050 CRC64;
                                                                                                                                                                                                  RC STRAIN-C57BL/6J; TISSUE-EMBRYO;

RX MEDLINE-21085660; pubmed-112178J;

RA Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,

RA Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,

RA Alzawa K., Isawa M., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Isawa M., Nishl K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Isawa M., Nishl K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Isawa M., Nishl K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Lawa M., Nishl K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., Klng B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Mikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewls S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewls S., Matsuo M., Rono H., Baldarelli R., Barsh G.,

RA Schilmi L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schilmi L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Blake J., Boffelli D., Bojunga N., Carnincl P., de Bonaldo M.F.,

RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hili D., Hofmann M., Hume D.A., Kamiya M., Lee N.M.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelii J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizki Y.,

RA Hayashizki Y.,
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Best Local S
Matches 9
                                                                        9130022019RIM.
9130022019RIM.
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentla;
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01-JUN-2001 (Tremblrel.
01-DEC-2001 (Tremblrel.
9130022019RIK PROTEIN.
                                    Pfam; PF00004; AAA;
SMART; SM00382; AAA
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                    ATP-binding
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9; Conservative
418 AA;
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1; Mismatches
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Last sequence update)
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Sclurognathi; Muridae;
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  94905BA9B097F0DE CRC64;
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018729;
01-NOV-1996 (TIEMBLIEL 0
01-JAN-1998 (TIEMBLIEL 0
01-DEC-2001 (TIEMBLIEL 1
C50C10 2 PROTEIN.
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MEDLINE-21173998; PubMed-11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwlnn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota: Metazoa: Nemat
Rhabditidae: Peloderinae;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PEPTIDOGLYCAN-BINDING PROTEIN, PUTATIVE.
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                                   Submitted (MAY-1996)
                                                                      McMurray
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_Tax1D-6239;
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TIGR; CC3322;
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Last sequence upo
                                   EMBL/GenBank/DDBJ databases
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Pred. No. 22;
2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                     Chromadorea;
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MEDLINE-21173698; PubMed-11259647;

RA NIerman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson R. R. Lisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., R. Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E. RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwlnn M.L., Haft D.H., R. R. Colonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry R. Witerback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulabacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL; AE005835; AAK23581.1; -.

BR TIGR; CC1602; -.

KW Hypothetical protein; Compla**
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Q9A7W7;
Q9A7W7;
Q1-JUN-2001 (TremBLrel. 17, I
Q1-JUN-2001 (TremBLrel. 17, I
Q1-DEC-2001 (TremBLrel. 19, I
HYPOTHETICAL PROTEIN CC1602.
                                                                                                                            09T133
09T133;
01-MAY-2000
01-MAY-2000
01-DEC-2001
   Viruses; dsDNA
                                                                                                    ENDDNDCLEASE.
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phireO3-12.
A viruses, n
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2; Mismatches
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Pred. No. 26;
1; Mismatches
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   stage;
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      Caudovirales;
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O1-NOV-1998 (TrEMBLrel. 08, C
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O1-HOV-1998 (TrEMBLrel. 08, C
PUTATIVE MEMBRANE PROTEIH.
SC9A10.05C.
                                                                                    Redenbach M., Kleser H.M., Denapaite D., Elcnner A. Redenbach M., Kleser H.M., Denapaite D., Elcnner A. Redenbach M., Hopwood D.A.;

*A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).

EMBL; ALO31260; CAA20292 l; -

EMBL; ALO31260; CAA20292 l; -
                                                                                                                                                                STRAIH-A3(2);
MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                            STRAIN-A3
                                                                                                                                                                                                                                                                                                                                              Streptomyces coellcolor. Bacteria; Firmicutes; Ac
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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J. Bacteriol. 183:1928-1937(2001).
EMBL, AJZ81805; CAB63604-1; -
SEQUENCE 153 AA; 17640 MW; 211571BB
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                                                                                                                                                                                                                                                                                                                                    Actinomycetales;
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NCBl_TaxID=110457;
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AWVSAHGVRQVGFF
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                                         Similarity 50.7; Conservative
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7; Conserva
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(AUG-1998)
                                                                                                                                                                                                                                                                    Taylor K.; (AUG-1998) to
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Pred. No. 16;
1; Mismatches
                                        Score 40; DB
Pred. No. 20;
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bacteriophage phiYeO3-12 of
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1D PH18
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DT 011
RR CY
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OCC BB
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Mol. Microbiol. 21:77-96(1996).

-1 - SHAILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCIPLES AND STATE CAA22785.1;

EMBL; AL035212; CAA22785.1;

R EMBL; AL035212; CAA22785.1;

R Pfam; PF00165; HTH_ARAC; 1.

R Pfam; PF00165; HTH_ARAC; 1.

R SMART; SM00342; HTH_ARAC; 1.

R PROSITE; PS01024; HTH_ARAC_FAMILY_1; 1.

R PROSITE; PS01024; HTH_ARAC_SAMILY_2; 1.

DHA-binding; Transcription regulation.

SEQUENCE 324 AA; 34650 MW; 2AFB5C250A7D003D CRC64;
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Q92554;
Q1-54;
Q1-54;
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Q1-554;
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OPPH18
O1-OCT-2000 (TrEMBL
O1-OCT-2000 (TrEMBL
O1-DEC-2001 (TrEMBL
CYSTEINE SYNTHASE.
XF0128
MEDLINE-20365717; PubMed-10910347;
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A.,
Simpson A.J. Alves L.M.C., Araya J.E., Baia G.S., B
Alvarenga R., Alves L.M.C., Araya J.E., Boxe J.M., E
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., E
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro I
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R.,
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Bentley S.D., Parkhill :
Submitted (JAN-1998) to
                                                                                                                                                                                     SEQUENCE FRI
STRAIN-9A5C
                                                                                                                                                                                                                                                                                                                                    Bacterla;
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"A set of ordered cosmids and a
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                                                                                            RA Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,
Ra Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernai G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Dominguez-Bernai G., Duchaud E., Durant L., Dussurget O.,
RA Butlar K.-D., Fsihi H., Garcia-dei Portillo F., Garrido P.,
RA Gautler L., Goebel W., Gomez-Lopez N., Haln T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerat U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Mudueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari N.,
RA Mordsiek G., Novelia S., de Pablos B., Perez-Dlaz J.-C., Purceil R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Varquez-Boland J.-A., Voss H., Wehland J., Cosaart P.;
RT Comparative genomics of Listeria specles.";
Sclence 294:849-852(2001).
RE Figh; AL596166, CAC96023.1; -.
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Bacteria; Firmicutes; Bacillus/Ciostridium group;
Bacilius/Staphylococcus group; Liateria.
NCBI_TaxID-1642;
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Search completed: September 13, 2002, 09:29:20 Job time: 1065 sec

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Result
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8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1987.DAT:
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10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1989.DAT:
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
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13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1993.DAT:
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15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
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20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
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27: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
28: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
29: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1999.DAT:
    US-09-446-543A-73_COPY_6_21
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4.447 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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AAG62534
AAB90999
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              Human oxytocin sec
1992 ligand peptid
Human CRH releasin
Prolactin releasin
Human type G prote
Human oxytocin sec
Human CRH releasin
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Human type G prote
Human type ligand
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AAB90996	AAB90994	AAG62527	AAG62519	AAY49302	AAY49301	AAB10358	AAB10350	AAW95175	AAW95191	AAW97234	AAW97232	AAW31374	AAW31387	AAG62530	AAB10361	AAW97226	AAW31390	AAG62533	AAB10364	AAW31393	AAG62532	AAB10363	AAW31392	AAB90995	AAB90991	AAG62531	AAY49291	AAB10362	AAW87615	AAW97235	AAW31391	AAG62536	AAB10367	
Prolactin releasin	Prolactin releasin	Rat CRH releasing	н	Lgand	ligand	Rat oxytocln secre	Bovlne oxytocln se	Murine pituitary-d	tuitary	Rat type ligand po	pituitary-	ine G pr	ດ		oxyto	type 1	type G pro	Human CRH releasin	oxytoc	type	CRH	ğ	Ō		ct in	_	11gar	oxyto	1922	type ligand	Œ.	relea	Human oxytocin sec	

## ALIGNMENTS

RESULT AAY 49293

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AAY49293 standard; peptide;

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Monoclonal antibody; 19P2 iigand; diagnosis; prolactin secretion; pltuitary; regulatory mechanism; central nervous system; pancreat

pancreatic

19P2 ilgand peptide fragment.

22-FEB-2000 AAY49293;

(flrst entry)

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Key
Modified-site
                                                                                                                  Homo saplens.
New monoclonal antibodies, useful in diagnosis, as drugs and
            WPI; 2000-039381/03.
                       Matsumoto H, Kitada C,
                                               21-MAY-1998;
                                                          20-MAY-1999;
                                                                     25-NOV-1999.
                                                                                 WO9960112-A1
                                   (TAKE ) TAKEDA CHEM IND LTD.
                                              98JP-0140293
                                                         99WO-JP02650
                                                                                                 Location/Qualifiers
                                                                                           /note- "C-termlna1 amide"
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studying

diseases related

to ligand abnormality

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RESULT
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Matches 13
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of projectin secretion), central mervous regulatory mechanism, and panceatic function regulatory mechanism. The antibody-based immunosassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAV49290-302 represent peptide fragments of the 1992 ligand.
ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancrestic function modulator. This ligand could have specific applications as a
                                                                                                                                                                    WPI; 1997-363672/33,
N-PSDB; AAV02431.
                            ilgand polypeptide corresponding to amino acid residues 34 to 5 sequence represented in AW31390 and is used in an assay to mon tigand binding to the G protein-coupled records.
                                                                                                        Claim
                                                                                                                                              Ligand
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odulator; pituitary; central nervous system
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                                                                                                                              peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary glam
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                                                                                                                                                                                                                                                                                                                                                                                                                                           agent.
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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. 1.8e-07; 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      nding; pharmaceutical; system; pancreas; pro
                                     used in an assay to monitor receptor protein. Pharmaceutical
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the 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      prophylactic;
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53 of
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Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour: emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommei syndrome; Argonz-del Castilo syndrome; forbes-Albright syndrome; iymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; contraceptive; placental function; choriocarcinoma; hydatid mole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trauma, growth hormone secretory diaeane, hyper and polyphagia, hyperipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turnor's syndrome, neurosis, asthma, rheumatoid arthritia, spinal injury transient brain ischaemia, epilepsy, amylotrophic lateral scierosis, acute mycocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosia and/or oligogalactia. Assays can also be developed to acreen compounds which as capable of altering the binding activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human type ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999
                                                                                                                                                                 WPI; 1999-105614/09
                                                                                                                                                                                                                                                 23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                         abnormai iipidmetaboiism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yndrome,
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98
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                                                                                                                                                                                                                                                                                                                                                                                                   unthrifty fetus; abnormal
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2.4e-07;
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The present sequence represents a human type ligand fragment. is used in the course of the invention. The apecification descan agent for modulating prolactin secretion which comprises a ligand polypeptide or a sait, for a 6 protein-coupled receptor

prolactin

receptor (GPCR) describes Claim syndrome,

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Page 166;

241pp;

English.

the of G protein-coupled receptor ligands - for modulating preservation or placental function, e.g. for treating menopausal

or placental function, e.g. tumours, autoimmune disease

autoimmune disease

or abnormal pregnancy

for modulating prolactin

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RESULT
AABI10365
ID AABI
XX AABI
XX AABI
XX AABI
XX AABI
XX HUMB
XX HUMB
XX HUMB
XX HOMC
XX VOIC
PN WO2C
XX OC-J
PF 22-C
PF 23-C
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                       This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the G protein-coupied receptor protein, It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g., weak pains and atonic bieeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This sequence represents a human peptide which acts as an oxytocin secretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Physiologically active polypeptide recognized as ligand by G protein coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                         Disciosure;
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                 The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 1972 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunocassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 1972 ligand.
                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                   New monocional antibodies, studying diseases related:
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                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat
 Sequence
                                                                                                                               Disciosure; Page 26; 73pp; Japanese.
                                                                                                                                                                                                         Matsumoto M,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                             The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysesic or for treating preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's
                                                                                                                                                                                                                                                                                                                                              hypercortisolaemia, secondary or enrouse hypercortisolaemia, secondary or enrouse hypercortisolaemia, secondary or enrouse hypercortison, hypogenadism, hair disease (including boredom, nausea, pigmentation, hypogenadism, hair close, and hypotension), adrenal giand hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; corticotrophln releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
        Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thlo1; hormone; growth factor; neurotransmitter.
                                                           Prolactin releasing poptide
                                                                                                                AAB90992;
                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
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26-SEP-2000; 2000JP-0297073.
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                                                                                     22-JUN-2001
                                                                                                                                       AAB90992 standard;
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half infrarediction protects) and interference with particular access.
        Query Match
Best Local Similarity
Matches 13; Conserv
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10-SEP-1999;
15-OCT-1999;
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peptidase
                                                                                                                                                                                   intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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Synthetic.
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99US-0153406.
99US-0159783.
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Pred. No.
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טB 22; ב.
2.4e-07;
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iength of in vivo a
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AAW31395
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                                             G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
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                                                                                                                                                                                       AAW31395 standard; Peptide;
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                Conservative
                              agent.
                                                                                                                          (first entry)
                                                                                           protein-coupled receptor ligand fragment
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                                           pancreas; prophylactic;
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RESULT
AAB10366
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Best Local S
Matches 13
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                     numan; oxytocin secretion promoter: G protein-coupled receptor treatment; disease; pain; atonic bleeding; uterine recovery fai caesarean section; artificial fertilization; galactostasis; goa voteins marketing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                     Homo sapiens.
                                                             veterinary
                                                                                                                             Human oxytocin secretion promoting
                                                                                                                                                          24-NOV-2000
                                                                                                                                                                                    AAB10366;
                                                                                                                                                                                                            AAB10366 standard:
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligand peptide for G protein-coupled receptor - function in the central nervous system, pancreas
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13: Conserv
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"Itada C:
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                                                              medicine;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                            peptide;
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86.7%;
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2.6e-07;
hes 2;
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pancreas and
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                                                                         goat; pig:
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RESULT 10
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI:
                               Kitada C,
                                                                             18-NOV-1999;
26-SEP-2000;
                                                                                                               17-NOV-2000;
                                                                                                                                      25-MAY-2001
                                                                                                                                                            WO200135984-A1
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                          Addison's
                                                                                                                                                                                                                   Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
                                                                                                                                                                                                                                                    Human CRH releasing protein related
                                                                                                                                                                                                                                                                             24-AUG-2001
                                                                                                                                                                                                                                                                                                    AAG62535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medicine
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                                                       (TAKE ) TAKEDA CHEM IND
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13; Conserv
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                                                                            99JP-0327900
2000JP-0297073
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                                                                                                                                                                                                       adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                         peptide;
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86.78;
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Pred. No. 2.6e
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2.6e-07;
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artificial
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RESULT AAW31396
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Best Local
Matches 1
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G proteir receptor ligand. This can be used to control the secretion of CRH and is useful as an analysist or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaidosteronism, hypercortisolaemia, secondary or chronic hypodarencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function
                                                                       Claim
                                                                                                                                                                                                       (TAKE
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                                                                                           Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                     Kawamata Y,
                                                                                                                                                                                                                                                                                           26-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       therapeut1c
                                                                                                                                                                                                                                                                                                                                                                                                     modulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                 protein-coupled receptor; iigand binding; pharmaceutical;
odulator; pituitary; central nervous system; pancreas; pro
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                                               sequence represents
                                                                                                                                 1997-363672/33.
DB; AAV02433.
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                                                                                                                                                                                                       ) TAKEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                      type
                                                                       2; Page 186;
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Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                              D)
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2.6e-07;
hes 2;
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RESULT 12
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Best Local S
Matches 13
This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bieeding, before and after expulsion of placenta uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cov. graft and mile.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; oxytocin secretion promoter; G protein
treatment; disease; pain; atomic biseding; un
cassarean section; artificial fertilization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia,
                                                                                                                                                                          Physiologically-active polypeptide recognized as ligand by protein-coupied receptor protein, for promoting secretion as drugs for diseases relating to oxytocin secretion and in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor eeding; uterine recovery far
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2.7e-07;
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                                                                                                                                                                           n of oxytocin,
in veterinary
                                                                                                                                                                                      of
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; goat; pig
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RESULT 1
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                                                                                           The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating discases associated with CRH secretion such as hypersidosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter.
                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                          Homo
                                                                      Sequence
                                                                                                                                                                                           Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                        Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; anaigesic; hypersidosteronism; hypercortisolaemia; hypoadrenocorticism; addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                    Kitada
                                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                  18-NOV-1999; 99JP-0327900.
26-SEP-2000; 2000JP-0297073.
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                                                                                                                                                                                                                                                                                                                                                                                         Human CRH
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                                       Local Similarity
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                                                                                                                                                                                                                                    Matsumoto
                                                                                                                                                                            Page 75; 90pp; Japanese.,
                                Conservative
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86.7%;
                                       96.2%;
86.7%;
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                               Score 77; DB Pred. No. 2.7e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         rclated peptide SEQ
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Pred. No. 2.76
0; M1smatches
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. 2.7e-07;
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PAWYXXRGIRPVGRF pawyasrg1rpvgrf

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This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the Sequence represented in ANA31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ijgand may be used as a pituitary function comodulator, a central nervous system modulator or a pancreatic function comodulator. This ligand could have specific applications as a complylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, comparations as a comparation of consciousness, anxiety syndrome, schizophrenia, comparation, provide tinama, dispercholesterolaemia, hyper-and polyphagia, comperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, cancer pancreatitis, renal disease, activation, infertility, spinocerebellar degeneration, considered pancreation, atopic dermatitis, osteoporosis and/or cancer pancreation, atopic dermatitis, osteoporosis and/or capable of altering the binding activity of the ligand affecting cancivation of the G protein-coupled receptor protein.
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Query Match
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Matches 13
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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modulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligand peptide for G protein-coupled receptor - a function in the central nervous system, pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                      Sequence
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DB; AAV02428.
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95JP-0343371.
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96JP-0211805.
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86.7%;
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Score 77; DB
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s and
                                                      Length 31;
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RESULT 15
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                                                                                                                                                                                     The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes is a spent for modulating prolactin secretion which comprises a cityand polypeptide or a salt, for a G protein-coupied receptor (GPCR) if the agents for promoting prolactin secretion can be used for citreating or preventing hypocovarianism, gonecyst cacogenesis, menopausal contraction in a domestic mammal and as an aphrodistac. The agents for citreating prolactin secretion can be used for treating or preventing thibiting prolactin secretion can be used for treating or preventing continuation, infertility, impotence, amenorabea, galactorrhea, galactorrhea, compast, infertility, impotence, amenorabea, galactorrhea, composed, contractions, the syndrome, spents for probes-Albright syndrome, tymphoma, Sheehan syndrome or dyscospermia. The inhibitory agents can also be used as contraceptives. The agents for codulating placental function can be used for treating or preventing control carcinoma, hydatid moie, irruption mole, abortion, unthrifty fetus, contraceptives.
                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ciaim 3; Page 159; 24lpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujii R, Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1998;
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                                                                                        Local Similarity
                                    1 PAWYXXRGIRPVGRF
pawyasrgirpvgrf
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                                                                                                                                                               31 AA;
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                                                                                        96.2%;
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                                                                     Mismatches
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3.9e-07;
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Perfect score:
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1: /cgn2_6/ptodata/2
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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US-09-421-208-46
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US-09-105-678A-43
US-09-105-678A-43
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US-09-421-208-43
US-09-421-208-44
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US-09-421-208-44
US-08-776-971-63
US-09-421-208-44
US-08-776-971-63
US-08-776-971-138
US-09-105-678A-34
US-08-776-971-50
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2.861 Million cell updates/s
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44, Appl
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46, Appl
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48, Appl
49, Appl
40, Appl
40, Appl
41, Appl
41,
                    Query Match
Best Local Similarity
Matches 13; Conserv
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Database

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	Sequence 31, Appl	Sequence 8, Appli	e 7,	e 42,	Sequence 36, Appl	52,	e 10,	42,	36,	Sequence 41, Appl	e 35,	e 51,	Sequence 9, Appli	41,	35	•		Sequence 98, Appi

## ALIGNMENTS

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FILING DATE: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: CONIIO, DAVId G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECHONE: 617-523-3400

TELEPHONE: 617-523-6440

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
Type:
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-105-678A-46
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: F10PPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: JP 172118/1997
TTTTITE CAMES 77-THE-1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Applicat patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 130 W
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09105678A
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Conservative

0

Score 77; D8 Pred. No. 9.6e 0; Mismatches

D8 3; 5.9.6e-08; 2;

Length 20 Indeis

0

Gaps

0

96.2%; 86.7%;

PAWYXXRGIRPVGRF

15

PAWYASRGIRPVGRF 20

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US 08-776-971-64
; Sequence 64, Application; Patent No. 6228984
; GENERAL INFORMATION:
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                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQ ID ND: 64: US-08-776-971-64
                                                                                 Matches
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INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIDE APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573
                                                                                                   Local
                                    1 PAWYXXRGIRPVGRF 15
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Conlin, David G.
REGISTRATIDN NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                           MDLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
PAWYASRGIRPVGRF 20
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                      TOPDLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DIKE, BRONSTEIN, RDBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08776971B
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Kitada, Chieko
DF INVENTION: POLVERDTEINS, THEIR PRODUCTION AND USE
OF SEQUENCES: 140
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujii, Ryo
Fukusumi, Shoji
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                                                                                                   96.2%;
                                                                         Score 77; DB 4; Length 20
Pred. No. 9.6e-08;
0; Mismatches 2; Indels
                                                                                                                    Length 20;
                                                                             0
                                                                             Gaps
                                                                             0
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Patent NO. VALUE :
GENERAL INFORMATION:
APPLICANT: Suenega, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Mishamura, Osamu
TITLE OF INVENTION: METHOD DF PR
                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                   US-09-105-678A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE IYPE: peptide US-09-421-208-46
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Matches
                                                                                                                                                                                                  Sequence 47
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/
FILING DATE:
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172
FILING DATE: 27-JUN-1997
AITORNEY/AGENT INFORMATION:
DAME: CON110 DAY14 G
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
DPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy disk
                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACIERISTICS
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CDRRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Ianaka, Yoko
APPLICANT: Nishimura, Dsamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIILE DE INVENTION:
SIREET: I30
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
mes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G. REGISTRATION NUMBER: 2
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                                 ADDRESSEE:
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                 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                               DIKE, BRONSTEIN, ROBERIS & CUSHMAN, LLP
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                     Score 77; DB 4; Le
Pred. No. 9.6e-08;
0; Mismatches 2;
                                                                              PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65, Applicati
Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 26-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING XYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617-523-3400
                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes I3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I PAWYXXRG1RPVGRF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Φı
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                           FURUSUM1, Shoji
Ritada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02109
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                                                                                                                                                                                                                               CITY: Boston
STATE: MA
                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                  STREET: I30 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/0877697IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 amino acids
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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RESULT 6
US-09-42I-208-47
/ Sequence 47, Application US/0942I208
/ Patent No. 6258561
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Best Local Similarity
PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105
APPLICATION NUMBER: US 19/105
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172IIB,
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET, NUMBER: 4846
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #I.30
CURRENT APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
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NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-NUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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86.7%;
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                                                                                                                                                       US 09/105,678
                         48466-342
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Pred. No. 1e-07;
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; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-09-105-678A-48
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US-09-105-678A-48
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us-09-421-208-47
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Best Local Similarity 86.7
Matches 13; Conservative
                                                              Matches
                                                                                           Ouery Match
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Patent No. 6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIN: 22 amino acids
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                 NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617.523-3400
                                                                                                                                                                                                                                                                                                                                                           SOFTMARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
PRIOR APPLICATION UNATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
ANDE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Fioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                              Local
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                             1 PAWYXXRGIRPVGRF 15
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                                                              1 Similarity
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130 Water Street
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                                                              Conservative
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                                                                            96.28:
86.78;
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                                                          Score 77; DB 3; L
Pred. No. 1.1e-07;
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US-08-776-971-66
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Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                     Matches
                                                                                                      Best Local Similarity
                                                                                                                         Ouery Match
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEO ID NO: 66:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 47176

TELEPNONE: 617-523-3400

TELEPNONE: 617-523-3400
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Versior
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                        1 PAWYXXRGIRPVGRF 15
6 PAWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Kitada, Chieko
TITLE OF INVENTICU: POLYPROTEINS, TNEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                             TYPE: amino acids
                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
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STATE: MA
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FILING DATE: 28-DEC-1996
                                                                                   Conservative
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Fujii, Ryo
Fukusumi, Shoji
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Kawamata, Yuji
                                                                                                      96.2%;
86.7%;
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                                                                                                      Score 77; DB 4;
Pred. No. 1.1e-07;
                                                                                   Mismatches
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RESULT 9 US-09-421-208-48

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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440
INFORMATION FOR SEQ IO NO:
SEQUENCE CHARACTERISTICS:
LENGTN: 22 amino acids
                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING OATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takco
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                     TITLE OF INVENTION: ME NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Conlin, Oavid G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
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                                 STATE:
                                               CITY:
                                                          STREET:
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les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                                          ADDRESSEE:
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                                                            130 Water Street
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                                                                                                                                    Nishimura, Osamu
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Tanaka, Yoko
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                                                                       DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                       METHOD OF PRODUCING A 19P2 LIGAND
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Pred. No. 1.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Worlya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
ATITLE OF INVENTION: METHOD O
NUMBER OF SEQUENCES: 52
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN. DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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Matches 13; Conserv
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INFORMATION FOR SEQ IO NO:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CORRENT APPLICATION ONTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CONILO, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION OATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADORESS:
ADORESSEE: OIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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1NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

3 :-

31 amino acids

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Query Match
Best Local Similarity
Watches 13; Conserve
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Patent No. 6228984
GENERAL INFORMATION:
                                                    REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: PT/J44371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 7/343371
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/29419
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-NGG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN. DAVID G.
REGISTRATION NUMBER: 27,026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l PAWYXXRG1RPVGRF 15
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                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DÂTA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSRWAN, LLP
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TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
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ZIP: 02109
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                                       LENGTH: 31 amino acids
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Kitada, Chieko
LNYENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.2%:
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Pred. No. 1.5e-07;
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SI
US-08-776-971-61
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                                                        Query Match
Best Local S
Matches 13
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Best Local Similarity
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 17211B/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1in, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                         TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
17 PAWYASRGIRPYGRF
                                                                                                                                                                STRANDEDNESS
TOPOLOGY: 1:
                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U:
ZIP: 02109
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                          1 PAWYXXRGIRPVGRF 15
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                                                          Similarity
13; Conserv
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6258561
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Tanaka, Yoko
                                                          Conservative
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                                                                        96.2%;
86.7%;
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86.7%;
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                                                       Score 77; DB 4; Le
Pred. No. 1.5e-07;
0; Mismatches 2;
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Pred. No. 1.5e-07;
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                                                                                      Length 31;
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RESULT

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// TOPOLOGY: linear
// MOLECULE TYPE: peptide
US-09-421-208-43

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US-09-105-678A-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matchea 13; Conserv
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APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTONNEY/AGENT INFORMATION:
NAME: CON11D, DAV1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440
INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                      Dogton
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130 Water Street
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Query Match
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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; MOLECULE TYPE: peptide
US-09-105-678A-44
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAVId G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PM PC POS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                          17 PAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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hypothetical prote	50S ribosomal prot	ribosomai protein	hypothetical prote	acetyitransferase	carcinoembryonic a		hypothetical prote	hypothetical prote	conserved hypothet	319K protein ndvB	vaiine tRNA synthe	valine tRNA synthe	valinetRNA ligas	valyi-tRNA synthet	acetate kinase - D

## ALIGNMENTS

cB3322 probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa (strain C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 C;Accession: CB3392 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Couiter, S.N.; Foiger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Qlson, M.V. Nature 406, 959-964, 2000 A;Titie: Compiete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337 A;Accession: CB3292 A;Status: preliminary A;Molecule type: DNA A;References: GB:AE004709; GB:AE004091; NID:9948904; PIDN:AAG06209.1; GSPDB:GN A;Experimental source: Strain PA01 C;Genetics: A;Gene: PA2821 C;Superfamily: plaice giutathione transferase	Query Match 95.0%; Score 76; DB 2; Length 83; Best Local Similarity 86.7%; Pred. No. 2.2e-06; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 PAWYXXRGIRPVGRF 15	PESULY 1  JC7607  prolactin-releasing peptide - rat  C;Species: Rattus norvegicus (Norway rat)  C;Date: 30-Jun-2001 *sequence_revision 30-Jun-2001 *text_change 30-Jun-2001  C;Accession: JC7607  R;Yannada, M; Ozawa, A.; Ishli, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001  A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959  A;Contents: Spleen A;Accession: JC7607 A;Molecule type: DNA A;Residues: 1-83 <yan> A;Cross-references: DDNA A;Cross-references: DDNA A;Cross-references: DDS-AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary. A;Introns: 33/1</yan>

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A; Experimental source: strain 9a5c

R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Aivarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Eas-Neto, E.; Docena, C.; El-Dorry, H.: Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junequolita, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E. A.Authora: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.G.; de Oliveira, M.C.; de Silva, R.G.; Santalii, R.V.; Sawasak A; Authora: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, Tsuhako, M.H.; Vailada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zandani, M.S.; V
                                                                                                                                                                                                                                                                                                                                                                       ARPI protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D1478; protein YDL167c
C;Species: Saccharomyces cerevisiae
C;Date: 15-reb-1996 #sequence_revision 01-Mar-1996
C;Accession: S61046; S31139; S67719
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                                         A;Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91579.1; PID:g1061272 R;Wehner, E.P.; Rao, E.; Brendel, M. Mol. Gen. Genet. 237, 351-358, 1993
                                                                                                                                                                                                                           A; Reference number: A; Accession: S61046
                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, November 1995 A;Reference number: S61010
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A; Residues: 1-719 < POH>
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A; Residues: 1-333 <Slm>
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Nature 406, 151-157, 2000
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   A; Title: Molecular structure and
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Xylella fastidiosa
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       genetic regulation
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Pred. No. 5.8;
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Pred. No. 3
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A; Reference number: Z19224
A; Accession: T20100
A; Status: preiiminary; translated
A; Molecule type: DNA
A; Residues: 1-338 <WIL>
                                                                                                                                                          hypothetical protein C50C10.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change C;Accession: T20100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Neison, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermoiaeva, M.; White, O.; Saizberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                 R; McMurray, A submitted to
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A; Residues: 1-433 <5T0>
A; Cross-references: GB:
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
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A; Map position: 4L
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A;Experimental source: strain S288C
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A; Residues: 1-719 < POW>
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A;Accession: S31139
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A;Accession: H87660
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number: Z19224
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Pred. No. 12;
                                                from G8/EMBL/DDBJ
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probable Inner membrane transport protein ECs0007 [imported] - Escherichia coli (strain C;Specles: Escherichia coli (strain C;Specles: Escherichia coli (strain C;Specles: 18-Jui-2001 #sequence_revision 18-Jui-2001 #text_change 03-Aug-2001 C;Accession: 690629
R;Hayashi, T.; Makino, K.; Ohnlshi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Nan, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Nattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genca, Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90629
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Science 277, 1453-1462, 1997
A;Tltle: The complete genome sequence of Escherichia coll
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A;Experlmental source: clone C50C10
C;Genetics:
            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <NA)
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A; Accession: G64720
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R;Blattner, F.R.; Plunket
A.; Rose, D.J.; Mau, B.;
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C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Aug-1999
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A;Map position: 5
A;Introns: 74/3; 144/3;
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A;Moiecule type: DNA
A;Residues: 1-476 <BLAT>
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                type: DNA
1-476 <NAY>
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Pred. No. 18;
1; Mismatches
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Pred. No.
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Query Match
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A;Cross-references: GB:BA000007; PIDN:BAB33430.1; PID:g13359463; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0007
C;Superfamily: sodium-dependent D-alanine/glycine transport protein
                                                                                                                                                                                                                                                                                                                                                              probable amino-acid transport protein STY0006 [Imported] - Salmo (Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C; Accession: AG0502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inner membrane transport protein [Imported] - Escherichia coii (strain 0157:N7,
C;Specles: Escherichia coil
C;Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change 14-Sep-2001
                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <PAR>
                                                                                                                                                               th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dow, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; PMID:11677608
A;Accession: AG0502
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A;Residues: 1-476 <STQ>
A;Residues: 1-476 <STQ>
A;Cross-references: GB:AE005174; NID:g12512682; PIDN:AAG54307.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
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                                                                      A; Cross-references: GB: AL513382;
                                                                                                                                                                                                                                                                                                              R;Parkhlll, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
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sodium-dependent D-alanine/glycine transport protein
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66.7%;
                                                                    PIDN:CAD01159.1; PID:g16501289; GSPDB:GN00176
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C;Genetics:
A;Gene: CC1602
C;Superfamily: ]
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R, Nierman, W. C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolorn, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.
A, Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: A87448
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              probable araC family transcription regulator - Streptomyces coelicolor C;Specles: Streptomyces coelicolor C;Specles: Streptomyces coelicolor C;Date: 03-Dec1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec C;Accession: T35901
                                                                                                                                                                                                                                                                                                    A: Experimental source: strain A3(2)
C: Genetics:
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A;Molccule type: DNA
A;ReBidues: 1-184 <HAR>
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A;Molecule type: DNA
A;Residues: 1-545 <STO>
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   R;Saunders, D.
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 Barrell, B.G.; Rajandream,
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A;Gene: valS
C;Superfamlly: val:
C;Keywords: ligase
                                                                                                                                                                                 R:Parkhill, J.; Wren, B.W.: Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davles, R.M.; Davls, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                              valine--tRNA ligase (EC 6.1.1.9) [imported] - Yersinia pestis (strain cO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: DNA
A;Residues: 1-790 <DEH>
A;Cross-references: EMBL:AL132959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; De Haan, M.; Maarse, A.C.; Grivell, L.A.; submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F15G16.60 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #t
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A:Molecule type: DNA
A:Residues: 1-324 <SAU>
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                                                              C; Genetics:
                                                                                  A;Cross-references: GB:AL590842; PIDN:CAC92673.1;
                                                                                                     A; Molecule type: DNA
A; Residues: 1-965 < KUR>
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A; Introns: 39/1; 678/2; 698/3; 773/2
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A; Accession: T47959
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                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                             C; Accession: AE0418
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                 Superfamily: valine -- tRNA ligase
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January 2000
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Copyright (c) 1993 - 2000 Compugen Ltd
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## ALIGNMENTS

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modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/snnounce/or send an email to license@isb-slb.ch).  EMBL; AB015419; BAA29027.1; - MIM; 602663; - HOTTODE; AM1dation; Signal. 2 BY SIMILARITY. 23 FREPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20. 34 53 PROLACTIN-RELEASING PEPTIDE PRRP20. 35 AMIDATION (G-54 PROVIDE AMIDE GROUP). 36 SEQUENCE 87 AA; 9639 MW; 229A2F3F50CF981B CRC64;	Regul. Pept. 83:1-10(1999).  Regul. Pept. 83:1-10(1999).		SUL RP_

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                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a coilaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to llcense@isb-sib.ch).
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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Matsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino K.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sumino Y., Fujino M.; "Tissue distribution (
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujii R., Fukusumi S., Hosoya M., Sekiguchi M., Kitada C., Kurokawa
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Mammalia; Eutheria;
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30-MAY-2000 (Rei. 39, Last sequence update)
30-MAY-2000 (Rei. 39, Last sequence update)
01-MAR-2002 (Rei. 4I, Last annotation update)
Prolactin-releasing peptide precursor (PTRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PTRP31; Prolactin-releasing peptide PTRP31; Prolactin-releasing peptide PTRP31; Prolactin-releasing
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                          1 PAWYXXRGIRPVGRF
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TISSUE SPECIFICITY: Widely expressed, with highest levels in
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PAWYTGRGIRPVGRF
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PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

ANIDATION (G-53 PROVIDE AMIDE GROUP).

DOC75A264EEE4F29 CRC64;
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Pred. No. 1.3e-07;
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T., Nishimura
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15-JUL-1998
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SEDUENCE
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or send a
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Kitada C., Masuo Y., Asano T., Matsumoto H., S
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protactin-releasing peptide precursor (PrRP) (Protactin-releasing peptide)
                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a coilaboration between the Swiss institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                                                                                  Homo sapiens
                                                                                                                                                       EXTL1 OR EXIL.
                                                                                                                                                                            Exostosin-like 1
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Bovidae; Bovinae; Bos.
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Eukaryota; Metazoa;
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                                                                                        s (Human).
                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
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                                                                                                                                                                                                                                                                                         STANDARD;
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  PubMed=9037597
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PROLACTIN-RELEASING PEPTIDE PRRP20.
ANIDATION (G-54 PROVIDE ANIDE GROUP
08AC35A13B0FA908 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 1;
Pred. No. 2.3e-07;
                                                                                      Catarrhini;
                                                                                                          Cranlata; Vertebrata;
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de PrRP31; Proiactin-
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                      NRP1_YEAST STANDARD; PRT; 719 AA P32770; Q12228; O1-CCT-1993 (Rel. 27, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation updata Asparagine-rich protein (ARP protein). NRP1 OR ARP1 OR ARP OR YDL167C.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WHYTE W., Spieker N., Van Roy N., De Paepe A., De Boulle K., Willems P.J., Van Hul W., Versteeg R., Spieman F.; "Refined physical mapping and genomic structure of the EXTL1 gene."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: APPEARS TO BE A TUMDR SUPPRESSOR (BY SIMILARITY).
Saccharomyces cerevisiae 
Eukaryota; Fungi; Ascomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entitles requires a license agreement (See http://www.isb-slb.ch/announce/
or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TD THE EXDSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                    AF083623; AAD02840.1;
AF083624; AAD02840.1;
AF083625; AAD02840.1;
AF083625; AAD02840.1;
AF083625; AAD02840.1;
AF083626; AAD02840.1;
AF083628; AAD02840.1;
AF083629; AAD02840.1;
AF083629; AAD02840.1;
AF083630; AAD02840.1;
AF083631; AAD02840.1;
AF153980; AAF73172.1;
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AF083633; AAD02840.
AF083623; AAD02840.
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cota; Saccharomycotina;
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hereditary
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COLT.STRCO STANDARD;

D EXTL_STRCO STANDARD;

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T 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable exodeoxyribonuclease VII large subun

Pxonuclease VII large subunit).
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SMART; SM00547; ZnE_RBZ; 2.
PROSITE; PS50102; RRM_RNP_1;
PROSITE; PS00030; RRM_RNP_1;
PROSITE; PS01358; ZF_RANBP2_1
PROSITE; PS50199; ZF_RANBP2_2
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CONFLICT
SEQUENCE
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Wehner E.P., Rao E., Brendel M.;
"Molecular structure and genetic regulation of SFA, a gene responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product."; Mol. Gen. Genet. 237:351-358(1993).
Streptomyces coelicore Bacteria; Firmicutes;
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NCBI_TaxID-4932;
[1]
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Pfam; PF00641; zf-RanBP; 2.
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zinc-finger; RNA-binding;
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ZF_RANBP2_1;
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RANBP2-TYPE
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Best Local S
Matches 9
[2]
SEQUENCE FROM N.A.
SETATIN-K12 / MG1655;
STRAIN-812 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Blattner F.C. Plunkett G. III, Bloch C.A.,
Chiley M., Collado-Vides J., Glasner J.D., RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; aL391754; CaC05901.1; ...
InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR002309; tRNA-synt_2.
                                                                                                                                           MEDIJNE-92334977; PubMed-1630901;
Yura T., Mor1 H., Nagai H., Nagata T., 1sh
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia
the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rajandream N.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INT
ACID-INSOLUBLE OLIGONUCLEOTIDES, WNICN ARE THEN DEGRADED F
ACID-INSOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: EXONUCLEOITLES (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: EXONUCLEOITLES (BY SIMILARITY).
-I- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Crcated)
01-JUL-1993 (Rel. 26, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a control between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical control of the statement is not removed.
                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECOL
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Pfam; PF01336;
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Rajandream M.A.;
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                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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NCBI_TaxID=1902;
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9; Conservative
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43882 MW; 1
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42.9%;
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1; Mismatches
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                      ., Perna N.T., Burland
Rode C.K., Mayhew G.F.
Goeden M.A., Rose D.J.,
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"Complete nucleotide sequence of bacteriophage locations of T7 genetic elements.";
J. Moi. Bioi. 166:477-535(1983).
                                                                                                                                                                  Viruses: dsDNA viruses,
T7-like phages.
NCBI_Tax1D=10760;
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InterPro; IPR002293; AA_rel_perme
InterPro; IPR001463; Na_ala_symp.
             MEDLINE=82078034; PubMed=7310871; Dunn J.J., Studier F.W.;
                                    [2]
SEQUENCE FROM N.A.
                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=83241725; PubMed=6864790;
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PROSITE; PS00873; NA_ALANINE_SYMP;
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EMBL; AE000111; AAC73118.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                             PAWYXXRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01235; Na_Aia_symp;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 66. 6; Conservative
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(Re1. 01,
(Re1. 32,
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Last sequence update)
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Last annotation update)
I (EC 3.1.21.2) (Endonuclease).
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                                                                                                                                                                                                 RNA stage; Caudoviraies; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB Pred. No. 3.9; 1; Mismatches
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 genetic left end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYE_BACHO STANOARD; PRT; 485 AA.

OPKGF6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Clutanyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
Bacitlus/Clostridium group:
Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., St
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V01127; CAA24345.1; -. EMBL; V01146; CAA24402.1; -. PIR; A00785; NEBP37. PIR; S42301; S42301.
                                                                                                                                         This SWISS-PRDT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                               halodurans and genomic sequence comparison w
Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-86665:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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FUNCTION: ENDOEDXYRIBONUCLEASE I, WHICH IS EXPRESSED IN THE BREAKDON STAGE, IS NECESSARY FOR TO GENETIC RECONBINATION AND THE BREAKDON OF HOST ONA. IN THE EARLY STAGE OF INFECTION, TO ONA REPLICATES VIA A LINEAR NONOMER. IN THE LATE STAGE, THE TO ONA REPLICATES VIA LINEAR CONCATEMERS SEVERAL GENOMES IN LENGTH. THE GENE 3 PRODUCT HAS ALSO BEEN IMPLICATED IN THE MATURATION OF THESE CONCATEMERS.

CATALYTIC ACTIVITY: Endomncledlytic cleavage to 5'-
                                                                                                                                                                                                                                                           diphosphate + L-glutamyl-tRNA(Glu).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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149 AA; 17172 MW: 0092AA28E3743BC1 CRC64;
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; OB
Pred. No. 2.9;
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                                                                                rmatics and the EMBL on There are no restrictions as its content la
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N., Kuhara S.
                                                                                                                                                                                                                                                                                                                                                  ERNA(Glu)
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|th Bacillus
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RESULT 10

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AC 09KPY
AC 09KPY
AC 09KPY
16-00
DT 16-00
DT
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STRAIN=EL TOR N16961 / SEROTYPE 01;

STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn N.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.O., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Oass S., Oin H., Oragoi I., Sellers P.

McDonald L., Utterback T., Ficischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Nekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYV_VIBCH
Q9KP73;
                  InterPro; IPR002300; tRNA-synt InterPro; IPR002412; tRNA-synt InterPro; IPR002303; tRNA-synt InterPro; IPR002303; tRNA-synt Pfam; PF00133; tRNA-synt_1; 1. PR1NTS; PR00986; TRNASYNTHYAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE
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                                                                                                                                                EMBL; AE004320; AAF95645.1;
HSSP: P96142; IGAX.
TIGR; VC2503; -
                                                                                                                                                                                                                                                       or send an
                                                                                                                                                                                                                                                                            entitles requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:477-483(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
NCBI_TaxIO=666;
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PROSITE; PS00178: AA_TRNA_LIGASE_I;
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InterPro; IPR001412; tRNA-synt_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "ONA sequence of both chromosomes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete
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SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY
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(EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
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ATP (BY SIMILARITY).
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Pred. No. 9.5;
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Best Local :
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Complete proteome.
SITE 52
SITE 54 58
OINDING 557 557
SEQUENCE 953 AA; 108170 N
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P19534;
01-FEB-199I
01-FEB-199I
16-OCT-2001
                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                    endothelial celis.";

EMBO J. 9:2701-2708(1990).

-I- FUNCTION: CADHERINS ARE CALCIUM OF THEY PREFERENTIALLY INTERACT WITH
                          DOMAIN
TRANSMEM
                                                                                              PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
                                                                                                                                                                    EMBL; X53615; CAA37677.1; -. PDIR; SI1693; LJBOCN.
HSSP; P15116; LNCI.
InterPro; IPR002126; Cadherin.
InterPro; IPR000233; Cadherin_C_term.
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90360979; PubMed=2390969;
Liaw C.W., Cannon C., Power M.D.,
"Identification and cloning of tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; B
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                                                                                                                         SMART:
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                                                                                                                                                                                                                                                                                                                                           SORTING OF NETEROGENEOUS CELL TYPES. N-CADHERIN MAY NEURONAL RECCONITION MECHANISM.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: CADHERINS ARE CALCIUM OEPENDENT CELL ADHESION PROT
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO
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PF01049; Cadherin_C_term;
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n; Glycoprotein; Transmembrane; C
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41 13
131 877 NEURAL-CADHERIN.
131 695 EXTRACELLULAR (P
696 717 POTENTIAL.
696 717 CYTOPLASMIC (POT
131 238 CADHERIN 1.
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(N-cadherin) (Cadherin-2) (Fragment).
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annotation
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Pred. No.
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 EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
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P (BY SIMILARITY).
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of cadherins
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                                                                                   Calcium-binding;
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MEDLINE-95048366; PubMed-7959764;
Wallis J.A., Fox M., Walsh F.S.;
"Structure of the human N-cadherin ge chromosomal mapping to 18g11.2.";
Genomics 22:172-179(1994).
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Best Local :
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01-NOV-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neural-cadherin precursor (N-cadherin) (Cadherin-2).
CDH2 OR CDHN OR NCAD.
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MEDLINE=91016946; PubMed=2216790;
Reid R.A., Nemperly J.J.;
"Human N-cadherin: nucleotide and
                                                                                                                                                                                                                                                   MEOLINE=90347462; PubMed=2384753; Walsh F.S., Barton C.H., Putt W., Spurr N., Goodfellow P.N.;
                                                                                                                                                                                                                                                                                                                                       gendothelial cells.*;
J. Cell Sci. 102:7-17(1992).
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-92363956; PubMed-1500442;
Salomon D. Ayalon O., Patel-King
"Extrajunctional distribution of
                                                                                                                                                                                                                  E-cadherin gene
                                                                                                                                                                                                                          "N-cadherin gene maps
                                                                                                                                                                                                                                                                                                        SEQUENCE OF 160-906 FROM
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Mammalia; Eutheria;
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 FUNCTION: CADHERINS ARE CALCIUM DEBENDENT CELL ADNESION PROTEINS. THEY PREFERENTIALLY INTERACT WITH MEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
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Primates;
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Catarrhini;
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N-cadherin
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InterPro; IPR00233; Cadherin_C_term.
Pfam; PF00028; Cadherin; 5.
Pfam; PF01049; Cadherin_C_term; 1.
PRINYS; PR00205; CADHERIN.
SMART; SM00112; CA; 5.
PROSITE; PS00233; CADHERIN_1; 3.
PROSITE; PS00236; CADHERIN_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: X57548; CAA40773.1; -.
EMBL: X54315; CAA38213.1; -.
EMBL: X42303; AAB22854.1; -.
EMBL: M34064; AAA03236.1; -.
EMBL: Z27420; CAA81799.1; -.
PIR: A38870; IJHUCN.
NSSP; P15116; INCJ.
MIM; 114020; -.
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 5 CADHERIN DDMAINS.
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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(Rel. 14, Rel. 14,
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CYTOPLASMIC
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CADHERIN 2.
CADHERIN 3.
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CADHERIN
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> T (ÎN REF. 1).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             MEDLINE=98318235; PubMed=9655503;
Tamura K., Shan W.S., Hendrickson W.A., Colman D.R.,
"Structure-function analysis of cell adhesion by neur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyatani S., Shimamura K., Hatta M., Matsunaga M., Hatta K., Takeichi M., Matsurari cadherin: role in selective Science 245:631-635(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89346748; PubMed-2762814; MEDLINE-89346748; PubMed-2762814; Metta
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
EMBL; M31131; AAA37353.1; -. EMBL; AB008611; BAA33549.1; -. EMBL; S45011; AAB23356.1; -. PIR; A32759: IJMSCN.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Hendrickson W.A.; "Structural basis of cell-cell Nature 374:327-337(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGKAPHY (1:9 ANGSTROMS) (
MEDLINE-95191680; PubMed-7885471;
Shaptro L., Fannon A.M., Kwong P.D., Ti
Gruebel G., Legrand J.-F., Als-Nielsen
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Neural-cadherin precursor (N-cadherin) (Cadherin-2).
CDH2.
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MEDLINE-98318235; PubMed-
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MEDLINE-97033837; PubMed-8879495;
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Miyatani S., Copel
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fetal, immature, and adult mice utilizing the polymorase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetal, immature,
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                                                                                                                                                                                                        NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: Type I membrane protein.
DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES C
DEVELOPMENT WITN HIGHEST LEVELS FOUND IN TESTE
                                                                                                                                                                             SIMILARITY: CONTAINS 5 CADHERIN DOMAINS
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land N.G., Gilbert
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Sciurognathi; Muridae; Murinae;
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PDB; INCH; 10-JUL-95.
PDB; INCI; 10-JUL-95.
PDB; INCJ; 18-MAR-99.
MGD; MGI:88355; Cdh2:
InterPro; IPR002126; Cadherin.
InterPro; IPR00233; Cadherin_C_term.
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Pfam; PF01049; Cadherin_C_term;
PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 5.
PRDSITE; PS00232; CADHERIN_1; 3
PRDSITE; PS50268; CADHERIN_2; 5
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Rat
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SIGNAL
                           SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

STRAIN-SPRAGUE-DAWLEY; TISSUE-TESTLS;

MEDLINE-98187820; PubMcd=9528971;

Chung S.S., Mo M.Y., Silvestrini 8., Lee W.M., Cheng C.Y.;

"Rat testicular N-cadharin: its complementary deoxyribonucleic cloning and regulation.";

cloning and regulation.";

cloning and regulation.";
                                                                                                                                                                   Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
NCBI_TaxID=10116;
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Pred. No. 22;
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NEURAL-CADHERIN.

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CADHERIN 3.

CADHERIN 4.

CADHERIN 5.
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Sciurognathi; Muridae;
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SEQUENCE FROM N.A.

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PAW---YXXRGIRPVGRF PAWNAAYRISGGDPTGRF

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Query Match Best Local S Matches 9

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Pred. No. 22; 0; Mismatches

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RESULT

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EMBL; AF097593; AAC83818.1; -.
EMBL; AB017695; BAA84919.1; -.
NSSP; P15116; INCJ.
InterPro; IPR002126; Cadherin.
InterPro; IPR00233; Cadherin.C_t
Pfam; PF00028; Cadherin, 5.
Pfam; PF01049; Cadherin_C_term; 1
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Signal. 1
SIGNAL 1
PRDPEP 28
CHAIN 160
   CARBDHYD
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE DAWLEY; TISSUE-Brbin;
ASBAI K., Tadd T., Yamamoto M., Tada A., Mizuno M., Eimoto T., Kato T.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITN THEMSELVES IN A HUMOPHILLO
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING DE HETEROCENBOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
NEURONAL RECOGNITION MECHANISM.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- TISSUE SPECIFICITY: IN TESTIS, EXPRESSED IN SERTOLI AND GERM
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DOMAIN
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SMART; SM00112; CA; 5.
PRDSITE; PS00233; CADHERIN_1;
PRDSITE; PS50268; CADHERIN_2;
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 4.
CADHERIN 5.
SER-RICN.
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EXTRACELLULAR (H
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A -> R (IN REF.

A -> V (IN REF.

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N -> K (IN REF.
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A -> R (IN REF. 2).
A -> V (IN REF. 2).
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sakine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanka T., Kubota K.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-1., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Ki.";
DNA Res. 6:83-101(199).
"It SIMILARITY: BELONGS TO THE LISP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
50S rlbosomal protein L15P.
RPL15P OR APE0343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein; SEQUENCE 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP000059; BAA79298.1; InterPro; IPR001196; Ribosomal_L15. PROSITE: PS00475; RIBOSOMAL_L15: 1.
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(without alignments)
8.876 Million cell updates/se
                                                                                                                                                                                         09w624 carassius a
093127 streptomyce
091022 pseudomonas
09ph76 xylella fas
09ph76 xylella fas
09a787 caulobacter
018729 caenorhabdi
09a787 caulobacter
                                    O9t133 bacteriopha
086838 streptomyce
09z554 streptomyce
09z554 streptomyce
09lgz0 oryza sativ
09vn94 drosophila
09m371 arabidopsis
09dlv4 mus musculu
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                  streptomyce
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45	44	43	2	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
37	37	37	37	37.5	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38.5	39	39	39	39
46.2	46.2	46.2	46.2	46.9	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5		48 8	48.8	48.8	48.8
234	178	160	114	333	950	703	536	536	536	536	536	536	536	536	481	419	416	398	359	238	194	127	97	238	555	425	390	340
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063112	Q97SU7	Q9LWD3	Q63104	Q9RJ10	Онхно	Q95Z10	Q95NQ0	Q95NR7	Q95NT6	Q95NU7	Q95PK5	Q95PK6	Q95PK7	Q95YN4	Q95WT7	Q9Y276	Q99ZA9	Q9RR92	088036	OPYEHO	Q9A9U0	<b>Q9HXA7</b>	033440	055075	000050	Q986U6	Q9PH18	Q18731
		Q91wd3 oryza sativ	Q63104 rattus norv	00	0		_	-		Q95nu7 drosoph11a					Q95wt7 drosophila	=		Q9rr92 deinococcus	treptomyce			~	033440 pseudomonas	055075 cricetulus	asperqillus	rhizobium	8	Q18731 caenorhabdi

## ALIGNMENTS

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Q93LZ7
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AC Q9
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Matches 10
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09w624;
01-NOV-1999 (TrEMBLTel. 1
01-NOV-1999 (TREMBLTel. 1
01-DEC-2001 (TREMBLTel. 1
C-RF AMIDE.
Q93LZ7
Q93LZ7;
Q1-DEC-2001 (TremBLrel. 19,
Q1-DEC-2001 (TremBLrel. 19,
Q1-DEC-2001 (TremBLrel. 19,
                                                                                                                                                                                                                                Satake H., Minakata H., Fujimoto M.;
"Carassius Rramide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 NW; DSDC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ctinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cyprinidae; Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-BRAIN;
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                                                                                                                     PAWYXXRGIRPVGRF 15
| || ||:||:||;
|EWYVGRGVRPIGRF 75
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10; Conserv
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Last annotation update)
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01-MAR-2001 (TYEMBLIEL 1
01-MAR-2001 (TYEMBLIEL 1
01-DEC-2001 (TYEMBLIEL 1
09РН76;
09РН76;
01-ОСТ-2000
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kormanec J., Bistakova J., Novakova R., Homerova D., Re; "Cloning and characterization of a new polyketide gene of Streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL, AY033994; AAK61719.1;
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AUR2B.
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SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL, AE004709; AAG06209.1; -.
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    (TremBLrel.
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                                                   PRELIMINARY;
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20 AA; 24716 MW;
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el. 19, Last annotation update)
S-TRANSFERASE.
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Pred. No. 2.8;
l; Mismatches
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Pred. No. 6;
l; Mismatches
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RESULT
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.E.R.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Lemos S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lombais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Margues M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Mono D.H., Naggi M.A., Nascimento A.L.T.O., Hetto L.E.S.,
RA Moni D.H., Naggi M.A., Nascimento A.L.T.O., Hetto L.E.S.,
RA Moni D.H., Naggi M.A., Nascimento A.L.T.O., Sattisa M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Pelxoto B.R., Pereita G.A.G., Pereita H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silva A.F., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
The Genome Secourne of the Dlant mathogen Xviella fastidicas **.
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Matches 8
                                                                                                                                                     01-JUN-2001
01-JUN-2001
01-DEC-2001
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Q9A382;
                                                                                                                 01-JUN-2001 (TremBLrel. 17, Last sequent 01-DEC-2001 (TremBLrel. 19, Last annotat PEPTIDOGLYCAN-BINDING PROTEIN, PUTATIVE CC3322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of the plant Nature 406:151-159(2000).

EMBL, AE003860; AAF82881.1; -.

InterPro; IPR00537; UblA.

Pfam; PF01040; UblA; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYDROXYBENZOATE OCTAPRENYLTRANSPERASE.
SEQUENCE FROM N.A.
STRAIN-ATCC 19089
                                                Caulobacter.
NCBI_TaxID-69394;
                                                                                     Bacteria;
                                                                                                     Caulobacter
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Proteobacteria;
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17,
19,
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Pred. No. 9.4;
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                                                                                   subdivision; Caulobacter
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Science 282:2012-2018(1998).
EMBL; Z72505; CAA96608.1; -
InterPro; IPR003839; DUF215.
Pfam; PF02688; DUF215; 1.
SEQUENCE 338 AA; 39053 MW;
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O1-NOV-1996 (TIEMBLITEL C
O1-JAN-1998 (TIEMBLITEL C
O1-DEC-2001 (TIEMBLITEL J
C50C10.2 PRDTEIN.
 Q9A7W7
Q9A7W7;
01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-99069613;
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NCBI_TaxID=6239;
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Pfam; PF01471; PG_binding_1; 1.
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TIGR; CC3322; -.
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Nierman W.C., Felo
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53.8%;
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D9T133;
01-MAY-2000 (TIEMBLIEL L
01-MAY-2000 (TIEMBLIEL L
01-DEC-2001 (TIEMBLIEL L
                                                                                                                                             "Complete genomic sequence of the lytic Yersinia enterocollitica serotype 0:3.";
J. Bacteriol. 183:1928-1937(2001).
EMBL; A.751805; CAB63604 1; -
SEQUENCE 153 AA; 17640 MW; 211571BBD
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T7-like phages
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Bacteria; Proteobacteria;
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Viruses; dsDNA viruses, n
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STRAIN-A3(2);
Parkhill J., Barrell I
Submitted (AUG-1998) t
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O1-NOV-1998 (TrEMBLrel. OB, Created)
O1-NOV-1998 (TrEMBLrel. OB, Last sequence update)
O1-NOV-1998 (TrEMBLrel. OB, Last annotation update)
PUTATIVE MEMBANE PROTEIN.
SC$A10.05C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycinese; Streptomycetaceae; Str
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ARAC FAMILY TRANSCRIPTIONAL REGULATOR.
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Streptomyces coellcolor.
Streptomyces coellcolor.
Bacteria; Elrmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
SEQUENCE FROM N.A.
STRAIN-83(2);
STRAIN-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapa
Kinashi H., Hopwood D.A.;
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"A set of ordered cosmils and a detalled genetic at the 8 Mb Streptomyces coelloclor A3(2) chromosome. MoI. Microbiol. 21:77-96(1996).
EMBL; AL031260; CAA20292.1; -
SEQUENCE 184 AA; 20178 MW; 58806A19FBFD6996 CR
                                                                                                                                                                                                      Bentley S.D., Parkhill J., I Submitted (JAN-1998) to the
                                                                                                                                                                                                                                         STRAIN-A3(2);
Bentley S.D.,
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Saunders D.C., Harris
Submitted (JAN-1999) |
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Submitted (AUG-1998) to
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Harris D., Ta
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17;
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hromosome.";
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IL SUDMITTED (JUN-2000) to the EMBL/GenBank/DDBJ databases.

IL SUDMITTED (JUN-2000) to the EMBL/GenBank/DDBJ databases.

C -1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER COVALENT ATTACHMENT OF UBIQUITIN TO OTHER COPOTEINS (BY SIMILARITY).

C -1- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + COPOTEINS (BY SIMILARITY) - CONCURATION.

C -1- PATHWAY: SECOND STEP IN UBLOUTIN CONUUGATION.

C -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-CONTURNING ENZYME FAMILY.

DR HISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-CONTURNING ENZYME FAMILY.

DR HISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-CONTURNING ENZYME FAMILY.

DR HISCELLANEOUS: BELONGS TO THE UBIQUITIN-CONTURATING ENZYME FAMILY.

DR HISCELANEOUS: UBAN96583.1; -.

DR HISCELANEOUS: UBAN96583.1; -.
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Matches 6
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01-OCT-2000 (TrEMBLr;
01-OCT-2000 (TrENBLr;
01-DEC-2001 (TrEMBLr;
01-DEC-2001 (TrEMBLr;
                                                                                                                   Pfam; pr00179; UO_con; 1.
SMART; SM00212; UBCc; 1.
SMART; SM00212; UBCc; 1.
PROSITE; PS50127; UBIDUITIN_CONJUGAT_2;
Ligase; Ubiquitin_conjugation.
SEQUENCE 540 AA; 60487 MW; 5DE1FF4E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL035212; CAA22785.1; -.
Interpro; IPR000005; HTHATAC.
Iften; PF00155; HTH_ATAC; I.
SMART; SM00342; HTH_ARAC, I.
PROSITE; PS00041; HTH_ARAC_FAMILY_I; I.
PROSITE; PS00124; HTH_ARAC_FAMILY_2; 1.
DNA-binding; Transcription regulation.
DNA-binding; Transcription regulation.
SEQUENCE 324 AA; 34650 MW; 2AFB5C250A7D003D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENE.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A set of ordered cosmids a
the 8 Mb Streptomyces coell
Mol. Microbiol. 21:77-96(19
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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[1]
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AWWRVRGLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t of ordered cosmids and a detailed genetic and Mb Streptomyces coellcolor A3(2) chromosome."; Mlcrobiol. 21:77-96(1996).
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                                                     Similarity
6; Conserv
                                                     Conservative
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2; Mlsmatches
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annotation update)
TO A REGION OF THE
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RESULT 13
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Best Local
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Q9VN94;
Q9VN94;
Q1-MAY-2000 (TrEMBLrel. 1:
Q1-MAY-2000 (TrEMBLrel. 1:
Q1-MAY-2000 (TrEMBLrel. 1:
Q1-MAY-2000 (TrEMBLrel. 1:
CG1113 PROTEIN.
CG1113 Droaphila melanogaster ()
Q9M371
Q9M371;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                          52
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                                                                                                          PAWSSOMGVRSLAKE
                                                                                                                                            PAWYXXRGIRPVGRF 15
                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                     FBgn0037304; CG1113.
562 AA; 63406 MW;
                 PRELIMINARY;
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Pred. No. 58;
3; Mismatches
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                                                                                                                                                                                                                                       RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Ndachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa N., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa N., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl R., Staubil F., Suzuki R., Tounton H., Baldareill R., Barsh G.,
RA Sokai K., Okido T., Frunno M., Aono H., Baldareill R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boiffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hovenstein M.J., Bult C., Fletcher C., Fujita M., Gerlboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Kuchle P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki N., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Wilming L.,
RA Mayashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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"Functional annotation of a full-length mouse cDNA col
Nature 409:685-690(2001).
EMBL; AKO21149; BABD32306.1; -.
MGD; MGI:1924786; CO30044P22Rik.
SEQUENCE 108 AA; 11922 MW; 218DC6056B7112E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing pr
Submitted (JAN-2000) to the
EMBL; AL132959; CAB71097.1;
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De Haan M., Maarse A.C., Grivell L.A.,
Mayer K.F.X., Quetier F., Salanoubat M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicota; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TremBLre1. 15,
01-0CT-2000 (TremBLre1. 15,
01-DEC-2001 (TremBLre1. 19,
HYPOTHETICAL 87.4 KDA PROTE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J; TISSUE-CORPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C030044P22RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 790 AA; 87376 MW; B222724B75690F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21085660; PubMed=11217851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C030044P22RIK PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F15G16.60
                                                                                                                                                                                                                 Hayashizaki Y
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| | ||::| ||:
70 PRTYGSRGLQPHGRW
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7; Conserv
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Rodentia;
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he EMBL/GenBank/DDBJ
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Last annotation update
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRIATUM;
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; Murinae; Mus
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RESULT 15
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ID 09x307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

C STRAIN=A372);

C STRAIN=A372);

X MEDLINE=97000351; PubMed=8843436;

A Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,

A Redenbach H., Hopwood D.A.;

T *A set of ordered cosmids and a detailed genetic and physical map for

T the 8 mb Streptomyces coelicolor A3(2) chromosome.";

L Mol. Microbiol. 21:77-96(1996).

L Mol. Microbiol. 21:77-96(1996).

R EMBL; AL360034; CAB95978.1; -.

Interpro; IPR000182; Acetyltransf_GCN5.

R Pfam; PF00383; Acetyltransf; 1.

R Ffam; PF00383; Acetyltransf; 1.

R SEQUENCE 179 AA; 19784 MW; 0693898A177C64C8 CRC64;
                                                                                                                                                                                                                                                                                          Query Match 48.8%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conservat
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09K3O7;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-A3(2);

Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

[3]
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STRAIN-A3(2);
Seeger K.J., Harris D.;
Seeger K.J., Harris D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.

Bacterla; Firmicutes; Actinobacterla; Actinobacterldae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID-1902;
[1]
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                                                                                                                                                                 138 AWYERRGYRRIG 149
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|:|: ||| |
38 PSWHNCRGISP 48
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Pred. No. 25;
0; Mismatches
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Pred. No. 15;
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Perfect score:
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DB seq length: 2000000000
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Match
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2: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1981.DAT: *
3: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1981.DAT: *
4: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1983.DAT: *
4: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1983.DAT: *
5: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1984.DAT: *
5: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1985.DAT: *
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9: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1987.DAT: *
10: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1989.DAT: *
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12: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1991.DAT: *
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16: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1995.DAT: *
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22: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1996.DAT: *
23: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1996.DAT: *
24: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA1996.DAT: *
25: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA2000.DAT: *
26: \SIDSI_gcgdata_hold-geneseq_geneseqp-cmbl_AA2000.DAT: *
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AAY49293
AAW31396
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AAG62534
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AAW31395
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                                                                                                                                                                                                                                                                            SUMMARIES
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(without alignments)
4.169 Million cell updates/sec
           19P2 ligand peptid
19P2 ligand peptid
Human type G prote
Human type ligand
Human oxytocin sec
19P2 ligand peptid
Human CRH releasin
Prolactin releasin
Human type G prote
Human oxytocin sec
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## ALIGNMENTS

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New monocional antibodies, useful in diagnosis, as drugs and
           WPI; 2000-039381/03.
                                                                                        Key
Modified-site
                                                                                                        Homo
                     Matsumoto H,
                               (TAKE ) TAKEDA CHEM IND
                                          21-MAY-1998;
                                                    20-MAY-1999;
                                                              25-NOV-1999.
                                                                         WD9960112-A1
                                                                                                        sapiens
                     Kitada C,
                                          98JP-0140293
                                                    99WO-JP02650
                                                                                        Location/Qualifiers
                                                                                   /note- "C-terminal amide"
                                LTD.
                     Hinuma
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'n
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Monocional antibody; 19P2 ligand; diagnosis; proiactin secretion; pituitary; regulatory mechanism; central nervous system; pancreat

pancreatic

19P2 iigand peptide fragment.

AAY49293;

22-FEB-2000

(first entry)

AAY49293 standard;

peptide;

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RESULT
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central narvous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19p2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosassy can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19p2 ligand.
                                                                                                                                                                                                                                                               Disclosure; Page 27; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                    New monoclonal antibodies, u
studying diseases related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsumoto H,
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regulatory mechanism; central nervous system; pancreat
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Pred. No. 1.6e
0; Mismatches
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d abnormality
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RESULT
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                        This sequence represents a peptide fragment from a novel human type caliform polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupied receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, composition, prophylactic application, prophylactic application, prophylactinaemia, hyperchoiesterolaemia, hypergiyceridaemia, hyperchoiesterolaemia, hypergiyceridaemia, hyperpolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, neurosis, asthma, rheumatoid arthritis spinal injury, translent brain ischaemia, epilepsy, amylotrophic lateral scierosis, acute myocardial infarction, infertility, spinocerebellar degeneration, colapsable of altering the binding activity of the ligand affecting activity of the ligand aff
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28-DEC-1995;
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                capable of aitering activation of the G
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N-PSDB; AAV02431.
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95JP-0343371.
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                                                                                                                                                                                                                                                                                                                                                                          258pp;
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              protein-coupied receptor
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85.7%;
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Pred. No. 1.6e-06;
0; Mismatches 2;
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                                                      The present sequence represents a human type ligand fragment. It

CL is used in the course of the invention. The specification describes

CL an agent for modulating prolactin secretion which comprises a

CL ligand polypeptide or a sait, for a G protein-coupled receptor (GPCR)

CL treating or preventing hypocovarianism, genecyst cacogenesia, menopausal

CL syndrome, suchyroid or hypometaboliam. They can by used for promoting

CL inhibiting prolactin secretion can be used for promoting

CL inhibiting prolactin secretion can be used for treating or preventing

CL inhibiting prolactin secretion can be used for treating or preventing

CL prolactinoma, infertility, impotence, amenorihea, galactorihea,

CL prolactinoma, infertility, impotence, amenorihea, galactorihea,

CL cromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome.

CL proles-Albright ayndrome, lymphoma, Sheelan syndrome or dyszocapermia.

CL proles-Albright ayndrome, lymphoma, Sheelan syndrome or dyszocapermia.

CL prolacting placental function can be used for treating or preventing

CL choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

aborting account of the second of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autolumnune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 166; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                            This Invention describes a novel oxytocin accretion-regulating agent which contains a ligand peptide or its asit for the 6 protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin accretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, atoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; oxytocln secretion promoter: G protein-coupled receptor protein: treatment: disease; pain; atonic bleeding: uterine recovery failure; co caesarean section: artificial fertilization; galactostasia: goat: pig;
                                                                                                                                                                                                                                                  Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting aecretion of oxytocin, as drugs for diaeaaes relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human oxytocin secretion promoting peptide
                                                             Sequence
                                                                                                                                                                                                                  Diacloaure: Page 63;
                                                                                                                                                                                                                                                                                                                          Matsumoto H.
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Matches 12
                                                                                                                                                                                                                                                                           The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism, the antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
Human; corticotrophin releasing hormone; CRH; G protein receptor analgesic; hyperaldosteronism; hypercortisoiaemia; hypoadrenocort Addison's disease; adrenal gland hyperfunction; obesity.
                                          Human
                                                                                                                                                                                                                                                             Sequence
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                                         CRH releasing
                                                                                                                                                                                                         12;
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              clonal antibodies, useful in diagnosis, diseases related to ligand abnormality
                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; 19P2 ligand; diagnosis; prolactin secretion; regulatory mechanism; central nervous system; pancreat
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                          peptide;
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                                        protein related peptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                   95.9%;
                                                                                                                                                                                                                                                                                                                                                                                        73pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinuma
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Pred. No.
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                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                    DB 21; Le
. 2.1e-06;
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                                          IJ
                                                                                                                                                                                                                           Length 20
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                                                                                                                                                                                                        Indels
                                          Ö
        hypoadrenocorticism;
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RESULT
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                    17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or smellorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypedarencorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                   Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidy1; maleimido group; amino hydroxy1; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                    17-MAY-2000;
                                                                                                                                                                    23-NOV-2000
                                                                                                                                                                                                                   WO200069900-A2
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     Prolactin releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB90992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB90992 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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26-SEP-2000; 2000JP-0297073.
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12; Conserv
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                                                                                                                    2000WO-US13576
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                    990S-0134406.
990S-0153406.
990S-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ζ
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
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RESULT
AAW31395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention deacribes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a cractive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase atabiliaed therapeutic peptides e.g. hormones, growth (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not auitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to aibumin prevents or reduces the action of peptidases to increase length of activity (haif iffe) and apecificity as bonding to large molecules decreases chaseogle to AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matchea
                                                                                                                         18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
Fujii R,
Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mod1fying
peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
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                                                                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                         26-DEC-1996;
                                                                                                                                                                                                                                                                                                           10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                           WO9724436-A2
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiena
                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic
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  Fukuaumi S,
Y, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-coupled receptor ligand fragment 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (firat entry)
                                                                                                                         96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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85.7%;
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                          Habata
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Pred. No. 2.1e
0; Mismatches
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                          Hosoya M;
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length of in vivo activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prophylactic;
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RESULT 10
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Best Local Similarity 85.
Matchea 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperlipidaemia, hypercholesterolaemia, hypergiyceridaemia, hypercholesterolaemia, hypergiyceridaemia, hypercholesterolaemia, disbetes, cancer, pancrestitis, renai disease, furner'a ayndrome, neurosis, asthma, rheunatoid arthritia, spinai injury, transient brain ischaemia, epilepsy, amylotrophic iateral scleroais, acute myocardial infarction, infertility, spinocerebeilar degeneration, bone fracture, trauma, atopic dermatitis, osteoporoais and/or oligogalactia, assays can also be developed to screen compounda which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper and polyphagia, hyperilpidaemia hyperological becase, hyper and polyphagia,
                                                                                                                                                                                                                                                                                                                  Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bieeding; uterine recovery failure; co caesarean section; artificial fertilization; galactoatasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ligand polypeptide corresponding to amino acid residues 34 to 54 of aequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceu compositions containing thia ligand may be used an a pituitary func
                                                                                                                                                                                                06-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB10366 standard: peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-363672/33.
N-PSDB; AAV02432.
                              WPI; 2000-452298/39
                                                              Matsumoto H,
                                                                                                                                                                  22-DEC-1999;
                                                                                                                                                                                                                                     WO200038704-AL
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                     veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                      Human oxytocin secretion promoting peptide SEQ
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useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair ioss, and hypotension), adrenal gland hypofunction and obesity. The
                                                           The present sequence describes a method of controlling the secretion coorticotrophin releasing hormone (CRH), involving the use of a G prote receptor ligand. This can be used to control the secretion of CRH and useful as an analgesic or for treating, preventing or amellorating
                                                                                                                                      Disclosure; Page 75; 90pp; Japanese
                                                                                                                                                                     Usc of G protein receptor corticotropin releasing ho
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26-SEP-2000; 2000JP-0297073.
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sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
n's disease; adrenal gland hyperfunction; obesity.
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                   This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in ANW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. A central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consclousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperprolactinaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, province, neurosis, astima, rheumatold arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardiai infarction, infertiiity, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or
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28-DEC-1995;
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modulator; pituitary; central nervous system; pancreas; prophylactic;
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                                                                                                     This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                        Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
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                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analyseic or for treating, preventing or ameliorating diseases associated with CRH secretion auch as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's hipercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
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26-SEP-2000; 2000JP-0297073
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                                              Human type G protein-coupled receptor ligand fragment
                                                                                 06-APR-1998
                                                                                                                AAW31391;
                                                                                                                                               AAW31391
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitada
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ia; hypoadrenocorticlsm;
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G protein-coupled receptor; ligand binding; modulator; pituitary; central nervous system

central nervous system;

pharmaceutical;

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pancreas; prophylactic;

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Search completed: September 13, 2002, 09:18:35 Job time: 500 sec
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                                                                                                                                                                                                                                                                        This sequence represents a poptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the certain polypeptide corresponding to amino acid residues 23 to 53 of the CC sequence represented in AAX31390 and is used in an assay to monitor CC indicated binding to the G protein roupled receptor protein. Pharmaceutical compositions containing this iigand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function composition, a central nervous system modulator or a pancreatic function modilator. This iigand could have specific applications as a composition, and is the protein system modulator or a pancreatic function composition, interpretable syndrome, schizophrenia, composition, growth hormone secretory disease, naxiety syndrome, schizophrenia, composition, growth hormone secretory disease, hyper-and polyphagia, composition of hyperinjedemia, hyperchoiesterolaemia, hypergiveridaemia, fully for the pancreatitis, renai disease, compositent brain ischaemia, epiiepsy, amylotrophic lateral scierosis, context myocardial infarction, infertiiity, spinocerebeliar degeneration, considered by the screen compounds which are capable of altering the binding activity of the ligand affecting activation of the C protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPT; 1997-363672/33.
N-PSDB; AAV02428.
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Kawamata Y, Kitada C;
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awyasrgirpvgrf 31
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95JP-0343371.
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Ouery Match Best Local S Matches

Similarity 12; Conser

Conservative

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Score 70; DB Pred. No. 1.2e 0; Mismatches

DB 3; 1.2e-06; 2;

Length 20; Indels

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Gaps

US-09-105-678A-46  Sequence 46, Application US/09105678A PATENT No. 6103882  GENERAL INFORMATION: APPLICANT: MORIYA, TAKAO APPLICANT: MORIYA, TAKAO APPLICANT: MORIYA, TAKAO APPLICANT: MAPLICANT: NISHIMURA, OSAMU TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street CITY: Boston STATE: MA COUNTRY: USA ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TIPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TIPE: FLOPS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/09/105,678A FILING DATE: 26-JUN-1996 PRIOR APPLICATION UNMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: RESISTRATION UNMBER: 48466-342 TELECOAMUNICATION INFORMATION: TELEFRAX: 617-523-3400 TELEFRAX: 617-523-3400 INFORMATION POR SEO ID NO: 46: SEQUENCE CHARACTER:STICS: LENGTH: 20 amino acids TYPE: maino acid STRANDEDNESS: TOPOLOGY: Linear MUS-09-105-678A-46	28 69 94.5 20 4 US-08-776-971-50 Sec 29 69 94.5 20 4 US-08-776-971-98 Sec 30 69 94.5 20 4 US-09-421-208-34 Sec 31 69 94.5 21 3 US-09-105-678A-41 Sec 32 69 94.5 21 3 US-09-105-678A-41 Sec 33 69 94.5 21 3 US-09-105-678A-41 Sec 34 69 94.5 21 4 US-08-776-971-9 Sec 36 69 94.5 21 4 US-08-776-971-51 Sec 37 69 94.5 21 4 US-09-421-208-41 Sec 39 69 94.5 21 4 US-09-421-208-41 Sec 39 69 94.5 21 3 US-09-105-678A-36 Sec 39 94.5 22 3 US-09-105-678A-36 Sec 39 94.5 22 4 US-09-105-678A-36 Sec 30 Se
	Sequence 50, Appl Sequence 98, Appl Sequence 34, Appl Sequence 35, Appl Sequence 41, Appl Sequence 9, Appli Sequence 35, Appl Sequence 35, Appl Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl Sequence 52, Appl Sequence 42, Appl Sequence 42, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 53, Appl Sequence 54, Appl Sequence 57, Appl Sequence 67, Appl Sequence 67, Appl Sequence 68, Appl

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AWYXXRGIRPVGRF 14

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APPLICATION:
CLASSIFICATION: CUNKNOWN>
LIOR APPLICATION: CUNKNOWN>
LIOR APPLICATION NUMBER: PCT/JP96/03821
ETLING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-ANR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 11-ANR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
ATTORIST NUMBER: JP 8/2
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US-08-776-971-64
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                                                                                                                                                            Query Match
Best Local S
                                                                                                                                    Matches
                                                           I AWYXXRGIRPVGRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
AWYASRGIRPVGRF 20
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                                                                                                                                                               Similarity
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ninuma, Shuji
Nabata, Yugo
Kawamata, Yuji
Nogoya, Masaki
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                                                                                                                                                               95.9%;
85.7%;
                                                                                                                             Score 70: DB
Pred. No. I.2e
0; Mismatches
                                                                                                                                0
                                                                                                                                . I.2e-06;
ches 2;
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Ouery Match
Best Local Similarity
Watches 12; Conserve
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                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6258561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118.

FILING DATE: 27-TUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REFERENCE/DOCKET NUMBER: 4846

TELECOMMUNICATION INFORMATION:

TELEPNONE: 617-523-3400
                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga Masato
APPLICANT: MOT19a, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METNOD OF
NUMBER OF SEQUENCES: SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
EILING DATE:
EILING DATE:
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                  TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 52
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 130 v
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                     7 AWYASRGIRPVGRF
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5. 6103882
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625856I
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           130 Water Street
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Pred. No. 1.2e-06;
D; Mismatches 2;
                                                                                   PRODUCING A 19P2 LIGAND
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Iinear
; MOLECULE TYPE: pept1
US-09-105-678A-47
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN. DAVID G
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-5400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
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LENGTH: 21 amino acids
                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-197

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 12; Conserv
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7 AWYASRGIRPVGRF 20
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHNAN, LLP
                                                                                                                                                                                                                                                                                                                                                     FukusumI, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
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                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                  STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                      OF SEQUENCES: 140
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Fujii, Ryo
Fujii, Shoji
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Habata, Yugo
Kawamata, Yuji
Hogoya, Masaki
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Pred. No. 1.3e-06;
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US-09-421-208-47
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            NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 488
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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NAME: COLLIN, DAVID G.
NAME: COLLIN, DAVID G.
RECISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 aming acids
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                  l AWYXXRGIRPVGRF 14
7 AWYASRGIRPVGRF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: I8-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: I5-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                     Conservative
                                                                                        95.9%;
85.7%;
                                                                                      Score 70; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP 7/343371
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                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          47176
                                                                                      DB 4;
1.3e-06;
                                                                                                      Length 21
                                                                     Indels
                                                                     0
                                                                   Gaps
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Sequence 47, Application US/0942I208 Patent No. 6258561 GENERAL INFORMATION: APPLICANT: Suenaga, Masato
APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: NIShimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 Boston 130 Water Street USA

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNGBER: US 09/I05,678
APPLICATION UNGBER: JP 172118/1997
ETILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US US/09/421,208

48466-342

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US-09-105-678A-48
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Best Local Similarity 85.7
                                                                         Query Match
Best Local :
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                     NAME: CON111, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: pepi
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Ogray
APPLICANT: Nishimura, Ogray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                         Local Similarity
nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                           LENGTH:
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               1 AWYXXRGIRPVGRF 14
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AWYASRGIRPVGRF 20
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6103882
                                                                                                                                                                                           amino acid
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                                                           Conservative
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                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHOD OF PRODUCING A 19P2 LIGAND
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85.7%;
                                                                       95.98;
85.78;
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                                                                     Score 70; DB 3; 1
Pred. No. 1.3e-06;
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Pred. No. 1.3e-06;
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                                                           Mismatches
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                                                                                   Length 22;
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; PRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
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                                                                           Matches
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                   1 AWYXXRGIRPVGRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FRATSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
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Kitada, Chiako
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 617-523-3400
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Nabata, Yugo
Kawamata, Yuji
AWYASRGIRPVGRF
                                                                                                                                                                                                                                            LENGIN: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                    FELEFAX: 617-523-6440
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                                                                           Conservative
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Nosoya, Masaki
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85.7%;
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mi, shoji
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                                                                         Score 70; DB 4;
Pred. No. 1.3e-06;
0; Mismatches 2
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RESULT 9 US-09-421-208-48

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                                                                                                                                                                                                                                                                   US-09-105-678A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CON111, David G.
REGISTRATION NUMBER: 27,026
REFERENCE_DOCKET NUMBER: 4846
TELECOMMUNICATION 1NFORMATION:
TELEPHONE: 617-523-340D
TELEPHAX: 617-523-644D
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                             sequence 9, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Moriyā, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METNOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/1D5,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNET/AGENT INFORMATION:
                                                                                                                APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                  STATE:
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                                                                                                                                                                                                                                                                                                                                  1 AWYXXRGIRPVGRF 14
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7 AWYASRGIRPVGRF 20
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                                                                 130 Water Street
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Tanaka, Yoko
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85.7%;
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GENERAL INFORMATION:
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Best Local !
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                                                                                       SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48:
TELECOMMUNICATION 1NFORMATION:
                                                         FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 48-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 L1GAND
NUMBER OF SEQUENCES: 52
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hes 12; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3D
                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AWYASRGIRPYGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
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85.7%;
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Pred. No. 1.9e-D6;
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                                                                                                                                                                                                                                                                                                                                                                                      ROBERTS & CUSHMAN, LLP
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US-08-776-971-61; Sequence 61, A
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             PRIOR APPLICATION DATA:

APPLICATION UNBER: PCT/JP96/03821

APPLICATION NUNBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUNBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/9419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 18-MAR-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: CON111, DAVId G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 47176

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFDRMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids
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GENERAL INFORMATION:
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Best Local (
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMEDTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hlnuma, Shuji
Habata, Yugo
Kawamata, Yuji
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12; Conserv
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TYPE: amino acid
STRANDEDNESS: single
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Fujli, Ryo
Fukusumi, Shojl
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Pred. No. 1.9e-06;
0; M1smatches 2;
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-61
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GENERAL INFORMATION:
                                                        Matches
                                                                     Query Match
Best Local :
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Best Local Similarity
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CONPOTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF FILING DATE: 26 JUN-1998
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masat
APPLICANY: MOTIYB, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Oss
TITLE OF INVENTION: METHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 18 AWYASRGIRPVCRF
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G. REGISTRATION NUMBER: 2
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                1 AWYXXRGIRPVGRF 14
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                                                      l Similarity
12; Conserv
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                                                        Conservative
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85.7%;
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                                                                                                                                                                                                                                                                                                      27,026
                                                     Score 70; DB 4;
Pred. No. 1.9e-06;
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Pred. No. 1.9e-06;
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RESULT

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RESULT I5
US-09-I05-678A-44
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; MOLECULE TYPE: peptide
US-09-421-208-43
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Best Local Similarity 85.7
Matches 12; Conservative
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                                                                                                                                                                                                                               Patent No. 6103882
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Sequence 44, Application US/09105678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FICPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #I.30
CURRENT APPLICATION DATA:
                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: MORIYa, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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ZIP: 02109
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                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                             18 AWYASRGIRPVCRF 3I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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             COUNTRY:
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USA
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85.7%;
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Pred. No. I.9e-06;
0; Mismatches 2; Indels
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                                                          Query Match
Best Local Similarity
Matches I2; Conserv
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INFORMATION FOR SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NDMBER: US/09/
EILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
APPLICATION STATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 8
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                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                     NAME: Conlin, David G. REGISTRATION NUMBER: 27,026
                1 AWYXXRGIRPVGRF 14
AWYASRGIRPVGRF 31
                                                              Conservative
                                                                                                                                                                            linear
                                                                                                                                                      peptide
                                                                             95.9%;
85.7%;
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                                                                           Score 70; D8 3;
Pred. No. 2e-06;
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                                                              Mismatches
                                                              2:
                                                                                          Length 32;
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Search completed: September 13, 2002, 09:20:58
Job time: 623 sec

Gaps

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: plr1:*
2: plr2:*
3: plr3:*
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Match
       554.88
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## ALIGNMENTS

RESULT JC7607

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RESULT 2 S61046 ARP1 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein D1478; protein YDL167c C;Species: Saccharomyces cerevisiae C;Species: S61046; S31139; S67719 R;Sohl, T.M. Submitted to the EMBL Data Library, November 1995 R;Reference number: S61010 A;Recession: S61046 A;Residues: 1-719 <poh> A;Residues: 1-719 <poh> A;Residues: 1-719 <poh> A;Cross-references: EMBL:Z67750; NID:g1061256; DIDN:CAA91579.1; DID:g1061272 A;Gross-references: EMBL:Z67750; NID:g1061256; DIDN:CAA91579.1; DID:g1061272 A;Wehner, E.P.; Rao, E.; Brendel, M. Mol. Gen. Genet. 237, 351-358, 1993 A;Title: Molecular structure and genetic regulation of SFA, a gene responsible for re A;Reference number: S31138; MUID:93247548 A;Scatus: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA</poh></poh></poh>	Query Match 94.5%; Score 69; DB 2; Length 83;  Best Local Similarity 85.7%; Pred. No. 1.2e-05;  Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Qy 1 AWYXXRGIRPVGRF 14	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-83 <yam> A; Residues: 1-83 <yam> A; Cross references: DDBJ:AB040612; DDBJ:AB040613 C; Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pitultary. C; Genetics: A; Gene: PTRP A; Introns: 33/1</yam></yam>	prolactin-releasing peptide - rat  C:Specles: Rattus norvegicus (Norway rat)  C:pate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001  C:Accession: JC7607  R:Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001  A:Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A:Reference number: JC7607; MUID:21092785; PMID:11178959  A:Accession. TC7607

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probable membrane protein - Streptomyces coelicolor C;Specles: Streptomyces coelicolor C;Specles: Streptomyces coelicolor C;Specles: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T35841
R;Hatrls, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1998 A;Accession: T35841
A;Accession: T35841
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: NA
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A:Cross-references: EMBL:X68020; NID:g577609; PIDN:CAA48159.1; PID:g288590
A;NOte: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Potl, T.M.
submitted to the Protoin Sequence Database, July 1996
A;Reference number: $67708
A;Accession: $67719
                                                                 A; Molecule type: DNA
A; Resldues: 1-149 <DUI>
R; Dunn, J.J.; Studler, F.W.
J. Mol. Blol. 148, 303-330, 1981
J. Mol. Blol. 148, 303-330, 1981
A; Title: Nucleotide sequence from the genetic left
A; Reference number: A92866; MUID:82078034
A; Accession: C92866
                                                                                                                                                                                                                                                                                                                                                                                                                                            endodeoxyribonuclease I (EC 3.1.21.-) - phage T7 C;Species: phage T7 C;Date: 01-Sep-1981 #sequencc_revision 24-Sep-1981 C;Accession: B94615; C92866; S42301; A00785 R;Dunn, J.J.; Thompson, K.
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A; Residues: 1-184 <NAR>
A; Cross-references: EMBL: ALO31260;
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A;Map position: 4L
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50.0%;
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Pred. No. 6.2;
1; Mismatches
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Pred. NO. 6.6;
3; Wismatches
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Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,633-kb pSymB megapiasmld A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95936
A;Asterine: ------
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A;Experimental source: strain 1021, megaplasmid psymb
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.N.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorbolter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the Legume symbiont Sinorhizoblum mellioti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:V01146; NID:9431187; PIDN:CAA24402.1; PID:915581 A;Note: the authors did not translate the codon for residue 1 C;Comment: Endodeoxyrlbonuclease I, which is expressed in the late stage, s a linear monomer. In the late stage, the T7 DNA replicates via linear cc C;Genetics:
glutamy1-tRNA synthetase gltX [imported] - Bacillus halodurans (strain C-125)
C;Specles: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E83663
                                                                                                    RESULT
E83663
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
G; Conserve
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C;Superfamily: phage T7 exodeoxyribonuclease
C;Keywords: hydrolase
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A; Residues: 1-149 < DUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SMb21253
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A; Residues: 1-256 < KUR>
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C;Species: Sinorhizobium meliloti
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8; Conserv
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Pred. No. 7.7;
1; Mismatches
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RESULT 7
D87357
hypothetical protein CC0871 [Imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Apr-2001 #text_change 20-Apr-2001
C;Accession: D87357
C:Accession: D87357
C:Accession: D87357
Ahlunm. T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Haft
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H72646
C;Accession: H72646
Title: Result 8
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodus A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E83663
                                                                                                                                                                                                                                                awa, H.; Takamlya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; NIR Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A; Reference number: A72450; MUID:99310339
A; Accession: H72646
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A;Title: Complete Genome Sequence of Caulobscter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87357
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A;Residues: 1-485 <370>
A;Cross-references: GB:AP001507; GB:BA0000004; NID:g10172612; PIDN:BAB03828.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Cross-references: DDBJ;AP000060;
A;Experimental source: strain K1
C;Genetics:
                                                                                                                      A; Molecule type: DNA
A; Residues: 1-238 <KAW>
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C;Genetics:
A;Gene: CC0871
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A; Residues: 1-194 <BTD>
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C;Superfsmily:
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                             Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no,
, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamaza
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Pred. No. 25;
2; Mlsmatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38;
Pred. No.
                                                                                   NID: 95104188; PIDN: BAA79576.1; PID: d1043362; PID: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutsmine--tRNA iigase homology
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15;
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acetate kinase - Delnococcus radiodurans (strsin R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #tex
C:Accession: B75254
R:White, O:Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.
S:Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacteriu
A;Reference number: A75250; MUID:20038896
A;Accession: B75254
A;Recession: B75254
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A; Residues: 1-333 <SIM>
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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717

A;Note: for s complete list of authors see reference number A59328 belo
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C;Species: xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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Best Local S
Matches 7
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Best Local
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7; Conserv
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7: Conserv
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63.6%;
                                                      the radioresistant bacterium MUID:20036896
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Pred. No. 26;
O; M1smatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                 03-Dec-1999 #text_change 17-Mar-2000
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                                                                                                                                                                                                        E.K.; Peterson, J.D.; Dodson, L.; Utterbsck, T.; Zslewski,
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A;Cross-references: GB:AE002089;

GB:AE000513; NID:g6460427; PIDN:AAF12139.1;

PID:9646

C Z

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A; Residues: 1-398 A; Molecule type: DNA A:Status: preliminsry

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A; Experimental
C; Genetics:
A; Gene: DR2602
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A35548

A35548

C; Specics: Rhizobium meliloti
C; Specics: Rhizobium meliloti
C: Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 08-Oct-1999
C; Accession: A35548
C; Accession: A35548
C; Accession: A35548
C; Accession: A35548
J. Biol. Chem. 265, 2843-2851, 1990
A; Title: The ndvB iocus of Rhizobium meliloti encodes a 319-kDa protein involved A; Accession: A35548; MUID:90153914
A; Accession: A35548; MUID:90153914
A; Accession: A35548; MUID:90153914
                                                                                                                                                                                                                                                                       A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-154 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein rPO2I72 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Caccession: AH.O.E.
R;Parkhili, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.: Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, din, Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.: Barre
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AH0264
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A:Molecule type: DNA
A:Rosidues: 1-2870 <IEL>
A:Cross-references: GB:J05219; NID:g152270; PIDN:AAA26305.1; PID:g152271
C:Keywords: transmembrane protein
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C; Superfamily: acetate
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                                                                                                Query Match
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Matches
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Best Local
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Best Local 9
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                          124 WYYIDGIRPSLGR 136
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les 6; Conserv
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(strain PCC 7120) plasmid pCC7

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                                                                                                    A: Map position:
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, Hosoya M., Kawamata C., Kurokawa T., Nishi of prolactin releasing 1999). tes prolactin through its rectly to secrete Pr. Y. Wishi oblowani A. Y. Wedulia oblowani A. Y. Wedulia oblowani A. Y. Wedulia oblowani A. Y. Wedulia oblowani I. Is pstitute of Bloinformat is copyright. It is pstitute of Bloinformat institutions as long tement is not removed. icense agreement (See Icense@isb-sib.ch).  027.1;  19nal. By SIMILARITY. PROLACTIN-RELE PROLACTIN-RELE PROLACTIN-RELE AMEDIATION (G-53 and DATION	Jence btati curs celea celea crani batar Mata a H.,	PIP_AERSO ARGA_ECOLI PPOX_HUMAN PPOX_HOUSE TDT_ONCMY KICH_YEAST ENV_MCFF CATA_CAUCR PBPB_HAEIN PBPA_ECOLI HGBB_HAEDU HGBB_HAEDU HGBB_HAEDU PRT; 87
g peptide elease and ceptor GPR AND HypOTH produced tics and lere are no a greater of the column of	ee) alate) RP) (Prolace) RP) (Prolace) Pertebrata; Hominidae; Hominidae; Hominidae; No M.; In. M.;	ENTS
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P81278;
                                                                                                         MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98268781; PubMed=9507765;
Hinuma S., Habata Y., Fujil R., Kawamata Y., Hc
Kitada C., Masuo Y., Asano T., Mattsumoto H., Se
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                       Regul. Pept. 83:1-10(1999).
                                                                                                                                                                                                                                                                                                                                                                                      sumino Y., Fujino M.;
"Tlssue distribution of prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                             Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
MEDLINE-98268781;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            releasing peptide
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                       AWYXXRGIRPVGRF
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AWYTGRGIRPVGRF
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red. No. 8.5e-07;
Mismatches 2;
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T., Nishimur
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a O., On
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NRP1_YEAST
ID NRP1_Y
AC P3277C
D7 01-0C1
D7 01-NOV
D7 01-MAR
DE ASPARE
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OS SACCIH
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RP SEQUEI
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Matches 12
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SIGNAL
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PEPTIDE
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2020 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
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  SEQUENCE FROM N.A
STRAIN-AH22;
                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovldae; Bovinae; Bos.
NCBI_TaxID=9913;
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Mammalla; Eutheria;
                                      Saccharomycetales;
NCBI_TaxID=4932;
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PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP
08AC35A13B0FA908 CRC64;
                                                     Saccharomycotina; Saccharomycetes; cetaceae; Saccharomyces.
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actyia; Ruminantia; Pecora;
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Sekiguchi M.,
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ENRN_BPT7 STAN
P00641;
21-JUL-1986 (Rel. 0
21-JUL-1986 (Rel. 0
01-NOV-1995 (Rel. 3
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InterPro; IPRO01876; Znf-RanBP.
Pfam; PF00076; rrm; 1.
Pfam; PF000641; zf-RanBP; 2.
SMART; SM00360; RRM; 1.
SMART; SM00367; ZnF_RBZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities a license agreement (see http://www.isb-slb.ch/announce/or scnd an cmail to llcense@isb-slb.ch).
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MEDLINE-83241725;
Dunn J.J., Studier
                                                       SEQUENCE FROM N.A.
                                                                                                               T7-11ke phages.
NCBI_TaxID-10760;
                                                                                                                                                                                                        Bacterlophage T7
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Wehner E.P., Rao |
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S0002326; NRP1.
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PS00030; RRM_F1; FALSE_NEG.
PS01358; ZF_RANBP2_1; 2.
PS50199; ZF_RANBP2_2; 2.
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e I (EC 3.1.21.2)
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Pred. No. 1.3;
3; Mismatches
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RANBP2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding;
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                                                                                                                                                                            stage;
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ADA9BC09FD582669
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                                                                                                                                                                            Caudoviraies; Podoviridae;
                                                                                                                                                                                                                                                                update) (Endonuclease).
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RESULT
SYE_BACHD
ID SYE_BACHD
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CO Bacte
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Q9KGF6;
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locations of T
J. Mol. Biol.
EMBL; V01127; CAA24345.1; -.
EMBL; V01146; CAA24402.1; -.
PIR; A00785; NBEP37.
PIR; S42301; S42301.
Hydrolase; Nuclease; Endonuclease.
SEQUENCE 149 AA; 17172 MW; D092AA28E3743BC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lab-slb.ch/announce/or send an email to license@isb-slb.ch).
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                                                                                                                                                                                        MEDLINE-20512582; PubMed-11058132; Takami H., Nakasone K., Takaki Y., Fuji F., Hirama C., Nakamura Y., O
                                                                                                                                                                                                                                                                                                                                          Bacillus halodurans.
Bacteria; Firmicutes; Bu
Bacillus/Staphylococcus
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16-OCT-2001 (Rel. 40, Las
16-OCT-2001 (Rel. 40, Las
Glutamyl-tRNA synthetase
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                                                                                                                                                                          Horikoshi K.;
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence of bacteriophage T7
  of T7 genetic elements.";
iol. 166:477-535(1983).
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                                                                                                                                                                                                                                                          / JCM 9153;
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57.18;
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Last annotation updat
ase (EC 6.1.1.17) (Glu
                                                                                                                                                                                                                                                                                                                                            Baclllus/Clostridlum us group; Bacillus.
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Pred.
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Ogasawara N.,
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with Bacillus subtilis.";
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Kuhara S.
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AND THE BREAKDOWN
DNA REPLICATES AS
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L outstation -
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AMINOACYL-TRNA SYNTHETASE FAMILY

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RESULT 7
EXLL_HUMN
ID LEXUL_N
AC 092935
DT 15-JUL
DT 15-
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Best Local S
Matches 7
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InterPro; IPR000924; CRNA-Synt_1c.
InterPro; IPR001412; tRNA-Synt_I.
Pfam; PF00749; tRNA-Synt_1c; 1.
Pfam; PF009779; TRNASYNTHGUU
PRINTS; PR00987; TRNASYNTHGUU
PROSITE; PS00178; AA_TRNA_LICASE_I; 1.
                                                                                                                                                       SEQUENCE FROM N.A. Van Roy N., Dc Psepe A., De Boulle K., Whyts W., Spleker N., Van Roy N., Dc Psepe A., De Boulle K., Willems P.J., Van Hul W., Versteeg R., Speleman F.; Willems P.J., Van Hul W., Versteeg R., Speleman F.; Refined physical mapping and genomic structure of the EXTL1 gene. "Refined (MAY-1999) to the EMBL/GenBank/DDBJ databases."

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases."

-I- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Type II mcmbrane protein. Endoplssmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998
15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE=97189339; PubMcd=9037597;
Wise C.A., Clines G.A., Massa H., Trask B.J.,
"Identification and localization of the gene
of the multiple exostoses gene family.";
Genome Res. 7:10-16(1997).
                                                                                                                               reticulum (By similarity).
-!- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Xu L., Deng H.X., "Mutations of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euksryota; Metazos;
Mammalia; Eutheria;
                                                          between
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  s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no wa
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Similsrity 58.3%;
7; Conservative
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Metazos; Chordats; C
Metazos; Primates; C
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(Rel. 36, Lsst sequence updste)
(Rel. 40, Lsst snnotation update)
(Rel. 40, Lsst snnotation update)
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EXT genes
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Prcd. No. 5.2;
2; Mismatches
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biosynthosis; Ligase; ATP-binding;
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5.2;
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RC STRAIN-Berkeley;

RX MEDLINE-20196006, PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Nahg Q., Chen L.X.,

RA George R.A., Lewis S.E., Richards S., Nelson C.R., MikLos G.L.G.,

RA George R.A., Lewis S.E., Bexter E.G., Nelt G., Nelson C.R., MikLos G.L.G.,

RA Hardon R.C., Bayayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burkis K.C., Busam D.A., Butler H., Csdieu E., Center A., Chandra I.,

RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dedson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evsngelista C.C., Ferraz C., Ferriera S., Fleischmsnn W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gusn P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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SEQUENCE
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01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Probable G-protein-coupled receptor Mt
like 10 protein)
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Eukaryota; Metazos; Arthropoda; Tracheata; Hexapoda; Insects;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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MIM; 601738; -.
InterPro; IPR004263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-oncogene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF083631;
AF083632;
AF153980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269
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Multigene family; Trsnsmembrane; Signi Multigene family; Signi Mul
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AAD02840.
AAF73172.
AAF73172.
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53.8%;
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Pred. No. 7.3;
2; Mismatches
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jaisii M., Kalush F., Karpen G.N., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krayltz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mishina N.Y., Hobarry C., Morris J., Mosbrefi A.,
RA McIkulov G., Mishina N.Y., Hobarry C., Morris J., Mosbrefi A.,
RA McIkulov G., Mishina N.Y., Hobarry C., Morris J., Melson O.L.,
RA McIkulov G., Mishina N.Y., Hobarry C., Morris J., Melson O.L.,
RA McIkulov G., Mishina N.Y., Hobarry C., Morris J., McDero D.,
RA McIkulov G., Mishina N.Y., Pan S., Poliard J., Puri Y., Reese M.G.,
RA Melson D.R., Pithman G.S., Pan S., Poliard J., Puri Y., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shine B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradiing A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodsee T., Weinsteck G.M., Welssenbach J.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Endin G.M., Venter J.C.,
RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.,
RN Licians S.M., Wers E.M., Rubin G.M., Venter J.C.,
RN Licians S.M., Wers E.M., Rubin G.M., Venter J.C.,
RN Licians S.M., Wers E.M., Rubin G.M., Venter J.C.,
RN Licians S.M., Wers E.M., Rubin G.M., Venter J.C.,
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"Drosophila melanogaster G prot.
J. cell Biol. 150:F83-F88(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00649; __PROTEIN_RECEP_F2_1;
PROSITE; PS00650; G_PROTEIN_RECEP_F2_4;
PROSITE: PS50261 _G_PROTEIN_RECEP_F2_4;
Receptor; G-protein_coupled_receptor; Tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: integral membrane protein (Potential). SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European
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   protein-coupled receptors.";
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MEDLINE-21396507; PubMed-11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe P., Bstut Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gioux S Godrie T., Goffeau A., Kahn D., Klas E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purneile B., Ramsperger U., Renard C., Thebauit P., Vandenboi M., Weidner S., Galibert F., Analysis of the chromosome sequence of the iegume symbiont Sinorhizoblum meilloti strain 1021.";

Sinorhizoblum meilloti strain 1021.";

Proc. Nati. Acad. Sci. U.S.A. 98:9877-9882(2001).

-i- FUKCTION: INVOLVED IN TNE PRODUCTION OF BETA-(1,2)-GLUCAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90153914; PubMed-2154461; relpi L., Dylan T., Ditta G.S., Helinski D.R., Stanfield Telpi L., Dylan T., Ditta G.S., Helinski D.R., Stanfield The ndvB locus of Rhizobium meliioti encodes a 319-kDa pinvolved in the production of beta-(1-->2)-glucan.*, D. Biol. Chem. 265:2843-2851(1990).
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Haemophius influenzae.
Bacteria, Profesharia
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STRAIN-RD / KW20 / ATCC 51907;
STRAINE-95350630; PubMed-75428
MEDLINE-9530630; Adams M.D.
                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                      Fieischmann R.D., Adbms M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fieids C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedbiom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Yenter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94341577; PubMed=8063112;
Clifton S.W., McCarthy D., Roe B.A.;
"Sequence of the rec-2 locus of Haemophilus
comms-ORF3 of Bacilius subtilis and msbA of E
Gene 146:95-100(1994).
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Science 269:496-512(1995).
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InterPro; IPR003753; EXONUC_VII_L.
InterPro; IPR002309; trNA-synt_2.
Pfam; PF02601; EXONUC_VII_L; 1.
Pfam; PF01336; trNA-anti; 1.
Hydrolase; Nuclease; Exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
NCBI_TaxID-1902;
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Q9FBM3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seeger K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
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Pred. No.
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Pfam; PF026 Pfam; PF013 Hydrolase;

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145929A8372B4E08 CRC64;

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RESULT 12

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046908;
15-DEC-1998
15-DEC-1998
15-JUL-1999
                                                                                                                                                                                                                                                         Interpro; IPRO00702; Ribosomai_L6.
Interpro; IPRO02358; Ribosomai_L6_1.
Pfam; PF00347; Ribosomai_L6; 1.
PRINTS; PR00059; RIBOSOMALL6.
PRODOm; PD002236; Ribosomai_L6; 1.
PROSITE; PS00525; RIBOSOMALL6_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dougias S.E., Penny S.L.,
"The plastid genome of the cryptophyte alga, Guillardia theta:
complete sequence and conserved synteny groups confirm its common
ancestry with red algae.",
J. MOL. Evol. 48:236-244(1999).
-1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND
LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                Ribosomal protein;
SEQUENCE 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF041468; AAC35717.1; HSSP; P02391; 1RL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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NC8I_TaxID=55529;
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SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INE-97283757; PubMed-9137835; S.L., Liu X.-Q., Douglas S.E.; large ribosomal protein gene ciuster of organization, sequence and evolutionary hem. Moi. Biol. Int. 41:1035-1044(1997).
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YKGKGIRYVGEF
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liarity 58.3%;
Conservative
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19527 MW;
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                                                                                      Score 35; DB Pred. NO. 11; 1; Mismatches
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Score 35; DB Pred. No. 25; 3; Nismatches

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ID CYCR_CHRVI
AC 08947;
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DE Photosynthe
GN Photosynthe
GN Chromatium;
OC Allochromatium;
OC Chromatium;
RR COISON G.E.
CO THIGHTLY
CC THISTORY
CC -1- SUBDELLIA
RT CHROTION
CC -1- SUBDELLIA
RT CHROTION
CC -1- SUBLIAN
CC -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       center proteins from Chromatium vinosum.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN A
TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PHOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000
30-MAY-2000
30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR003158; Cytc_RC.
InterPro: IPR000345; Cytc_hem
Pfam; PF02276; Cytc_RC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB011811; BAA32742.1; HSSP; P07173; 6PRC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromatium vinosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Primary structure of genes encoding light-harvesting
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PTM: BINDS FOUR HEME GROUPS PER MOLECULE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 transport;
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R., Knaff D.B.
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in; Duplication;
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Last sequence up
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HEME 1 (CO).
IRON 1 (HEME A.
(BY SIMILARITY).
HEME 2 (COVALENT) (B.
'USME 2 (COVALENT) (BY S'
'USME 2 (HEME AXIAL LIT'
'VILARITY)
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                                                          HEME 2 (COVALENT IRON 2 (HEME AXI (BY SIMILARITY))
HEME 3 (COVALENT HEME 3 (COVALENT IRON 3 (HEME AXI (BY SIMILARITY))
HEME 4 (COVALENT HEME 4 (COVALENT IRON 3 (HEME AXI (BY SIMILARITY))
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IRON 4 (HEME AXIAL (BY SIMILARITY). 96BCD91FF1B9AE7E
                                                                                                                                                                                                                                                                                                                                                                                      PHOTOSYNTHETIC REACTION CENTER CYTOCHRONE
                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
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                                                                                                                        (HEME AXIAL
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RESULT 14

THIL\_ZOORA P07097; 01-APR-1988

STANDARD; 97,

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palmer M.A.J., Differding E., Gamboni R., Williams S.F., Walsh C.T., Sinskey S.J., Masamune S.; "Biosynthetic thiolase from Zoogloes ramigera. Evidence mechanism involving Cys-378 as the active site base."; J. Biol. Chem. 266:8369-8375(1991).

-I- CATALYTIC ACTIVITY: 2 acetyl-CoA - CoA + acetoacetyl-PATHWAY: FIRST STEP IN POLY-BETA-HYDROXYBUTYRATE BIOLING THE BIOL
                                                                                                       PROSITE; PS00098; THIOLASE 1;
PROSITE; PS00099; THIOLASE 3;
PROSITE; PS00737; THIOLASE 2;
Transferase; Acyltransferase;
INIT_MET 0
                                                                            INIT_MET
                                                                                                                                                                                                                                                                                                                                                     PIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGENESIS OF CYS-377.
MEDLINE-91217075; Pubmed-1673680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus Characterization of the genes encoding beta-ketothiolase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peoples O.P., Masamune S., Walsh C.T., Sinskey A.J.;
"Biosynthetic thiolase from Zoogloea ramigera. III. Isolation and characterization of the structural gene.";
J. Blol. Chem. 262:97-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-ATCC 19623 /
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01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J02631; AMA27706.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetoacetyl-CoA reductase."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89359356; PubMed-2670935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87083504; PubMed-2878929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acetyl-CoA acetyltransferase (EC
                                                                                                                                                                                                                                                                                            Interpro; IPR002155; Thiolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISION TO 130
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                                                                                                                                                                                                                                                                                                                  A26121; XXGZAC.
A27754; A27754.
; P27796; 1AFY.
                                                                                                                                                                                                                                  PF00108; thiolase; 1. PF02803; thiolase_C; 1.
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  40342 MW;
SUBSTRATE BINDING (BY SIMILARITY).
BASE.
C->G: LOSS OF ACTIVITY.
; 6D2351A1BC0E4EDD CRC64;
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; 1.
; PNB biosynthesls.
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2.3.1.9) (Acetoacety1-CoA thiolase).
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01-0CT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _GEOCN
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00091; Lubulin; 1.

PRINTS; PR01161; TUBULIN.

PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.

PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.

Microtubules; CTP-binding; Multigene family.

NP_BIND 142 GTP (POTENTIAL)

SEQUENCE 453 AA; 50399 MW; 2EA9DBA0246EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: $69627; AAB20557.1; ALT_SEO. PIR; $18597; $18597 InterPro; IPR002453; Beta_tubulln. InterPro; IPR000217; Tubulin_FtsZ. InterPro; IPR003008; Tubulin_FtsZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss institute of Dioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-slb.ch/moor send an emmail to license@isb-sib.ch).
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-i- FUNCTION: TUBULLY IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.

-i- SUBUNIT: DIMER OF ALPNA AND BETA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=92079883; PubMed=1836049;
Gold S.E., Casala W.L., Keen N.T.;

"Characterization of two beta-tubulin genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candidum."
Mol. Gen.
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Eukaryota; Fungi; Ascomycota; Saccharomycotlna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - 1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Dlpodascaceae; Galactomyces
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266 RGIQPLGR 273
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Pred. No. 29;
1; Mismatches
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2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
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6: sp_manmal:*
7: sp_mhc:*
8: sp_organe1:
9: sp_phage:*
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Match
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Q91920 orya sativ
Q9k397 streptomyce
Q9k397 streptomyce
Q92ve9 rhizobium m
Q986u6 rhizobium 1
Q00050 aspergilius
Q9a9u0 caulobacter
Q9yeh0 asropyrum p
Q9ph76 xylella fas
Q9rr92 deinococcus
Q9rr92 deinococcus
Q95wf7 drosophila
Q95yh7 drosophila
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Q9t133 bacteriopha
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## ALIGNMENTS

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Q9w624;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
C-RF AMIDE
Q93LZ7
Q93LZ7; PRELIMINARY;
Q93LZ7;
Q1-DEC-2001 (TremBLre1. 19,
Q1-DEC-2001 (TremBLre1. 19,
Q1-DEC-2001 (TremBLre1. 19,
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"Carassius Rramide (C-RF amide).":
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cypriniformes; Cyprinidae; Carassius.

Cypriniformes; Cyprinidae; Carassius.
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3 WYVGRGVRPIGRF :
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SEQUENCE FROM N.A.

Pajunen M.I., Kiljunen S.J., Soederholm M.

"Complete genomic sequence of the lytic ba

"Craninia enterocolitica serotype O:3.";

J. Bacterioi. 183:1928-1937(2001).

EMBL; AJ251805; CAB63604.1;

SEQUENCE 153 AA; 17640 MW; 211571BBDE6
                                                            086838;
01-NDV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9T133;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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T7-like p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kormanec J., Bistakova J., Novskova R., Homerova D., Rei 'Cloning and characterization of a new polyketide gene of Streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64:
PUTATIVE MEMBRANE
SC9A10.05C.
Streptomyces coeif
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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NCB1_TaxID=1894;
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bacteriophage
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Pfam; PF00179; UQ_con: 1.

SMART; SM00212; UBCc; 1.

SMART; SM00212; UBCc; 1.

PROSITE; PS50127; UBIQUITIN_CONJUGAT_2;

Ligase; Ubiquitin conjugation.

CPOTENCE 540 AA; 60487 MW; 5DE1FF4E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000
01-0CT-2000
01-DEC-2001
                                                                                                                                                                                       Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUE PROTEINS (BY SIMILARITY).

2. CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSING PYROPHOSPHATE + PROTEIN N-UBIQUITYLLYSING.

2. PATHWAY: SECOND STEP, IM UBIQUITIN CONJUGATION.

2. MISCELLANEOUS: A CYSTEIME RESIDUE 18 REQUIRED FOR UBITIOLESTER FORMATION (BY SIMILARITY).

2. SIMILARITY: BELONGS TO THE UBIQUITIN-COMJUGATING ENZINGLES A CASACSESS 1.
                                                                                                                        EMBL; AP002481; BAA96583.1; -. HSSP; P06104; IAYZ. InterPro; IPR000608; UBQ_conjugat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. NIPPONBARI
Sasaki T., Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridipiantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                 "Oryza sativa nipponbare(GA3) genomic clone:P0702F03.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_Tax1D-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harris D., Taylor K.;
Submitted (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRA1N-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces ACEI_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A set of ordered cosmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97000351; PubMed-8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
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OCT-2000 (Trembirel. 15, Last sequence update)
DEC-2001 (Trembirel. 19, Last annotation update
AU070209(R3722) CORRESPONDS TO A REGION OF TN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ROM N....
NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J., Barrell (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMIMARY;
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to the
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EMBL/GenBank/DDBJ
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                  5DE1FF4EEB75A86E CRC64;
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a; Poales; Poaceae;
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OF THE
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Best Local S
Matches 7
                                                 Q92VE9

Q92VE9;
Q92VE9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q2-PETICAL PROTEIN SMB21253.
NSMB21253.
NSMB21253.
Rh1zobium meliloti (Sinorhizobium meliloti).
Q2-PETICAL PROTEIN SMB21253.
Rh1zobium meliloti (Sinorhizobium meliloti).
Q3-PETICAL PROTEIN SMB21253.
Rh1zobium meliloti (Sinorhizobium meliloti).
Q4-PETICAL PROTEIN SMB21253.
Rh1zobiaceae; Sinorhizobium.
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Best Local
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Seeger K.J., F
Submitted (JU)
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09K3Q7;
01-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A set of ordered cosmids and a detailed the 8 Mb Streptomyces coeilcolor A3(2) ch Moi. Microbiol. 21:77-96(1996).
EMBL; AL360034; CAB95978.1; ...
InterPro; IPRO00182; Acetyltransf_GCN5.
Priom: PF00583; Acetyltransf; 1.
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STRAIN-A3(2);
Cerdeno A.M., Parkhill
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrei. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase.
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Kinashi H., Hopwood D.A.;
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Redenbach M., Kieser H.M., Denapaite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 58.: 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%;
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EMBL/GenBank/DDBJ databases.
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2: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
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Pred. No. 15;
0; Mismatches
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Last sequence update)
Last annotation updat
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01-JUL-1997
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"The complete sequence of the 1,683-kb psymb megaplasmid from the fixing endosymbiont Sinorhizobium mellioti.";

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).

EMBL; ALGO3644; CRC49157.1; -
Plasmid: Hypothetical protein; Complete proteome.

SEQUENCE 256 AA; 28459 MW; 54B054834CEC7C39 CRC64;
  Aspergillus niger var. awamorii.
Eukaryota; Fungi; Ascomycota; Pe
Eurotiales; Trichocomaceae; mito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuhi C., Yamada M., Tabata S.; Nakazaki N., Shimpo S., Sugimoto M. "Complete genome structure of the nitrogen-fixing accommendation of the nitrogen-fixing accommendation of the nitrogen-fixing accommendation of the nitrogen-fixing accommendation of the nitrogen fixing accommendation of the nitrog
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STRAIN-1021;
MEDLINE-21396508; PubMed-11481431;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation updatance transfer, SUBSTRATE BINDING PROTEIN.
                                                                                      TRANSPOSASE.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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60.0%;
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Pred.
Pezizomycotina; Eurotiomycetes;
itosporic Trichocomaceae; Aspergillus.
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Matches 7
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01-JUN-2001
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STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed-11259647;
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Interpro; IPR001878; Enf_CCHC.
SMART; SM00343; Enf_CCHC; 1.
SEQUENCE 555 AA; 62978 MW;
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Nyyssonen E., Amutan M., Enfield L., Stubbs J., Dunn-Coleman N.S.
"The transposable element Tani of Aspergillus niger var. awamori,
new member of the Fotl family.";
Mol. Gen. Genet. 253:50-56(1996).
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Amutan M., Nyyssonen E., Stubbs J.,
"Identification and cloning of a mo
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STRAIN-UVX143F DERIVED FROM NRRL3112: TRANSPOSON-VADER;
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154
                                            1 AWYXXRGIRPVGRF
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A Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barraco M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R. S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraco D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., Ei-Dorry H., Refincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Ferroga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Rraga J.S., Franca S.C., Franco M.C., Frohme M. Furlan J.P., R. Kraga J.S., Jooldman M.H.S., Gomes S.L., Kitajina J.P., R. Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., R. Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., R. Krieger G.G.M., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
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01-NOV-1999 (
01-MAR-2001 (
HYPOTNETICAL
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Kawarabayasi Y., Nino Y., Horikawa H., Yamazaki S., Halkaw,
Jin-no X., Takahashi M., Sakine M., Baba S.-I., Ankai A., I
Hosoyama A., Fukui S., Nagai Y., Nishijama K., Nakazawa H.
Takaniya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
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01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation updat
HYDROXYBENZOATE OCTAPRENYLTRANSFERRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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DNA Res. 6:83-101(1999).
EMBL; AP000060; BAA79576.1; -.
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7; Conservative
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
L 26.1 KDA PROTEIN APEO606.
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Pred. No. 31;
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de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,

A Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,

duaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,

de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Jr.,

da Silva A.C.R., da Silvestri H.L.Z., Siqueira M.J. de Souza A.A.,

da Silveira J.F., Silvestri H.L.Z., Siqueira M.J. de Souza A.A.,

da Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

van Vallada N., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,

A Zago M.A., Zatz M., Meidanis J., Setubal J.C.,

"The genoma aequence of the plant pathogen Xylella fastidiosa.",

RT "The genoma eaquence of the plant pathogen Xylella fastidiosa.",

DR EMBL; AED03860; AAR828811; -.

DR Pfam; PP01040; UDIA, 1.

DR PROSITE; PS00943; UBIA, 1.

DR PROSITE; PS00943; UBIA, 1.

DR PROSITE; PS00943; UBIA, UNKNOWN_1.
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Q9RR92;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
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                                                                                                                          InterPro; IPRO00890; Acetate_kin.
Pfam; PF00871; Acetate_kinase; 1.
PfINTS; PR00471; ACETATEKNASE.
PROS1TE; PS01076; ACETATE_KINASE_2; UNKNOWN_1.
KInase; Complete proteome.
KInase; Complete proteome.
SEQUENCE 398 AA; 41798 MW; 79EB59FE97A15FC
                                                                                                                                                                                                                     radiodurans Rl.";
Science 286:1571-1577(1999).
EMBL; AE002089; ARF12139.1; -.
TIGR; DR2602; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermus/Deinococcus
NCBI_TexID=1299;
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Moon D.H., Nac
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Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
r., Nobrega E.G., Nunes L.R., Oliveira M.A.,
a M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
                                              Conservative
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Q95YN4;
Q1-DEC-2001 (TrEMBLrel. 19, C
Q1-DEC-2001 (TrEMBLrel. 19, L
Q1-DEC-2001 (TrEMBLrel. 19, L
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STRAIN-YAK.30;
Duvernell D.D., Schmidt P.S., Eanes W.F.;
Duvernell D.D., Schmidt P.S., Eanes W.F.;
*Molecular population genetics of a methuselah
*Molecular population to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                   STRAIN-ZIM(S)24;
DUVERTNEII D.D., Schmidt P.S., Eanes W.F.;
DUVERTNEII D.D., Schmidt P.S., Eanes W.F.;
MOIECULAR population genetics of a methuselah
submitted (AUG-2000) to the EMBL/GenBank/DDBJ d
EMBL; AF300396; AAK97885.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Search completed: September 13, 2002, 09:29:21 Job time:  $1066\ \text{sec}$ 

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

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Human type G prote
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## ALIGNMENTS

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AAY49293 standard; peptide;

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    Hew monoclonal antibodies,
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useful in diagnosis, as drugs and
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Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.

19P2 ligand peptide fragment. 22-FEB-2000 (first entry)

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Matches 11
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1922 ilgand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitury function regulatory mechanism (e.g. promotion of projectin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosassay can also be applied in ciarlifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
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                                                                                                                                     Disclosure; Page 27; 73pp; Japanese
                                                                                                                                                                 New monocional antibodies, studying diseases related (
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regulatory mechanism; central nervous system; pancreat
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RESULT
AAW31394
    This sequence represents a peptide fragment from a novel human type colligand polypeptide corresponding to amino acid residues 34 to 53 of the consequence represented in AAW31390 and is used in an assay to monitor cliqued binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function compositions containing this ligand may be used as a pituitary function composition containing this ligand may be used as a pituitary function composition containing this ligand may be used as a pituitary function condulator. This sigand could have specific applications as a comphylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, contrama, growth hormone secretory disease, hyper-and polyphagia, contrama, growth hormone secretory disease, hyper-and polyphagia, contrama, diabetes, cancer, pancreatitits, renal disease, curvanta, hyperpolactinaemia, diabetes, cancer, pancreatitits, spinal injury, contransient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, content myocardial infarction, infertility, spinocerebeilar degeneration, confident brain ischaemia, epilepsy, amylotrophic lateral sclerosis, and content pratial assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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Best Local
                                                                                                                                                                                              This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the 6 protein-coupled receptor protein. It is useful in the form of drugs for amellorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, iterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; oxytocin secretion promoter; G protein-coupled receptor protein treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat; pig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human oxytocin secretion promoting
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Best Local S
Matches 11
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Human; corticotrophin releasing hormone; CRH; G protein receptor ligand analgesic; hyperaldosteronism; hypercortisoiaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                               Human
                                                                                                                                        24-AUG-2001
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                                                                                          CRH releasing
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Best Local :
         17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadronocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                      Protection; endogenous therapeutic peptide; peptidese; conjugation; blood component; modification; succinimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence describes a method of controlling the secretion conticotrophin releasing hormone (CRH), involving the use of a G prote receptor ligand. This can be used to control the secretion of CRH and
                                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                        AAB90992 standard;
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                                                      17-MAY-2000; 2000WO-US13576
                                                                            23-NOV-2000
                                                                                                   WO200069900-A2
                                                                                                                                                                                                   Prolactin releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE )
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26-SEP-2000; 2000JP-0297073.
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8 wyasrgirpvgrf
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         99US-0134406.
99US-0153406.
99US-0159783.
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RESULT
AAW31395
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modulator: pituitary; central nervous system: pancreas; pro
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Fujii R, F
Kawamata Y.
                                                    (TAKE ) TAKEDA CHEM IND LTD
                                                                                                          28-DEC-1995;
15-MAR-1996;
                                                                                                                                                 18-SEP-1996;
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Fukusumi S,
Y, Kitada C;
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                                                                                                                                                                                                                                                                                                                                                    pituitary;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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84.68;
               Habata
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Pred. No. 9.26
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               Rosoya M;
                                                                                                                                                                                                                                                                                                                                                      pancreas; prophylactic;
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RESULT 1
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Best Local Similarity 84.0
Matches 11: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB10366 standard; peptide;
                          WPI: 2000-452298/39
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                                                                                                                                                                                                                                      Homo sapiens.
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                                                     Mataumoto H,
                                                                                     (TAKE ) TAKEDA CHEM 1ND
                                                                                                                   25-DEC-1998;
                                                                                                                                               22-DEC-1999;
                                                                                                                                                                                                                                                                  veterinary medicine; milk production.
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                           The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadremocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair
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                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                  Use of G protein receptor ligand or peptide corticotropin releasing hormone secretion -
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26-SEP-2000;
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2000JP-0297073
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Pred. No.
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   gland
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plgmentation, l
nd hypofunction
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9.7e-06;
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   hypogonadism,
n and obesity.
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                                                                ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesteroiaemia, hyperglyceridaemia, hypercholesteroiaemia, hyperglyceridaemia, figure, and polyphagia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperrolactias, spinal injury, transfent hasin tachaemia, antienay ambumatoid arthritis, spinal injury, transfent hasin tachaemia, antienay ambumatoid arthritis, spinal injury.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
transient brain ischaemla, epilepsy, amylotrophic lateral scierosis, acute myocardial infarction, infartillity, spinocerebeilar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which as capable of altering the binding activity of the ligand affecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor;
modulator; pituitary; centre
                                                                                                                                                                                                                                              This sequence represents a peptide fragment from a novel human
                                                                                                                                                                                                                                                                           Claim 2; Page 186;
                                                                                                                                                                                                                                                                                                       function
                                                                                                                                                                                                                                                                                                                      Ligand
                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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invention.
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                                                                                                                           258pp; English.
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Pred. No. 9.
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9.7e-06;
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              screen compounds which are
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                                                                                                              This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This
                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                               Human; oxytocin secretion promoter; G protein-coupled recept
treatment; disease; pain; atonic bleeding; uterine recovery
caesarean section; artificial fertilization; galactostasis;
                                                                                                                                                                                                                        Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for disesses relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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wymsrgirpvgrf 20
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nilarity 84.6%;
Conservative
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                                  Score 66; DB 21;
Pred. NO. 1e-05;
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                                                                                                        peptide which acts
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Pred. No. le-(
0; Mismatches
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ding; uterine recovery failure; co
zation; galactostasis; goat; pig;
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ie-05;
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                                                                                                       goat and pig. T
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AAG62536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysisc or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's hypercorticism, and the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of G prote corticotropin
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                                                                                 Human type G protein-coupled receptor llgand fragment
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26-SEP-2000;
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                                                                                                                                                                                                                                                                     standard;
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2000JP-0297073
                                                                                                                                                (first entry)
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adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                  Peptide;
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G protein-coupled receptor; ligand binding; modulator; pituitary; central nervous system

system; pancreas; prophylactic;

pharmaceutical;

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                                                                                  밁
                                                                                                                                                                                                                                                      This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupied receptor protein. Pharmscentical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC traums, growth hormone secretory disease, hyper-and polyphagia, CC hyperilpideemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinsemis, diabetcs, cancer, pancreatitis, renai disease, CC hyperprolactinsemis, diabetcs, cancer, pancreatitis, spinal injury, CC transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or capsble of sltering the binding sctivity of the ligand affecting CC activation of the C protein-coupled receptor protein.
                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ciaim 2; Page 184; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-363672/33.
N-PSDB; AAV02428.
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Kawamata Y, Kitads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-1996;
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                                                                                              1 WYXXRGIRPVGRF 13
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                                                                                                                                               Conservative
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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Pred. No. 1.5e-05;
0; Mismatches 2;
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Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match
  US-09-446-543A-73_COPY_8_21
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Gapop 10.0 ,
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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US-09-105-678A-46
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US-09-421-208-43
US-09-421-208-43
US-09-421-208-44
US-08-776-971-63
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2.503 Million cell updates/s
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        sequence
 Sequence
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        46, Appl
46, Appl
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51, Appl
43, Appl
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44, Appl
45, Appl
46, Appl
47, Appl
48, Appl
49, Appl
40, Appl
App1
                                                       ; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-46
         Query Match
Best Local S
Matches 11
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11;

Conservative

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Similarity

95.78; 84.6%;

Score 66; DB Pred. No. 2.7e 0; Mlsmatches

DB 3; 2.7e-06; 2;

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US-08-776-971-64
                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: US-08-776-971-64
                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ 1D NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application Patent No. 6228984
GENERAL INFORMATION:
                                                                                                    Query Match
Best Local :
                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 6/59419

FILING DATE: 15-MRR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusuml, Shoji
  В
                                      1 WYXXRGIRPVGRF 13
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukusum1, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal
WYASRGIRPYGRF 20
                                                                                                 Simliarity
                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Conlin, David (
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08776971B
                                                                                   Conservative
                                                                                                 95.7%;
                                                                                                                                                                                                        SEQ ID NO:
                                                                            0; · Mismatches
                                                                          Score 66; DB 4; Length 20; Pred. No. 2.7e-06; O; Mismatches 2; Indels
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-46
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US-09-421-208-46
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Matches
                                                                                                                                                                                              Sequence 47
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONlin, David G.
REGISTRATION NUMBER: 27,02
                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-523-6440
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                               tent No.
                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #I.0, Version #1.30
CURRENT APPLICATION DATA:
                        NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 W
CITY: Boston
STATE: MA
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/421,208 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UP 21P: 02109
                                                                                                                                                                                                                                                                                                                                             Local Similarity 84.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                               ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                            1 WYXXRG1RPVGRF 13
                                                                                                                                                                                                                                                                               WYASRG1RPVGRF 20
                                                                                                                                                                             7, Application US/09105678A
6103882
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        130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                              95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 09/105,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP 172118/1997
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                                                                                                                                                                                                                                                                                                                                             Score 66; DB
Pred. No. 2.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        DB ...
2.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 APTORNEY/AGENT INFORMATION:
NAME: COLLE DATA:
DAME: JP 172118/1997 ATTORNEY/AGENT INFORMATION:
NAME: COLLE DATA:
DAME: JP 172118/1997 APPLICATION:
NAME: JP 172118/
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 21 amino acids
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REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                           COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTMARE: FESACSED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nabata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
TiTLE OF INVENTION: POLYPROTEINS, TNEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
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11 Similarity 84.6%;
11; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 130 Water Street
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Pred. No. 2.8e-06;
0; Mismatches 2
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RESULT 6
US-09-421-208-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47,
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Best Local Similarity
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1in, DAVId G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CNARACTERISTICS:
                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      STATE: MA
COUNTRY: US
ZIP: 02109
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FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
PILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, DAVIDER STREET: 130 Water Street
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TYPE: amino acid
STRANDEDNESS: single
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84.6%;
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2.8e-06;
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SOFTWARE: PACHATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING OATE: 26-7UN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING LOATE: 27-7UN-1997
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-7UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAV1d G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECHONE: 617-523-3400
INFORMATION: FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH 22 Amino acids
TYLET 22 Amino acids
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-47
                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-48
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US-09-105-678A-48
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GENERAL INFORMATION:
                                                              Matches
                                                                         Query Match
Best Local (
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ENERGY 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suchaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                           WYXXRGIRPVGRF 13
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WYASRGIRPVGRF 20
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                                                                           Similarity
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                                                           Conservative
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84.68;
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                                                                         95.7%;
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                                                                         Score 66;
Pred. No.
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Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROBERTS & CUSHMAN, LLP
                                                         ore 66; DB 3; L
ed. No. 2.9e-06;
Mismatches 2;
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                                                                                        Length 22;
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                                                           Indels
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                                                           Gaps
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US-08-776-971-66

Sequence 66, Application US/08776971B

; Patent NO. 6228984

; GENERAL INFORMATION:
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MOLECULE TYPE: protein
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FRAGMENT TYPE: internal
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
                                                                   Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                               TELEPHONE: 617-523-6440
INFORMATION FOR SEQUENCE CHARACTORS

TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 66:
8
                                 1 WYXXRGIRPVGRF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBR: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUKUSUMI, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADORESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinuma,
WYASRGIRPYCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-KAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                      Similarity
                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                   LENGTH: 22 amino acids
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Habata, Yugo
Kawamata, Yuji
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                                                                                    95.7%;
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                                                                   0;
                                                                  Score 66; DB 4;
Pred. No. 2.9e-06;
0; Mismatches 2
                                                                                                                                                                            66:
                                                                                                   Length 22;
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                                                                  Gaps
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RESULT 9 US-09-421-208-48

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RESULT 10
US-09-105-678A-9
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                                                                                                                                                                                                                                       Sequence 9, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.7%;
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COD110, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                            APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 617-523-6440
                                             STREET: 130 W
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, brown---
connect: 130 Water Street
ZIP: 02109
                              STATE: MA
                                                               ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                  Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 4;
Pred. No. 2.9e-06;
0; Mismatches 2
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Best Local S
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
RUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CNARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || ||||||||
19 WYASRGIRPVGRE
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ZIP: 02109
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               DDRESSEE:
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                                                                          Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                          130 Water Street
                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 31;
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43:

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; TOPOLOGY: iinear
; MOLECULE TYPE: peptide
US-09-105-678A-43
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local S
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                                                      TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ IO NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  APPLICATION NUMBER: PCT/JP96/03821
FILING OATE: 28-OEC-1996
APPLICATION NUMBER: JP 7/343371
FILING OATE: 28-OEC-1995
APPLICATION NUMBER: JP 8/59419
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/211805
FILING OATE: 12-NAG-1996
APPLICATION NUMBER: JP 8/21805
FILING OATE: 12-NG-1996
APPLICATION NUMBER: JP 8/246573
APPLICATION NUMBER: JP 8/246573
FILING OATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 WYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING OATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUKUSUMI, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                    REFERENCE/DOCKET NUMBER: 47176 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADORESS:
NOORESSEE: OIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
TYPE: amino acid
STRANOEONESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 Water Street
                                        LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08776971B
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Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
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; FRACMENT TYPE: Internal
; SEQUENCE OESCRIPTION: SEQ ID NO: 61:
US-08-776-971-61
                                                                                                                                 ; MOLECULE TYPE: US-09-42I-208-9
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                                                                        Query Natch
Best Local (
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ IO NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING OATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, OAVID G.
NAME: CONLIN, OAVID G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CONPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NETHOD OF PROOUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADORESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION OATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 m
                                                                                                                                                              STRANDEONESS:
TOPOLOGY: linear
19 WYASRGIRPVGRF 31
                                                                      Local
                                                                                                                                                                                                                                                                                                             NAME: Conlin, Cavid G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING OATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                           I WYXXRGIRPVGRF 13
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6258561
                                                                      Similarity
                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 Water Street
                                                                                                                                                                                                           31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moriya, Takeo
Tanaka, Yoko
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                               peptide
                                                                      95.7%;
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84.6%;
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                                                     Score 66; OB 4; L
Pred. No. 4.3e-06;
0; Nismatches 2;
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Pred. No. 4.3e-06;
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                                                                                    Length 31;
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                                                        Indels
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                                                       Gaps
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RESULT

US-09-421-208-43

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RESULT 15
US-09-105-678A-44
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; TOPOLOGY: 11near
; MOLECULE TYPE: peptide
US-09-421-208-43
                                                                                                                                                                                                                                  Sequence 44, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.7
Best Local Similarity 84.6
Matches 11: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN. DAVIG G.

REGISTRATION NUMBER: 27.026

REGISTRATION NUMBER: 27.026

REGISTRATION NUMBER: 48466-342

TELECOMNUNICATION INFORMATION:

TELEPHONE: 617-523-6440

TELEPAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIN: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Ma
APPLICANT: MOOIlya, Tak
APPLICANT: Tanaka, Yok
APPLICANT: Nishimura,
APPLICANT: Nishimura,
TITLE OF INVENTION: ME
NUMBER DF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
COMPUTER: IBM PC com
                                                                                                                        APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING
NDMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patchtin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                CITY: Boston
                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                      19 WYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 02109
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STREET: 130 Water Street
               COUNTRY:
                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                        I WYXXRGIRPVGRF 13
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ASD
WA
                                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN. LLP I30 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 amino acids
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Morlya, Takeo
Tanaka, Yoko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/421,208
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                                                                                                                                          A 19P2 LIGAND
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 44
SEQBENCE CHARACTERISTICS:
FRIGHT: 32 amino acids
                                                                                                                                                    Query Match
Best Local Similarity
Matches II; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 172118
ETLING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #I.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105.678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                         19
                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                           WYXXRGIRPVGRF 13
                                                                                         WYASRGIRPVGRF
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                         31
                                                                                                                                                                       95.7%;
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                                                                                                                                                      Score 66; DB 3;
Pred. No. 4.4e-06;
0; Mismatches 2
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                                                                                                                                                      0;
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perfect score:
sequence:
Total number of hlts satisfying chosen parametera:
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                                     Searched:
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69
                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                               September 13, 2002, 09:24:01; Search time 172.41 Seconds (without alignments) 7.803 Million cell updates/sec
                                   283138 seqs, 96089334 residues
                                                                                                                               1 WYXXRGIRPVGRFX 14
                                                                                                                                                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
   283138
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Minlmum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summarles

Database : P1R\_71:\*
1: p1r1:\*
2: p1r2:\*
3: p1r3:\*
4: p1r4:\*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s dcrlved by analysis of the total score distribution.

## SUMMARIES

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	2	31	30	
35	<u>ა</u>	35	35	35	ន	<b>3</b> 5	<u>ა</u>	35	<u>3</u> 5	<u>ა</u>	<b>3</b> 5	35	ü	<u>ა</u>	35	
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N	N	N	N	N	N	ພ	N	H	N	N	N	N	N	N	N	
B82557	E82221	S06446	A84562	T45447	B70821	D84396	S18597	XXGZAC	A97751	D71686	T39533	T44866	D97897	D95026	G72674	
hypothetlcal prote	DNA gyraae, chaln	citrolysin-related	probable integral	probable two-compo	hypothetical prote	slgnal recognition	tubulin beta chain	acety1-CoA C-acety	hypothetical prote	hypothetical prote	hypothet1cal prote	hypothet1cal prote	50S rlbosomal prot	rlbosomal protein	hypothetical prote	

## ALIGNMENTS

RESULT 2 \$61046 ARP1 protein - yeast (Saccharomyces cerevislae) ARP1 protein - yeast (Saccharomyces cerevislae) N:Alternate names: protein D1478; protein YDL167c C:Specles: Saccharomyces cerevision 01-Mar-1996 #text_change 29-Oct-1999 C:Acceasion: \$61046: \$31139; \$67719 R:Pohl, T.M. aubmitted to the EMBL Data Library, November 1995 A;Reference number: \$61010 A;Acceasion: \$61046 A;Molecule type: DNA A;Residuems: 1-719 + COHI> A;Cross-referencem: EMBL:267750: NID:g1061256; PIDN:CAA91579.1; PID:g1061272 A;Title: Molecular atructure and genetic regulation of SFA, a gene responsible for re A:Reference number: \$31138; MDID:93247548 A:Accession: \$31138; MDID:93247548 A:Molecule type: DNA A;Molecule type: DNA	Query Match  94.2%; Score 65; DB 2: Length 83;  Best Local Similarity 84.6%; Pred. No. 4.3e-05:  Matches 11; Conservative 0: Mismatches 2: Indels 0; Gaps 0;  Qy 1 WYXXRGIRPVGRF 13	RESDLT 1  JC7607  JC7607  prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30.Jun-2001 #sequence_revision 30.Jun-2001 #text_change 30.Jun-2001 C:Accesaion: JC7607 R:Yamada, M: Ozawa, A: 1shli, S: Shlbusawa, N.; Haahida, T.; Ishlzuka, T.: Hoaoya, R:Yamada, M: Ozawa, A: 1shli, S: Shlbusawa, N.; Haahida, T.; Ishlzuka, T.: Hoaoya, R:Yamada, M: Ozawa, A: 1shli, S: Shlbusawa, N.; Haahida, T.; Ishlzuka, T.: Hoaoya, R:Yamada, M: Ozawa, A: 1shli, S: Shlbusawa, N.; Haahida, T.: Hoaoya, R:Yamada, M: Ozawa, A: Commun. 281, S3-56, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959 A:Contenta: Spleen A:Accession: JC7607 A:Molecule type: DNA A;Residues: 1-83 <yam> A;Residues: 1-83 <yam> A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C:Comment: This peptide induces arachidonic acid metabolite release from rat antcrior release, and stimulation of ACTH secretion from the pitultary. C;Genetica: A;Introna: 33/1</yam></yam>

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PICC. Natl. Acad. Sci. U.S.A. 98, 9889-9994, 2001

A:Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing end. A:Reference number: A95842; MUID:21396508; PNID:11481431

A:Accession: E95936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL591985; PIDN:CAC49157.1; PID:g15140642; GSPDB:GN001
A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallbert, F:, Finan, T.N.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F:; Ba:
peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; F
L:, Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.N.; Kiss, E.; Komp, A;Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.N.; Kiss, E.; Komp, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number; A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein [imported] - Sinorhizobium mellloti (strain 1021) magaplasmid C;Speckes: Sinorhizobium mellloti
C;Date: Sinorhizobium melltoti
C;Date: Sinorhizobium mellloti
C;Date: Sinorhizobium melllo
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A; Reference number: S67708
A; Accession: S67719
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A;Cross-references: EMBL:X68020; NID:g577609;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: SMb21253
A;Genome: plasmi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Moiccule type: DNA
A; Residues: 1-719 <PDW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the nucleotide sequence was R;Pohi, T.M.
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-256 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A: Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gcne: SGD:NRP1; ARP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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6; Conserv
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6; Conservative
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Pred. No. 7.8;
2; Mismatches
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Pred. No.
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Wong, K.; Yeh, K
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N.A.; Fisher, R.F.
                                              N.; Fuji,
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                                                  Hira
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A;Experimental source: strain 9a5c
R;Simpson, A,J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, N.; Alvarenga, R.
Briones, M.R.S.; Beeno, N.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, N.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.N.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martino
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Mijaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Dliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sancelli, R.V.; Sawa
A;Authors: da Sliva, A.C.R.; da Sliva, F.R.; da Sliva, A.M.; Sliva Jr., W.A.; da Sliva
A;Authors: da Sliva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sancelli, R.V.; Sawa
A;Authors: da Sliva, A.J. da Sliva, F.R.; da Sliva, A.M.; Sliva Jr., W.A.; da Sliva
A;Authors: da Sliva, A.J. da Sliva, F.R.; da Sliva, A.M.; Sliva Jr., W.A.; da Sliva
A;Reference number: A59328
A35548
319K protein ndvB - Rhizobium meiiloti
C;Species: Rhizobium meliloti
C;Date: 21-Sep-1990 #sequence_revision
C;Accession: A35548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000 (;Accession: H82852 R;anonymous, The Xyleila fastidiosa Consortium of the Organization for Nucleature 406, 151-157, 2000 R;anonymous, The Xyleila fastidiosa Consortium of the Organization for Nucleature 406, 151-157, 2000 R;anonymous R; The genome sequence of the plant pathogen Xyleila fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: NB2852
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A;Molecule type: DNA
A;Residues: 1-485 <STD>
A;Cross-references: GB:AP001507; GB:BA0000004; NID:g10172612; PIDN:BAB03828.1;
A;Cross-references: Strain C-125
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C;Superfamily: 4-hydroxybenzoate octaprenyltransferasc
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A;Cross-references: GB;AE003860; GB;AE003849; NID:g9104830;
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A;Gene: gltx
C;Superfamily: glutamate--tRNA ligase, glutamine--tRNA
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Matches 7; Conserv
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Pred. No. 19;
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S.E

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A;Molecule type: DNA
A;Residues: 1-2870 <IEL>
A;Cross-references: GB:J05219; N1D:g152270; PIDN:AAA26305.1; PID:g152271
C;Keywords: transmembrane protein
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A;Title: The ndvB locus of Rhizoblum melliotl encodes a 319-kDa A;Refercnce number: A35548; MUID:90153914
A;Accession: A35548
                                                                             R:Dunn, J.J.; Studier, F.W.
J. Mol. B101. 148, 303-330, 1981
A;Tille: Nucleotide sequence from the genetic left end A;Reference number: A92866; MUID:82078034
A;Accession: C92866
                                                                                                                                                                                                                                                                           C;Species: phage T7
C;Date: 01-Sep-1981 #sequence_revision 24-Sep-1981
C;Accession: B94615; C92866; S42301; A00785
R;Dunn, J.J.; Thompson, K.
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C;Supcrfam1ly:
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C;Species: Yersinia pestis
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
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                                       A; Molecule type: DNA
A; Residues: 1-149 <DU2>
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A; Residues: 1-149 <DU1>
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                      Cross-references:
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8; Conserv
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5; Conserv
ences: GB:V01127; NID:915498;
Studier, F.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical
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                                                                                                                                                                                                                                                              Sequence Database, September 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAC90980.1;
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Pred. No. 1.7e
2; Mismatches
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Pred. No. 12;
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1.7e+02;
3;
                    PIDN:CAA24345.1;
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                                                                                                                                                                                                                                                                                                                         #text_change 11-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 154;
                                                                                                                     of bacterlophage T7
                  PID: g15517
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A;Cross-references: GB:AL591985; PIDN:CAC48476.1; PID:915139948; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
A;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R. L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.N.; Wong, K.; Yeh, A;Title: The composite genome of the legume symblont Sinorhizoblum mediloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; He Proc. Natl. Acad. Sci. U.S.A. 91, 9889-9894, 2801
A;Title: The complete sequence of the 1,683-kb psymB megapiasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95851
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change
C;Accession: D95851
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A;Tittle: Complete nucleotide sequence of bacteriophage T7 DNA and the locations A;Reference number: S42283; MUID:83241725
A;Accession: S42301
A;Molecule type: DNA
A;Residues: 1-149 < DNA
A;Residues: 1-149 < DNA
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C; Superfamily: phage T7 exor
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A;Note: the authors did not translate the codon for residue 1
C;Comment: Endodeoxyribonuclease I, which is expressed in the late stage, is necessar a linear monomer. In the late stage, the T7 DNA replicates via linear concatemers s
                                                                                                                                                                                                                                      A; Genome: plasmid
                                                                                                                                                                                                                                                                 A; Gene: SMb 20076
                                                                                                                                                                                                                                                                                                                  A; Contents: annotation
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A; Residues: 1-338 <KUR>
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Best Local :
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Best Local
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87
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6; Conser
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7; Conservative
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46.2%;
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58.38;
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Pred. No. 32;
2; Mismatches
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conserved hypothetical membrane protein SMb20863 [imported] - Sinorhizoblum C;Species: Sinorhizoblum meliloti C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001 C;Accession: E95986

C;Accession: R;Flnan, T.M.

T.M.; Weldner,

S

Wong, A. 98,

K.; Buhrmester, 9889-9894, 2001

J

Chain,

P.; Vorholter,

F.J.;

Sinorhizobium

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A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Recession: E9586
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-343 <KUR>
A:Residues: 1-343 <KUR>
A:Residues: 1-343 <KUR>
A:Residues: 1-373 <KUR
A:Residues: 1-373   KUR

                                                                                                                                  beta-glucosidase (EC 3.2.1.21) oleR [validated] - Streptomyces antibioticus (ATCC 11891) (Species: Streptomyces antibioticus A; Variety: ATCC 11891 (C; Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 (C; ACCESSION: T51112 R; Quirrezabalaga, I.; Dlano, C.; Mendez, C.; Salas, J.A. submitted to the EMBL Data Library, September 1999 A; Reference number: 225300 A; Accession: T51112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable oxidase - Streptomyces coelicolor
[;Species: Streptomyces coelicolor
[;Species: Streptomyces coelicolor
[;C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
[;Accession: T34570
[;Accession: T3
         A;Status: prcliminary; translated A;Molecule type: DNA A;Residues: 1-769 <QUI>
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C; Genetics:
A; Gene: SCDEDB: SC10A5.02
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A;MOlecule type: DNA
A;Residues: 1-395 <MUR>
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A;Gene: SMb20863
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Best Local
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A;Cross-references: EMBL:AF055579; PIDN:AAC12650.1
A;Experimental source: ATCC 11891
C;Genetics:
A;Gene: oler
C;Function:
A;Cross-references: EMBL:X78470
C;Superfamily: acetate--CoA ligase homology; acyl carrier pro
C;Keywords: carrier protein
F;1-102/Domain: acetate--CoA ligase homology (fragment) <ACl>
F;119-142/Domain: acyl carrier protein homology (fragment)
                                                                                                                    A;Status: preliminary; nucleic acid sequence A;Molecule type: DNA A;Residues: 1-142 <TUR>
                                                                                                                                                                                                                                                                                                   bacitracin synthetase - Bacilius licheniformis (fragment) C;Species: Bacilius licheniformis C;Date: 27-Apr-1996 #sequence_revision l3-Mar-1997 #text_change C;Date: 25-Apr-1996 #sequence_revision l3-Mar-1997 #text_change C;Accession: S60747
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Tille: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630
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C;Keywords: glycosidase;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:30:47 : Search time 80.21 Seconds (without alignments) 6.758 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_8\_21

1 WYXXRG1RPVGRFX 14

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues 105224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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# ALIGNMENTS

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EMBL; AB015419; BAA29027.1;  MIN: 602663;  HORMONE; Amidation; Signal.  SIGNAL 1 22  PEPTIDE 23 53  PROLACTIN RELEASING PEPTIDE PRRP31.  PEPTIDE 34 53  MOD_RES 53 53  MOD_RES 53 53  AMIDATION (G-54 PROVIDE AMIDE GROUP).  SEQUENCE 87 AA; 9639 MW; 229A2F3F50CF981B CRC64:	ichi M., Kitada C., Kurokawa T., Nishimura O., Onda H., or., Fujino M.; pe distribution of prolactin-releasing peptide (PrRP) and i or." Pept. 83:1-10(1999). INCTION: Stimulates prolactin (PRL) release and regulates t pression of prolactin through its receptor GPR10. May stim ictotrophs directly to secrete PRL. ISSUE SPECIFICITY: MEDULIA OBLONGATA AND HYPOTHALAMUS. ISSUE SPECIFICITY: MEDULIA O	ubMed=9607765; ., Fujii R., Kawamata Y., Hogoya M., Asano T., Matsumoto H., Sekiguch ura O., Onda H., Fujino M.; ing peptide in the brain."; 1998).	RESULT 1  PRRP_HUMAN STANDARD; PRT: 87 AA.  AC P81277:  DI 30-MAY-2000 (Rel. 39, Created)  DI 30-MAY-2000 (Rel. 39, Last sequence update)  DI 30-MAY-2020 (Rel. 41, Last annotation update)  DI 01-MAR-2022 (Rel. 41, Last annotation update)  DE Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing  DE hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-  DE releasing peptide PrRP20].  GN Homo saplens (Human).  OS Homo saplens (Human).  OS Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;  OC Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;

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                                                                                                                                                                                                                                                                                                                                                                                                                   Fujii R., Fukusumi S., Hosoya M., Kawamata )
Sekiguchi M., Kitada C., Kurokawa T., Nishin
Sumino Y., Fujino M.;
"Tissue distribution of prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=98268781; PubMed=9607765; Hinuma S., Habata Y., Fujii R., Kawamata Y., Ho Kitada C., Masuo Y., Asano T., Matsumoto H., Se Kitada C., Masuo Y., Asano T., Matsumoto M., Fujino M., Kurokawa T., Nishimura O., Dnda H., Fujino M., "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31, Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRRP_RAT
P81278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
T1SSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammaiia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (
Eukaryota; Metazoa;
                                                                                                                                                                       SIGNAL
                                                                                                                                                                                               EMBL; AB015418; BAA29026.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10498338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_Tax1D=10116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              releasing peptide
6
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                                                                                                                                                                                                                                                                                                                expression of prolactin through its receptor GPRIO. May stimula lactotrophs directly to secrete PRI. TISSUE SPECIFICITY: Widely cxpressed, with highest levels in medulia oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                II. Pept. 83:1-10(1999).
FUNCTION: Stimulates prolactin
WYTGRGIRPVGRF
                        WYXXRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WYASRGIRPVGRE
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                                                                                                                                                                                   Amidation;
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Da; Chordata:
La; Rodentia;
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                                                                                                             signal;
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9215 MW;
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                                                             94.2%;
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BY SIMILARITY.
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                                                             Score 65;
Pred. No.
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Pred.
                                                                                                                                          PRDLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                DOC75A264EEE4F29 CRC64;
                                                                                                                            AMIDATION (G-53 PROVIDE AMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteieostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             T., Nishimura O., Dnda
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3e-06;
                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                      peptide (PrRP) and
                                                                                                                                                                                 of basic
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Sekiguchi M.
                                                                          Length 83
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                                                                                                                                                                                 residues
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RESULT 3
PRRP_BOLT
ID PRRP_B AC
P81264
DT 30-MAY
DR BOS ta
BOS ta
BOS ta
CO HOUSE
TISSUE
RN HIJUMA
RA KITAGA
RA KITA
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NRP1_YEAST
ID NRP1_YEAST
GAFFFFF GROOCKARA
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Best Local S
Matches 11
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing Prolactin-releasing peptide PrRP31; Prolactin-releasing Prolactin
                                                                                                                                                 P32770; Q12228;
Q1-0CT-1993 (Rel. 27, Created)
Q1-0CT-1993 (Rel. 27, Created)
Q1-NDV-1997 (Rel. 35, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Asparagine-rich protein (ARP protein).
Asparagine-rich protein (ARP protein).
NRP1 DR ARP1 DR ARP DR YDL167C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycettes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOTMONE,
SIGNAL
PEPTIDE
PEPTIDE
MDD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PRDT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hinuma S., Habata Y., Fujii R., Kawamata Y., H
Kitada C., Masuo Y., Asano T., Matsumoto H.,
Kurokawa T., Nishimura O., Onda H., Fujino M.,
"A projactin-releasing peptide in the brain.",
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPR10. Maj lactotrophs directly to secrete PRL.
-i- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                         Saccharomycetales,
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Co
Bovidae; Bovinae; Bos.
                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98268781; PubMed=9607765;
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22
PROLACTIN-RE
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PROLACTIN-RE
53
AMIDATION (G
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                                                                                                                                   Saccharomycetaceae;
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PROLACTIN-RELEASING PEPTIDE PI
AMIDATION (G-54 PROVIDE AMIDE
08AC35A1380FA908 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE PRRP31.
PEPTIDE PRRP20.
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RESULT SE BAC OF DE CONTROL OF CO
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Best Local
Matches
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InterPro: IPR001876; Znf-RanBP.
InterPro: IPR001876; Znf-RanBP.
Pfam; PF00076; rrm; 1.
Pfam; PF00641; zf-RanBP: 2.
SMART: SM00360; RRM; 1.
SMART: SM00547; ZnF_RBZ: 2.
SMART: SM00547; ZnF_RBZ: 2.
PROSITE; PS00100; RRM; 1.
PROSITE; PS00100; RRM; RNP_1; FALSE_NEG.
PROSITE; PS01358: ZF_RANBP2_1; 2.
PROSITE; PS01358: ZF_RANBP2_2; 2.
                                                                                                GLTX OR BN0109.

Bsctlius halodurans.

Bscteria, Firmicutes, Bsc

Bscillus/Stsphylococcus 9.

NCBI_TaxID=86665,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYE_BACHD
                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Giutamyi-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZN_FING
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Wehner E.P., Rso E., Brendel M.;
"Molecular structure and genetic regulation of SFA, a gene
"molecular structure to formaldehyde in Saccharomyces
responsible for resistance to formaldehyde in Saccharomyces
cerevisiae, and characterization of its protein product.";
moi. Gen. Genet. 237:351-358(1993).
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EMBL; Z67750; CAA91579.1;
EMBL; Z74215; CAA98741.1;
PIR; S31139; S31139.
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       SEQUENCE FROM N.A. STRAIN-C-125 / JCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P04170: 6RXN.
SGD; S0002326; NRP1.
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                                                                                                                                                                                                                                                                                              (GluRS).
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6: Conserv
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384
510
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                                                                                                                                             Bscilius/Clostridium us group: Bacillus.
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Pred. No. 1.5:
2: Mismatches
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I -> N (I
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RNA-BINDING (F
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ADA9BC09FD582669
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MBL outstation -
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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EXL1_HUMAN
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Best Local S
Matches 7
                                                                                                                                                       SEQUENCE FROM 1
Xu L., Deng H.:
"Mutations of "
                                                                                                                                                                                                                                                                          WEDLINE-97189339; PubMed-9037597; Wise C.A., Clines G.A., Massa N., Trask B.J., "Itask B.J., "It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AXOSLOL.

EXTL1 OR EXTL.

Homo sapiens (Human).

Homosapiens (Homan).

Homosapiens (Homan).

Homosapiens (Homan).
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SEQUENCE
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SITE
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-!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) - AMP + diphosphate + L-glutamy1-tRNA(Glu).
-!- SUBGUIT: MONOMER (BY SIMILARITY).
-!- SUBCILLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Gytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa:
Msmmalla: Eutherla:
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updste)
Exostosin-like 1 (Exostosin-L) (Multiple exostosis-like
EXTL1 OR EXTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20512582; PubMed-11058132:
Takami H., Nakasone K., Takaki Y., Macno G., S
Takami H., Nakasone K., Takaki Y., Ogssawars N.,
Fuji F., Hirama C., Nakamura Y., Ogssawars N.,
Horikoshi K.:
"Complete genome sequence of the alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS: PR00987: TRNASYNTHGLU.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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Interpro; IPR001412: tRNA-synt_1.
Pfam; PF00749: tRNA-synt_1c: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-slb.ch).
   SEQUENCE FROM Wuyts W., Spie
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-97189339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q92935;
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W., Spieker
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                                                                                             (AUG-1998)
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ATP (BY SIMILARITY)
, 7D34A862918F57B6
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Catarrhini; Hominidae;
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                                                                                                                                                   n Q., Liu C.
hereditary
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   De Paepe
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   7.
                                                                                                                                                                                                                                                                                                                                           third member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
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RESDLT
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Best Local S
Matches 7
SEDULNAL.

STRAIM-BEERKeley;

MEDLINE-20196006; PubMed-10731132;

Adams M.D., Celniker S.E., Hoit R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Hoit R.W., Noskins R.A., Galle R.F.,

Levis S.E., Richards S., Ashburner M., Henderson S.N.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Probable G-protein-coupled receptor Mth-11ke
11ke 10 protein).
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EMBL;
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Eukaryota; Metazoa; Arthropoda;
Pterygota; Neoptera; Endopterygo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DROME
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-!- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                         SEDUENCE FROM N.A.
                                                                                                                                                                                                                                                                    Ephydroidea; Dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D9WOR5;
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BL; AP083623; AAD02840.1; JOINED
BL; AP083624; AAD02840.1; JOINED
BL; AP083625; AAD02840.1; JOINED
BL; AP083626; AAD02840.1; JOINED
BL; AP083627; AAD02840.1; JOINED
BL; AP083628; AAD02840.1; JOINED
BL; AP083629; AAD02840.1; JOINED
BL; AP083630; AAD02840.1; JOINED
BL; AP083631; AAD02840.1; JOINED
BL; AP083630; AAD02840.1; JOINED
BL; AP183391; AAP73172.1; JOINED
BL; AP183980; AAP73172.1; JOINED
BL; AP183980; AAP73172.1; JOINED
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PF03016; Exost
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AF083633; AAD02840.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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RA Beeson K.Y., Benos P.V., Serman S.P., Bhandari D., Boishakov S.,
RA Borkova D., Soctchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Soctchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawiey S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawiey S., Dahlke C., Dungor-Rocha S., Dunkov S.C., Dunn P.,
RA Cherry J.M., Deng E., Downes M., Dugan-Rocha S., Dunkov S.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov S.C., Dunn P.,
RA Borkova D., Sornell J.N., Gu Z., Gunar P., Harris M.,
RA Glodek A., Gong F., Gorrell J.N., Gu Z., Gunar P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Nouston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menscol D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Poilard J., Puri V., Reese M.G.,
RA Reinert K., Remingston K., Sunnders R., Dc., Scheeler F., Shen H.,
RA Syler B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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RA Syler B.C., Scheeler F., Wenter E., Wang S., Yao O.A.,
RA Yeng X.H., Zhong F. N., Zhong W., Zhou X., Smith H.O.,
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Abrll J.F.
Ballew R.B
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-I- SUBCELLULAR LOCATION: Inter-
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Brody T., Cravchil
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Proc. Nati. Acad. Sci. U.S. A. 98:9877-9882(2001).

-!- FUNCTIDN: INVDLVED IN THE PRODUCTION OF BETA-(1,2)-GLUCAN.

IT IS INVDLVED NOT ONLY IN INVASION BUT ALSO IN BACTERDID
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FRDM N.A.

MEDLINE-90153914; PubMed-2154461;

Ielpl L., Dylan T., Ditta G.S., Helinski D.R., Stanfield S.W.;

"The ndvB locus of Rhizoblum melilot1 encodes a 319 kDa protein

involved in the production of beta-(1->2)-glucan.";

J. Biol. Chem. 265:2843-2851(1990).
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21-JUL-1986 (Rel. (
01-NDV-1995 (Rel.
                                                                                                                                                                                                                                                   *Nuclectice sequence from the genetic left end of bacteriophage DNA to the beginning of gene 4.";
J. Mol. Biol. 148:303-330(1981).
-!- FUNCTION: ENDODEDXXIBDNUCLEAGE I, WHICH IS EXPRESSED IN THE STAGE, IS NECESSARY FOR T7 GENETIC RECOMBINATION AND THE BR DF HOST DNA. IN THE EARLY STAGE OP INFECTION, T7 DNA REPLICATES A LINEAR MONDMER. IN THE LATE STAGE, THE T7 DNA REPLICATES LINEAR CONCATEMERS SEVERAL GENDMES IN LENGTH. THE GENE 3 PRINTS ALSO BEEN IMPLICATED IN THE MATURATION DF THESE CDNCATE HAS ALSO BEEN IMPLICATED IN THE MATURATION DF THESE CDNCATE CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
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                                                                          use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
EMBL; V01127; CAA24345.1; EMBL; V01146; CAA24402.1; PIR; A00785; NEBP37.
                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA
T7-llke phages
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TRANSMEM 41
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                                                                                                                                                                               between
                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-82078034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-83241725; PubMed-6864790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage
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                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                    phosphooligonucleotide end-products.
                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics institute. There are no restrict by non-profit institutions as long as its content is
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166:477-535(1983).
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(Endonuclease).
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Hydrolase; Nu
SEQUENCE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9530630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.O., Shirley R., Llu L.-I., Glodek A., Keiley J.M.,

Weidman J.F., Philips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Witerback T.R., Hanna M.C., Nguyen O.T., Saudek D.M., Brandon R.C.

Fine L.O., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _HAEIN
                                                EMBL;
TIGR;
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sclence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence of the rec-2 locus of Haemophilus influenzae: comE-ORF3 of Bacillus subtilis and msbA of Escherichla come 146:95-100(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94341577; PubMed=8063112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P44408;
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                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MIGHT CONTRIBUTE TO TRANSFORMATION AS A MEMBER OF A MEMBERANE BOUND PORE COMPLEX AT THE BASE OF THE TRANSFORMASOME. IT COULD DIRECTLY INTERACT MITH TRANSFORMING DNA OURING TRANSLOCATION INDIRECTLY BY PARTICIPATING IN THE ASSEMBLY OF THE PORE.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
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U32691; AAC21739.1;
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Similarity 58.
7; Conservative
                                                                                                                                            an email to license@lsb-sib.ch).
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                      IPR001279;
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Nuclease;
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17172 MW; D092AA28E3743BCI CRC64;
                      Beta_lactam_met
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l; Mismatches
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable exodeoxyrlbonuclease VII large subunit (EC (Exonuclease VII large subunit).
XSEA OR SCK7.29C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: BIOIRECTIONALLY DEGRADES SIMELE-STRANDED ON INTACTOR ACTO-INSOLUBLE OLIGONOCLEGATIDES, WHICH ARE THEN DEGRADED FINTO SMALL ACID-SOLUBLE OLIGONUCLEOTIOES (BY SIMILARITY).

- CATALYTIC ACTIVITY: EXONUCLEOLYTIC CLEAVAGE In either 5'-
or 3'- to 5'-direction to yleid 5'-phosphomononucleotides.

- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNIT
                                          EMBL; AL391754; CAC0590I.1; -. InterPro; IPR003753; Exonuc_VII_L. InterPro; IPR002309; tRNA-synt_2.
                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                     Pfam; PF02601; Exonuc_VII_L; Pfam; PF01336; tRNA_antl; 1.
                                                                                                                                                                                                                                                                                              Rajandream M.A.;
                                                                                                                                                                                                                                                                                                         Seeger K.J.,
                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                        SIMILARITY: BELONGS TO THE XSEA FAMILY.
                                                                                                                                                                                           SUBCELLULAR
                                                                                                                                                                                                        SIMILARITY).
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6; Conserv
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Streptomycineae; Streptomycetaceae; Streptomyces.
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Pred. No.
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POTENTIAL.
VENTAVSGYVEVNFFQDRLEIQQARTKFSPWYARVIGLSKE
VENTAVSGYVEVNFFQDRLEIQQARTKFSPWYARVIGLSKE
PRIKGTKGTMRAIFTIR (IN REF. 1).
F31104595CB4E47A CRC64;
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**Hydroiase**;

Nuclease;

Exonuciease

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145929A8372B4E08 CRC64;

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RESULT 12
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ID RK6_GU
AC 046908
AC 046
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046908;
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15-DEC-1998
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                            Interpro; IPR000702; Ribosomal_L6.
Interpro; IPR002358; Ribosomal_L6_1.
Pfam; PF00347; Ribosomal_L6; 1.
PR1NTS; PR00529; RIBOSOMALL6.
ProDom; PD002236; Ribosomal_L6; 1.
PROSITE; PS00525; RIBOSOMAL_L6_1; 1.
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NCBI_TaxID-55529;
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Eukaryota; (
                                                                                                                                                                                             Ribosomal protein; Chioroplast. SEQUENCE 179 AA; 19527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Mol. Biol.
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                                      2 YXXRG1RPVGRF
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SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOWAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INE-97283757; PubMed-9137835; S.L., Liu X.-Q., Douglas S.E.; S.L., Liu X.-Q., Douglas S.E.; large ribosomal protein genc cluster of a cryptomonad plastid: large ribosomal protein genc cluster of a cryptomonad plastid: organization, sequence and evolutionary implications.*; hem. Mol. Biol. Int. 41:1035-1044(1997).
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YKCKCIRYVCEF 168
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P02391; 1RL6.
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THIL_ZOORA
  Query Match
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Matches 6
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01-APR-1990
01-OCT-1996
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MUTAGEN
SEQUENCE
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ACT_SITE
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PIR; A26121; XXGZAC.
PIR; A27754; A27754.
HSSP; P27796; LAFY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Secor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16. Characterization of the genes encoding beta-ketothiolase and acetoacetyl-CoA reductase.";
J. Blo1. Chem. 264:15293-15297(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRALN-ATCC 19623 / I-16-M;
MEDLINE-87083504; PubMed-2878929;
MEDDINE-87083504; PubMed-2878929;
MEDDINE-87083504; PubMed-2878929;
MEDDINE-8708504; PubMed-2878929; PubMed-2878929; 
                                                                                                                                                                                                                      pfam; pF02803; thioiase_C; 1.
pROSITE; pS00090; THIOLASE_1;
pROSITE; pS00099; THIOLASE_3;
pROSITE; pS00737; THIOLASE_2;
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P07097;
                                                                                                                                                                                                                                                                               InterPro, IPR002155; Thiola Pfam; PF00108; thiolase; 1. Pfam; PF02803; thiolase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paimer M.A.J., Differding E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91217075;
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6; Conserv
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391 AA; 40342 MW;
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34, Last annotation update)
transferase (EC 2.3.1.9) (Ac
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BASE,
C->G: LOSS OF ACTIVE
W; 6D2351A1BC0E4EDD (
  <u>ب</u>
  Score 35; DB
Pred. No. 20;
2; Mismatches
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                DB
20;
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                                                                                                 ACTIVITY.
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  Indels
                                                                                                                                                            SIMILARITY).
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RGIQPLGR

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TBB2\_GEOCN 932925;

STANDARD;

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RESULT 15
SR54_HALN1
ID SR54_H
AC 09HMN5
DT 16-0CT
DT 16-0CT
DT 16-0CT
DT 16-0CT
C Signal
GN SR546
OS Naloba
OC Haloba
OX NCBLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRESULT 14
TRES_GEOCN
ID TRES_GEOCN
ID TOLONO
DT 01-NOV
DT 15-JUL
OC ENKARY
OC SACCHA
OX NCELT
RN HEDLIN
RA GOLD S
RT CANDID
RT INTERF
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SQ SEQUEN
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Best Local S
Matches 5
                                                                                                            Q9HMN5;
16-OCT-2001
16-OCT-2001
16-QCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: S69627; AAB20557.1; ALT_SEQ.

PIR: S18597; S18597.

InterPro; IPR002453; Beta_tubulin.

InterPro; IPR00217; Tubulin.

InterPro; IPR003008; Tubulin_Ftsz.

Pfam; Pf00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SNISS-PROT entry is copyright. It is produced through a coilaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(lsb-sib.ch).
                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-QCT-2001 (Rel. 40, Last ann
16-QCT-2001 (Rel. 40, Last ann
11gnal recognition 54 kDa prot
SRP54 OR VNG2459G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-92079883; PubMed-1836049;
Gold S.E., Casale W.L., Keen N.T.;
Gold S.E., Casale W.L., Keen N.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rei. 27, Created)
01-NOV-1995 (Rei. 32, Last sequence update)
15-JUL-1999 (Rei. 38, Last annotation updat
Tubulin beta-2 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO1161; TUBULÍN.
PROSITE; PS0022P; TUBULIN. 1.
PROSITE; PS0022B; TUBULIN. 8_AUTOREG; 1.
Microtubules; GTP-binding; Multigene family.
NP_BIND 142 148 GTP (POTENTIAL)
SEQUENCE 453 AA; 50399 MW; 2EA9D8A0246EO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gold S.E., Casaie W.L., Keen N.T.; "Characterization of two beta-tubulin genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales;
NCBI_TaxID=27317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geotrichum candidum (Oospora lactis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                     Archaea; Euryarchaeota;
                                                         Nalobacterium sp. (strain
                                                                                                                                                                                         SR54_NALN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candidum."
                   Malobacterium
                                                                                                                                                                                                                                                                                      399 WYTGEGMEPV 408
                                                                                                                                                                                                                                                                                                                          1 WYXXRGIRPY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.

SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.

SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Genet. 230:104-112(1991).
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                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                 50.7%;
                                                                                         Last sequence update)
Last annotation update)
kDa protein (SRP54).
                                     Halobacteriales; Nalobacteriaceae;
                                                         NRC-1).
                                                                                                                                                                                                                                                                                                                                                              Score 35; DB
Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2EA9D8A0246E0371 CRC64;
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Search completed: September 13, Job time: 1137 sec

2002,

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A Shukia N.D., Lasky S.R., Bailga N.S., Thorsson V., Sbrogna J.,
A Shukia N.D., Lasky S.R., Bailga N.S., Thorsson V., Sbrogna J.,
A Shukia N.D., Lasky S.R., Bailga N.S., Thorsson V., Sbrogna J.,
A Swartzell S., Weir D., Nall J., Danson M.J., Hough D.W.,
A Leithauser B., Keller K., Cruz R., Dangon M.J., Hough D.W.,
A Maddocks D.G., Jablonski P.E., Krebs M.P., Apevine C.M., Dals N.,
A Maddocks D.G., Jablonski P.E., Krebs M.P., Apudich J.L., Jung K.-H.,
A Alam M., Freitas T., Nou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Alam M., Freitas T., Nou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
T "Genome sequence of Halobacterium species NRC-1.";
T "Genome sequence of Halobacterium species NRC-1.";
T "Genome sequence of Halobacterium species NRC-1.";
C -1- FUNCTION: BIRDS TO TNE SIGNAL SEQUENCE OF PRESECRETORY PROTEIN
C -1- SUBUNIT: ARCHAEAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 75 RNA
MOLECULE OF 300 NICLEOTIDES AND TWO PROTEIN SUBUNITS: SRP54 AND
                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                       NP_BIND
NP_BIND
NP_BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-20504483; PubMed-11016950;
MEDLINE-20504483; PubMed-11016950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE005125; AAG20536.1; -. InterPro; IPR000897; SRP54. Pfam; PF00448; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000819; SRP54; 1. PROSITE; PS00300; SRP54; FA
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                                                                                                                                                                                                                                                                                                                                Signal
120
                                      1 WYXXRGIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRP19 (BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

DOMAIN: HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; TN

M-DOMAIN BINDS THE 7S RNA IN PRESENCE OF SRP19 AND ALSO BINDS

SIGNAL SEQUENCE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
WFSKKGLRP
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                                                                             Conservative
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460 M
1111 G
1188 G
245 G
458 P
50149 MW;
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cle; GTP-binding; RNA-binding;
                                                                                                                                                                                                             G-DOMAIN (BY SIMILARITY).
M-DOMAIN (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                           Score 35:
Pred. No.
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                                                                                                                                                                           8361B782E651352E CRC64;
                                                                         Mismatches
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23;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 s
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BG
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1: sp_acchea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1:*
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:*
12: sp_verteb:*
13: sp_verteb:*
14: sp_urclass
15: sp_acteri:
16: sp_acteri:
17: sp_archeap
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Match
   US-09-446-543A-73_COPY_8_21
69
1 WYXXRGIRPVGRFX 14
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sp_unclassified:*
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(without alignments)
7.766 Million cell updates/s
09w624 carassius a
093127 streptomyce
09t133 bacteriopha
092ve9 rhizobium m
09ph76 xylella fas
095wt7 drosophila
095pk6 drosophila
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36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36.5	37	37	37	37	37	37	37
52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.9	53.6	53.6	53.6	53.6	53.6	53.6	53.6
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P79750	Q47673	097180	Q9VXK4	Q9M371	050431	Q93GZ5	Q9A7W7	Q9LGZ0	Q9KRY1	Q99TD8	8X7460	Q979S0	Q93EC5	Q18729	Q98BC2	Q92SA6	Q9PHR2	053929	086838	Q45285	Q46610	054728	Q92NX4	068843	054095	Q95U70	Q9W1G4	Q92UH4
0		O97180 drosophila	۵		O50431 mycobacteri	w	Q9a7w7 caulobacter			Q99td8 staphylococ		0 thermopla		caenorhabdi		Q92sa6 rhizobium m		9			a		4			Q95u70 drosophila	Ω	Q92uh4 rhizobium m

# ALIGNMENTS

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RESULT
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Best Local Similarity 69.1
Matches 9; Conservative
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09W624;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
C-RF AMIDE.
 Q93L27
Q93L27;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
                                                                                                                                                                                                                      Satake H., Minakata H., Fujimoto M.;
"Carassius Rramide (C-Rr amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                      Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Qstariophys1;
Cypriniformes; Cyprinidae; Carassius.
NCBI_TaxID=7957;
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                                                                                                             1 WYXXRGIRPVGRE
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63 WYVGRGVRPIGRE
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1 (Tremblrel. 19,
1 (Tremblrel. 19,
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                                                                                                                                                           Score 62; DB 13; Length 117;
Pred. No. 0.00026;
2; Mismatches 2; Indels
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Best Locai
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MEDLINE-2112559; PubMed-11222590;
MEDLINE-21125594; PubMed-11222590;
Pajunen M.I., Kiljunen S.J., Soederholm M.

"Complete genomic sequence of the lytic ba

"Complete genomic sequence of the lytic ba

"Crainia enterocolitica serotype 0:3.";

J. Bacteriol. 183:1938-1937(2001).

EMBL; AJS51805; CAB63604.1; -

SEQUENCE 153 AA; 17640 MW; 211571BDDE6
                                  Q92VE9;
Q92VE9;
Q1-DEC-2001 (TrEMBLrel. 19, Cre
Q1-DEC-2001 (TrEMBLrel. 19, Lag
Q1-DEC-2001 (TrEMBLrel. 19, Lag
UVPOTHETICAL PROTEIN SMB21253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09T133;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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Viruses; dsDNA viruses, n
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY033994; AAK61719.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FRON N.A. STRAIN-CCM3239;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
      Rhizobium
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Pred. No. 6;
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A HO P.L., Hoheisei J.D., Junqueira M.E., Kemper E.L., Kitejims J.P.,
A Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
A Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
A Marques M.V., Martins E.A.L., Martina E.M.F., Matsukums A.Y.,
A Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorelio C.B.,
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Moon D.H., Nagai M.A., Robrita B.L.T., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A Quaggio R.B., Pereira G.A.G., Pereira H.A. Jr., Peaquero J.B.,
A Quaggio R.B., Foberto P.G., Santelli R.V., Sawasaki H.E.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Zago M.A., Zatz M., Meldanis J., Setubal J.C.,

"The genome sequence of the piant pathogen Xyleila faatidiosa.";
U Nature 406:15I-159(2000).
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorai E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H. Colauto N.B., Colombo C., Costa F.E., Costa M.C.R., Costa-Neto C.M. Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Franca S.C., Franco M.C., Fronce M., Franco M.C., Franco M.C., Fronce M., Franco M.C., Franco M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; AL603644; CAC49157.l; -.
Piasmid; Hypothetical protein; Complete proteome.
SEQUENCE 256 AA; 28459 MW; 548064834CEC7C39 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alph
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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S., Bove J.M., Briones M.R.S.,
E.A., Carraro D.M., Carrer H.,
Costa M.C.R., Costa-Neto C.M.,
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Pfam; PF01040; UbIA; 1.
PROSITE; PS00943; UBIA; UNKNC
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SEQUENCE 333 AA; 3793I MM;
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STRAIN-ZIK(S)24;
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Duveznell D.D., Schmidt P.S., Eanes W.F.;
Wholecular population genetics of a methuselah
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"Molecular population genetics of a methuselah paralog."
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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               STRAIN-YAK_5:
Duvernell D.D. Schmidt P.S., Ear
Duvernell D.D. Schmidt P.S., Ear
Molecular population genetics of
Submitted (AUG-2000) to the EMBL;
EMBL; AF300419; AAK97897.1;
EMBL; AF300418; AAK97897.1; JOIN
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-YAK_4;
DUVERNELL D.D., Schmidt P.S., Eanes W.F.;
"Molecular population genetics of a methuselah submitted (AUG-2000) to the EMBL/GenBank/DDBJ d EMBL; AF300417; AAK97896.1; -...
EMBL; AF300416; AAK97896.1; JOINED.
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SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Last se
01-DEC-2001 (TrEMBLrel. 19, Last an
G_PROTEIN-COUPLED RECEPTOR PROTEIN.
                                                                                                              Drosophila yakuba (Fruit fly).
Bukaryota; Metazoa: Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                          MTH.
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Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydroldea; Drosophilldae; Drosophlla.
                                                                                SEQUENCE FROM N.A.
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                                                                                                     NCBI_TaxID=7245;
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Simllarity 46.2%;
6; Conservative
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EMBL/GenBank/DDBJ o
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Pred. No. 58;
2; Mismatches
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Best Local S
Matches
  STRAIN-VARIOUS STRAINS:
Duvernell D.D., Schmidt P.S., Eanes W.F.;
PMOlecular population genetics of a methuseIah pai
submitted (AUG-2000) to the EMBL/GenBank/DDBJ data
EMBL; AF300408; AAK97891.1; -.
EMBL; AF300364; AAK97869.1; JOINED.
EMBL; AF300363; AAK97869.1; -.
EMBL; AF300366; AAK97869.1; -.
EMBL; AF300366; AAK97870.1; -.
EMBL; AF300366; AAK97870.1; JOINED.
EMBL; AF300365; AAK97871.1; -.
EMBL; AF300367; AAK97871.1; JOINED.
EMBL; AF300370; AAK97871.1; JOINED.
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Q95NU7;
O1-DEC-2001 (TrEMBLrel. 19, C
O1-DEC-2001 (TrEMBLrel. 19, I
O1-DEC-2001 (TrEMBLrel. 19, I
G PROTEIN-COUPLED RECEPTOR.
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Q95PK5;
O1-DEC-2001 (TremB1
O1-DEC-2001 (TremB1
O1-DEC-2001 (TremB1
G PROTEIN-COUPLED F
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"Molecular population genetics of a methuselah
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ d
EMBL; AF300421; AAK97898.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                Drosophlla melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda: Tracheata; Hexapoda: Insecta;
Eukaryota; Neoptera; Endopterygota: Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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Duvernell D.D.,
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DrosOphila yakuba
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6; Conservative
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STRAIN-YAK_23, BG1013, AND YAK_2;

STRAIN-YAK_23, BG1013, AND YAK_2;

Duvernell D.D., Schmidt P.S., Banes W.F.;

"Molecular population genetics of a methuselah pa:

EMBL, AR$00413; AAK$7894.1; JOINED.

EMBL; AR$00410; AAK$7892.1; JOINED.

EMBL; AR$00412; AAK$7892.1; JOINED.
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01-DEC-2001 (TrEMBI
G PROTEIN-COUPLED I
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Eukaryota: Metazoa: Arthropoda: Tracheata; Hexapoda: Insecta;
Pterygota; Meoptera; Endopterygota: Diptera; Brachycera; Musc
Ephydroldea; Drosophilidae; Drosophila.
NCBI_TaxID=7245;
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AF300389
AF300390
AF3004003
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6; Conservative
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1 (TrEMBLrel. 19,
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COUPLED RECEPTOR P
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AC p95ND0

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE G-PROTEIN-COUPLED RECEPTOR PROTEIN.

OS Drosophila simulana (Pruit fly).

OC EUKaryotu, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomor
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Best Local S
Matches
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A Duvernell D.D., Schmidt P.S., Eanes W.F.,
T "Nolecular population genetics of a methuselah paralog.";
L Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AP300360; AAK82820.1; -.
R EMBL, AP300359; AAK82820.1; -.
R EMBL, AP300342; AAK82811.1; -.
R EMBL, AP300341; AAK82811.1; -.
R EMBL, AF300344; AAK82811.1; -.
R EMBL, AF300344; AAK82812.1; -.
R EMBL, AF300354; AAK82812.1; -.
R EMBL, AF300354; AAK82812.1; -.
R EMBL, AF300353; AAK82817.1; -.
R EMBL, AF300353; AAK82817.1; -.
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p95NR7;
p95NR7;
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p1-pc2-2001 (TrembLrel. 19, Last aequence update)
p1-pc2-2001 (TrembLrel. 19, Last annotation update)
p1-pc2-2001 (TrembLrel. 19, Last annotation update)
p1-pc2-2001 (TrembLrel. 19, Last annotation update)
p-profile almulane (Fruit fly).
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SEQUENCE 536 AA; 61768 MW; 58E
STRAIN-VARIOUS STRAINS;
Duvernel1 D.D., Schmidt P.S., Eanes W.F.;
"Molecular population genetics of a methuselah paralog.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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; Pred. No. 58;
2; Nismatches
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RA Adams M.D., Celaiker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Nenderson S.N.,
RA George R.A., Lewis S.E., Richards J., Ashburner M., Nenderson S.N.,
RA George R.A., Lewis S.E., Richards J., Ashburner M., Nenderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang D., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang D., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Nelt G., Nelson C.R., Niklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Nelt G., Nelson C.R., Niklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Bexman B.P., Bahadari D., Botlahakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bahadari D., Botlahakov S.,
RA Burtis K.C., Busam D.A., Butler N., Cadieu E., Center A., Chandra 1.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Dodaon K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Doblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.N.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Narris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Narris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Narris M.,
RA Harris N.L., Narvey D., Helman T.J., Wei M.-H., Ibeyram C.,
RA Alali M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
RA Lasko P., Let Y., Levitsky A., Mostla M.P., Nepherson D.,
RA Merkulov G., Nilshina N.V., Mobarry C., Norris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duery Match
Beat Local S
Matches 6
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D9W043;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, I
01-DEC-2001 (TrEMBLrel. 19, I
CG5707 PROTEIN.
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Drosophila melanogaater (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Nexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
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SEDUENCE
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskarn D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skung A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yel J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
RE EMBL, AE003474; AAR47616.1].
DR EMBL, AE003474; AAR47616.1].
DR EMBL, AE003474; AAR47616.1].
DR EMBL, AE003474; AAR47616.1].
SQ SEQUENCE 332 Abhydrolase.
DR InterPro, IPR000379; BEST:HL03644.
DR Figns: PSpn0025593; BEST:HL03644.
DR Figns: PSpn0025593; BEST:HL03644.
DR Figns: PSpn0025593; BEST:HD03644.
DR Figns: PSpn0025593; BEST:HD03644.
DR Figns: PSpn00279; BEST:HD03644.
DR Figns: PSpn00
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                                              19P2 ligand peptid
19P2 ligand peptid
Human type G prote
Human type ligand
Human oxytocin sec
19P2 ligand peptid
Human CRH releasin
Prolactin releasin
Human type G prote
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oxytocin sec
CRH releasin
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# ALIGNMENTS

RESULT
AAY49293
ID AAY4
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AC AAY4
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AAY49293 standard;

peptide;

15 ₿ \_

Monocional antibody; 19P2 ligand; diagnosia; prolactin secretion; pltuitary; regulatory mechanism; central nervous ayatem; pancreat

pancreatic.

19P2 llgand peptide fragment.

22-FEB-2000 AAY49293;

(first entry)

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New
             WPI; 2000-039381/03.
                       Mataumoto H,
                                               21-MAY-1990;
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Modlfled-alte
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 monocional antibodies,
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of projectin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in ciarifying the physiological functions of the ligand and its derivative sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.
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                                                                                                                                Disclosure; Page 27; 73pp; Japanese
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               sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic prophylactic or therapeutic agent for dementia, depression, hyperkinetic trauma, growth hormone secretory disease, hyper- and polyphagia, trauma, growth hormone secretory disease, hyper-lipidaemia, hypercholesterolaemia, hyperglyceridaemia, spinal injury, hyperprojactinaemia, disbetes, cancer, pancreatitis, renai disease, hyperilipidaemia, ceurosis, asthma, rheumatoid arthritis, spinal injury, transfent brain ischaemia, spilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebeilar degeneration, bone fracture, trauma, atopic dermatitis, osteoprosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
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N-PSDB; AAV02431.
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                                               The present sequence represents a human type ligand fragment. It

Consequence is used in the course of the invention. The specification describes

an agent for modulating prolactin secretion which comprises a

Consequence in the course of the invention. The specification describes

consequence in the course of the invention is specification describes

consequence in the course of the invention in the comprises and the secretion can be used for protein. The agents for protein phypowerlanism, gonecyst cacogenesis, menopausal

consequence enthyroid or hypometabolism. They can by used for promoting

consequence in a domestic mammal and as an aphrodisiac. The agents for

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                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                      This invention describes a novel oxytocin secretion-regulating agent which contains a ligand poptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for amellorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                           Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; oxytocin secretion promoter; G protein-coupled receptor prote treatment; disease; pain; atonic bleeding; uterine recovery failure; caesarean section; artificial fertilization; galactostasis; goat: pl
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                                                         Sequence
                                                                                promoter
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                                                                                                                                                                                                                                                                                                                                                                 25-DEC-1998;
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10; Conserv
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           DH 21;
0.00048;
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les 2;
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Matches 10
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  anaigesic;
Addison's
                                             Human CRH releasing protein
                                                                        24-AUG-2001
                                                                                               AAG62534;
                                                                                                                    AAG62534 standard;
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monoclonal antibodies, studying diseases related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1998;
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corticotrophin releasing hormone; CRH; G protein receptor ligand;
sic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
n's disease; adrenal gland hyperfunction; obesity.
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83.3%;
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                                             related peptide SEQ ID ND:
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Matches 10
         17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analysisc or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypeadremocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                       Homo sapiens.
Synthetic.
                                                                                                                                                    Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyi; maleimido group; amino; hydroxy1; thio1; hormone; growth factor; neurotransmitter.
                                                                                                  WO200069900-A2
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26-SEP-2000; 2000JP-0297073
                                                     17-MAY-2000; 2000WO-US13576
                                                                          23-NDY-2000
                                                                                                                                                                                                   Prolactin releasing peptide SEQ
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99US-0159783.
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CC AABS0829 to AAS9241 represent peptides which can be used in the creases are considered in the present invention.
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15-MAR-1996;
12-AUG-1996;
 Fujii R,
Kawamata
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                                            (TAKE ) TAKEDA
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95JP-0343371.
96JP-0059419.
96JP-0211B05.
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              Habata
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              Hosoya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulator, a central nervous system modulator or a pancreatic function conditator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperprolactinaemia, disbetes, cancer, pancreatitis, renal disease, hyper-prolactinaemia, disbetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, neurosis, asthma, rheumatoid arthritis, spinal injury, translent brain ischemenia, epilepsy, amylotrophic lateral scicrosis, acute myocardiai infarction, infertillty, spinocerebeliar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 54 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cialm 2; Page 186; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                      treatment; disease; pain;
                                                                                                                                                                                                                                                                                                                                                                                       Human oxytocin secretion promoting peptide SEQ
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                               WPI; 2000-452298/39
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                                                                                                 (TAKE ) TAKEDA CHEM IND
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DB; AAV02432.
                                                                                                                                                                                                                                                                                                                  oxytocin secretion promoter; G protein-coupled receptor protein; ent; disease; pain; atonic bleeding; uterlne recovery failure; coent; disease; pain; atonic bleeding; uterlne recovery failure; pain section; artificial fertilization; galactostasis; goat; pig;
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Physiologically-active polypeptide recognized as ligand

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The present sequence describes a method of controlling the secretion of conticotrophin releasing hormone (CRH), involving the use of a G protein receptor ilgand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolsemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, plgmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the 6 protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostesis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
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                                                                                                                                                                                Use of G protein receptor ligand or corticotropin releasing hormone secu
                                                                                                                                                                                                                                   WPI; 2001-355552/37.
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26-SEP-2000;
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CC ligand polypeptide corresponding to amino acid residues 34 to 55 of the CS sequence represented in ANW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hypercidaemia, phyperchaetinaemia, diabetes, cancer, pancreatitis, renai disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renai disease, cc Turner's syndrome, neurosia, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral scierosis, cc bone fracture, trauma, atopic dermatitis, osteoporosis and/or collopolatetia. Assays can also be developed to screen compounds which are CC capable of altering the binding activity of the itenna affection.
      RESULT 1
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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function in the central nervous system,
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modulator; pituitary; central nervous system
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                                                                                                This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameilorating, preventing and treating diseases relating to oxytocin secretion e.g. weak palms and atonic bleeding, before and after expulsion of placenta, uterine recovery fallure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                          Human; oxytocln secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; co caesarean section; artificial fertilization; galactostasis; goat; pig;
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                                                                                                                                                                                                              of oxytocin,
in veterinary
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AAW31391
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AAG62536
ID AAG625
                                                                                                                                                                                                                                                                                                               Query Match
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Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analycsic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity, The present sequence is a peptide used in the exemplification of the
G protein coupled receptor; ligand binding; pl modulator; pltultary; central nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG62536 standard; peptlde;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of G protein receptor ligand or peptide cortlcotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CRH releasing
                                                    Human type G proteln-coupled receptor ligand fragment
                                                                                       06-APR-1998
                                                                                                                          AAW31391;
                                                                                                                                                        AAW31391
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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26-SEP-2000;
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sic; hyperaidosteronism; hypercortisoiaemia; hypoadrenocorticism;
n's disease; adrenai gland hyperfunction; obesity.
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                                                                                                                                                                                                                                                                                                             l Similarity
10; Conserv
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                                                                                                                                                                                                                                                                                                               Conservative
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2000JP-0297073.
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Pred. No.
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                 pharmaceutlcal;
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pancreas; prophylactic;

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Search completed: September 13, 2002, 09:18:35 Job time: 500 sec
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                                                                                                                                                                                                                                             This sequence represents a peptide fragment from a novel human type colligand polypeptide corresponding to amino acid residues 23 to 53 of the consequence represented in AAW31390 and is used in an assay to monitor cligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This sigand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, schizophrenia, compositions of consciousness, anxiety syndrome, schizophrenia, compositions, growth hormone secretory disease, hyper- and polyphagia, hyperfipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperfipidaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, epilepsy, anylotrophic lateral sclerosis, caute myocardial infarction, infertility, spinocerebeliar degeneration, counter myocardial infarction, infertility, spinocerebeliar degeneration, counter fracture, trauma, atopic dermatitis, osteoporosis and/or collogogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cativation of the G protein-coupled receptor protein.
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Matches 10
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligand peptide for G protein-coupied receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV02428
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Kawamata Y, Kitada C;
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                                                                                                                     1 YXXRGIRPVGRF 12
                                                                                   1997-363672/33.
                                                                                                                                                      l Similarity 83.0
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                                                                                                                                                                      94.8%;
                                                                                                                                                      Score 55; DB 18; Length 31; Pred. No. 0.00076; O; Mismatches 2; Indels
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   and is derived by a
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   protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Match
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Maximum Match 100%
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58
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/Pdctiles1.pep:*
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US-09-105-678A-46
US-09-421-208-47
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-48
US-09-105-678A-8
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-43
US-08-776-971-138
US-08-776-971-138
US-08-776-971-138
US-08-776-971-138
US-08-776-971-138
US-09-105-678A-44
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2.324 Million cell updates/s
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46, Appl
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49, Appl
40, Appl
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Query Match
Best Local Similarity
Matches 10; Conserv

Conservative

0

94.8%; 83.3%;

Score 55; DB Pred. No. 0.00

лв ј, J. 00017; Z;

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US-09-105-678A-46  IS-09-105-678A-46  IS-09-105-678A-46	28 54 93.1 20 4 US-OB-776-971-98 S 29 54 93.1 20 4 US-OB-776-971-98 S 30 54 93.1 20 4 US-OB-776-971-98 S 31 54 93.1 20 4 US-OB-421-208-34 S 32 54 93.1 21 3 US-OP-105-678A-41 S 33 54 93.1 21 3 US-OP-105-678A-41 S 34 93.1 21 4 US-OB-776-971-91 S 35 54 93.1 21 4 US-OB-776-971-91 S 36 54 93.1 21 4 US-OB-776-971-91 S 37 54 93.1 21 4 US-OB-776-971-91 S 39 54 93.1 21 4 US-OP-421-208-41 S 40 93.1 22 3 US-OP-105-678A-76 S 41 93.1 22 4 US-OB-776-971-10 S 42 54 93.1 22 4 US-OB-776-971-52 S 43 54 93.1 22 4 US-OB-776-971-52 S 44 93.1 22 4 US-OB-776-971-52 S 45 93.1 31 3 US-OP-105-678A-7 S 46 93.1 31 3 US-OP-105-678A-7 S 47 93.1 31 3 US-OP-105-678A-8 S 48 93.1 31 3 US-OP-105-678A-8 S
P2 LIGAND	Sequence 50, Appl Sequence 98, Appl Sequence 40, Appl Sequence 41, Appl Sequence 41, Appl Sequence 9, Appli Sequence 51, Appl Sequence 35, Appl Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl Sequence 36, Appl Sequence 37, Appl Sequence 42, Appl

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US-08-776-971-64
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Patent No. 6228984
GENERAL INFORMATION:
                                                                                           Query Match
Best Local S
                                                                           Matches
                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-AWR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 96
APPLICATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 47176
TELECOMMUNICATION : 107-523-3400
TELECHNONE: 617-523-3400
TELECHNONE: 617-523-6440
                                                                                                                                                                                       MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPROTEINS, NUMBER OF SEQUENCES: 140
                                    YXXRGIRPVGRF 12
YASRGIRPVGRF 20
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                                                                         Similarity 83.:
10; Conservative
                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
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ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                               LENGTN: 20 amino acids
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Kitada, Chieko
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Nabata, Yugo
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Fujii, Ryo
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Best Local Similarity
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                                                 APPLICANT: MOTIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: MENOD OF P
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atenc NO. ---
GENERAL INFORMATION:
NODETCANT: Suenaga,
                                                                                                                                                                                  GENERAL INFORMATION:
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
PILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
ADDRESSEE: DIKE, CALL
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                               9 YASRGIRPVGRF 20
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                                DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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83.3%;
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Pred. No. 0.00017;
Pred. No. 0.00017;
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                                                                                         PRODUCING
                                                                                         A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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us-08-776-971-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6228984
GENERAL INFORMATION:
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Patent No. 6228984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION UNDATA:
APPLICATION UNDATA:
APPLICATION UNDATA:
APPLICATION UNDATA:
FILING DATE: 28-DEC-1996
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les 10; Conserv
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                  FURUSUMI, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
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YASRGIRPVGRF
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                       OF SEQUENCES: 140
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83.3%;
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Pred. No. 0.00018;
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; Sequence 47, Application US/09421208

; Patent No. 6258561
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Best Local Similarity
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: 27.026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                  COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Ose
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                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
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TELEPHONE: 617-523-3400
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FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-KAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Pred. No. 0.00018;
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-47
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US-09-105-678A-48
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Best Local Similarity
Matches 10; Conservai
                                                                                                                            Matches
                                                                                                                                                          Duery Match
Best Local :
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLIT DEVIL TO DEVIL TO THE PARTICE TO T
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
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INFORMATION FOR SEQ
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REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conlin, David G
REGISTRATION NUMBER: 2
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   9
                                                              1 YXXRGIRPVGRF 12
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YASRGIRPVGRF 20
                                                                                                                         1 Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                            Conservative
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ilarity B3.3%;
Conservative
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OR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suenaga,
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                                                                                                                  Score 55; DB 3; L
Pred. No. 0.00019;
0; Mismatches 2;
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Pred. No. 0.00018;
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FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-66
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US-08-776-971-66
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                                                                                        Query Match
Best Local Similarity
                                                                          Matches
                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
9 YASRGIRPYGRF 20
                                   1 YXXRGIRPVGRF 12
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
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KItada, Chieko

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP B/211805 FILING DATE: 12-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                     ENGTH: 22 amino acids
                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hosoya, Masaki
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                                                                                        94.8%;
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1, Shoji
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                                                                    Score 55; DB 4;
Pred. No. 0.00019;
0; Mismatches 2
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                                                                                                         Length 22;
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RESULT 9 US-09-421-208-48

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US-09-105-678A-9
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Dest Local Similarity
Matches 10; Conserv
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TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTN: 22 smino acids
                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UU-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                       APPLICANT: Tanaka, Yoko
APPLICANT: NIShimura, Osamu
APPLICANT: NIShimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
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                                                                       STREET:
                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                  9 YASRGIRPVGRF 20
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6258561
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                                                                  130 Water Street
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Tanaka, Yoko
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Tanaka, Yoko
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                                                                                      BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Pred. No. 0.
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0.00019;
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Best Local S
Matches 10
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172
APPLICATION NUMBER: JP 177
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026 .
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                       APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD OF PRODOCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, RODERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #I.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                             STREET: 10.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin polonomer's
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                                                                                                                                                                                                                                                                                                                                                                                            130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishimura, Osamu
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Pred. No. 0.00027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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SEQUENCE CHARACTERISTICS:
                                                   INFORMATION PDR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDLECULE TYPE: peptide
                                                                                                                                                       APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/216573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON1In, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPDLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 YASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hinuma, Shujl
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
FukusumI, Shoji
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                                                               TELEPAX: 617-523-6440

WATION PDR SEO TD WOMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDMPUTER: IBM compatible
DPERATING SYSTEM: DOS
SDFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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CDMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
PRIDR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDRRESPONDENCE ADDRESS:
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                TYPE: amino acid
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Clry: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDUNTRY: OSA
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Kitada, Chieko
DF INVENTIDN: PDLYPRDTEINS, THEIR PRODUCTIDN AND USE
OF SEQUENCES: 140
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Pred. No. 0.00027;
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STRANDEDNESS:
TDPDLOGY: 11nc;
HDLECULE TYPE: |
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; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SE
US-08-776-971-61
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                                                                     Query Match
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Patent No. 6258561
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Best Local (
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                                                                                                                                                                                                                                                                                                           FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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STREET:
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BOSTON
WA
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EILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
20 YASRGIRPVGRF 31
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                                                         Conservative
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                                                       Score 55; DB 4; L
Pred. No. 0.00027;
0; Mismatches 2;
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Pred. No. 0.00027;
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RESULT

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TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 4

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-421-208-43; Sequence 43, Applicat: patent No. 6258561; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                            US-09-105-678A-44
                                                                                                                                                                                                                                  Sequence 44, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27.026

REFERENCE/DOCKET NUMBER: 48466-342

TELEPHONE: 617-523-3400
                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                           APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tanaka, Yoko
APPLICANT: NIShimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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STREET: 10
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Boston
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STREET: 13
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            CQUNTRY:
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USA
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                                                              E: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
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Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                  94.88;
83.38;
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Pred. No. 0.00027;
Pred. No. 0.0027;
                                                                              ROBERTS & CUSHMAN, LLP
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INFORMATION FOR SEQ ID NO: 44
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 32 amino acids
                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 10; Conserv
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON110, DBV1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECHMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READNALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                               20 YASRGIRPVGRF
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Pred. No. 0.00028;
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### ALIGNMENTS

A;Accession: U., A;Accession: U., A;Accession: A;Accessio A;Molecule type: DNA
A;Residues: 1-485 <STD>
A;Cross references: GB:AP001507; GB:BA0000004; NID:gi0172612; PIDN:BAB0:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: gltX
C;Superfamily: glutamate--trna ligase; glutamine--trna ligase homology giutamyi-trNA synthetase gltX [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (C;Species: Bacillus halodurans) (Bacillus halodura 밁 Ş C;Genetlcs: A;Gene: PrRP A; Status: preliminary A; Introns: 33/1 Query Match
Best Local Similarity
Matches 10; Conser 41 YTGRGIRPVGRF N μ YXXRGIRPVGRF Conservative 52 12 93.1%; 83.3%; Score 54; DB 2; Pred. No. 0.0015; D; Mismatches 1 metabolite release from rat anterior the pituitary. <u>ب</u> Length 83; Indels R.; Masui, N.; Fuji, F.; PIDN:BAB03828.1; GSPDB:G Bacllius halodurans 0 Gaps 0

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A;Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DN A;Reference number: A92866; MUID:82078034
A;Recession: C92866
A;Accession: C92866
A;Accession: C92866
A;Cross-references: GB:V01127; NID:g15498; PIDN:CAA24345.1; PID:g15517
A;Cross-references: GB:V01127; NID:g15498; PIDN:CAA24345.1; PID:g15517
R;Dunn, J.J.; Studler, F.W.
J. Mol. Biol. 166, 477-535, 1983
A;Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locatio A;Reference number: S42283; MUID:83241725
A;Respion: S42301
A;Accession: S42301
A;Accession: S42301
A;Accession: S42301
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A;Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24402.1; PID:g15581
A;Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24402.1; PID:g15581
A;Cross-references: EMBL:V01146; NID:g431187; DIDN:CAA24402.1; PID:g15581
A;Cross-references: EMBL:V01146; NID:g15431187; DIDN:CAA24402.1; PID:g15581
A;Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24402.1; PID:g15581
A;Cross-references: EMBL:V01146; NID:
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A; Map position: 25.04-20
C; Superfamily: phage T7
C: Revwords: hydrolase
                                                                                                                                                                                                                                         R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heldelberg B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; R n, J.; Ermolaev.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
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c;Date: 01-Sep-1981 #sequence_revision 24-Sep-1981
C;Accession: B94615; C92866; S42301; A00785
R;Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, Se
                                                  A;Status: prelimlnary
A;Molecule type: DNA
A;Residues: 1-545 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein cc1602 [Imported] - Caulobacter crescentus C:Species: Caulobacter crescentus C:Species: Caulobacter crescentus C:Date: 20-Apr-2001 *text_change 10-May-2001 C:Date: 20-Apr-2001 *text_change 10-May-2001 C:Date: 20-Apr-2001 *text_change 10-May-2001 *text_change 10-May
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A; Accession: B94615
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A; Residues: 1-149 <DUi>
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     GB:AE005673; NID:g13422999;
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1; Mismatches
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PIDN:AAK23581.1; GSPDB:GN00148
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R;De Haan, M.; Masrse, A.C
submitted to the Protein S
A;Reference number: Z24480
A;Accession: T47959
A;Status: prellminary
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A; Gene: CC1602
C; Superfamily:
                                                                                             A; Map position: 3
A; Introns: 39/1; 6
A; Note: F15G16.60
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: G70875
                                                                                                                                                                                                                                                                                                                                                hypothetical protein F15G16.60 - Arabidopsis thallana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #t.C;Accession: T47959
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                                                                                                                                                          C;Genetics:
                                                                                                                                                                        A;Cross-references: EMBL:AL132959
A;Experimental source: cultivar Columbia;
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A; Residues: 1-790 <DEH>
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c;Species: Mycobacterlum tuberculosis
c;Species: Mycobacterlum tuberculosis
c;Date: 17-Jull-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
c;Accession: G70875
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                                                                                                                  678/2;
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Ce: strain H37Rv
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                 62.18;
50.08;
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Score 36; DB
Pred. No. 57;
3; Mlsmatches
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Pred.
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                 57;
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Holroyd,
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Similarity 6; Conserv

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R;Hosking, J.A., Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Althors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Alther Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D97897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 ribosomal protein L6 [imported] - Streptococcus pneumoniae (strain R6) C;Speciea: Streptococcus pneumoniae C;Capeciea: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001 C;Accession: D97897
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Biaszczak, L.; Burgett, S.; De
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C:Date: 03-Aug-2001 #aequence_revision 03-Aug-2001
C:Accession: D95026
C:Accession: D95026
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A;Accession: D95026
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Science 293, 498-506, 2001
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C;Superfsmily: Escherichia coli ribosomal protein
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C; Superfamily:
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A; Residues: 1-178 <KUR>
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A; Rcsidues: 1-178 < KUR>
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Best Local
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Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                     Score 35; DB
Pred. No. 19;
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C; Accession: B70821
R; Cole, S.T.; Brosch, R;
Connor, R; Davies, R;
Rsjandream, M.A.; Rogers,
Nature 393, 537-544, 1998
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A;Gene: phbA

G;Superfamily: acetyl-CoA scetyltransferase
C;Keywords: scyltrsnsferase; coenzyme A; homotetrsmer; ketone body metabolism;
F;2-391/Product: acetyl-CoA acetyltransferase #status predicted <MAT>
F;89/Active site: Cys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Peoples, O.P.; Masamune, S.; Walsh, C.T.; Sinskey, A.J.
J. Biol. Chem. 262, 97-102, 1937
A;Title: Biosynthetic thiolase from Zoogloea ramigera. III.
A;Reference number: A26121; MUID:87083504
A;Accession: A26121
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                                                                                    hypothetical protein Rv0982 - Mycobacterium tubercuiosis (strsin H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-
                                                                                                                                                               RESULT
B70821
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A;Map position: 2
A;Introns: 53/1;
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A; Residues: 1-391 < PEO>
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A; Residues: 1-272 <w00>
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Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Devlin, K.; Feltwell, T.; Genties, S.; Hamlin, N.; H. J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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43';
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R;Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, chardson, D.; Ermolaeva, M.D.; Vanathevan, J.; Bass, S.; Qln, H.; Dragoi, I.; Seile I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Scquence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID: 20406833
                                                      A;Cross-references: GB:AE004205; GB:AE003852; NID:99655740; PIDN:AAF94417.1; GSPDB:GN00:A;Experimental source: serogroup Q1; strain N16961; biotype El Tor
                                                                                                        A; Moiecuie type: DNA
A; Residues: 1-894 <HEI>
                                                                                                                                                                                                                                                                                                        C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C:Accession: E82721
                                                                                                                                                                                                                                                                                                                                                  DNA gyrase, chain A VC1258
C; Species: Vibrio choierae
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C; Superfamily: envZ protein; sensor histldlne kinase homology
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A;Accession: T45447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable two-component system sensor [imported] - Mycobacterlum leprae C;Spccies: Mycobacterlum leprae C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 02-Sep-2000
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A;Accession: B70821
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A;Experlmental source: cosmid L373
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|188 GLRPVGR 194
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February 1998
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A;Molecule type: DNA
A;Residues: 1-7463 <SAU>
A;Cross-references: EMBL:AL035640;
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: cdaPSI; SCQEDB:SCE63.03c
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A; Accession: T36248
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) Chain A; phage T4 DNA topoisomerase

Query Match
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0,

Qy 4 RGIRPVGR 11
Db 733 KGVRPMGR 740

RESULT 14
B82557
hypothetical protein XE2445 [imported] - Xyielia fastidiosa (strain 9a5c)
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CDA peptide synthetase I - Streptomyces coelicolor C;Specles: Streptomyces coelicolor C;Specles: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000 C;Accession: T36248
R;Saunder, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Ra:submitted to the EMBL Data Library, March 1999
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Dueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

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A; Molecule type: DNA
A; Residues: 1-1056 <SIM>
A; Residues: 1-1056 <SIM>
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO03849; NID: g9107631; PIDN: AAF85244.1;
A; Cross-references: GB: AEO04053; GB: AEO04053; AEO04055; AEO04055; AEO04055; AEO04055; AEO04055; AEO04055; AEO04055; AEO04055; AEO04055;
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C;Date: 18-Aug-2000 #sequence_revision
A; Status: preliminary; translated from
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A;Note: for a complete list of authors see reference number A59328 bel
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C;Species: Xyleiia fastidiosa
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PIDN:CAB38518.1;

GSPDB:GN00070;

SCQEDB:SCE63.03c

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C;Superfamily: acetate--CoA ligase homology; acyi carrier protein homology C;Kcywords: Carrier protein; phosphopantethelne; phosphoprotein F;516-1074/Domain: acetate--CoA ligase homology #Ritatus atypical <ACL1> F;1090-1118/Domain: acyi carrier protein homology <ACC12> F;1715-2184/Domain: acyi carrier protein homology <ACC12> F;2200-2268/Domain: acyi carrier protein homology <ACC2> F;2804-3249/Domain: acyi carrier protein homology <ACC2> F;2804-3249/Domain: acyi carrier protein homology <ACC2> F;2804-3332/Domain: acyi carrier protein homology <ACC4> F;4762-4830/Domain: acyi carrier protein homology <ACC4> F;4762-4830/Domain: acyi carrier protein homology <ACC4> F;5363-5786/Domain: acyi carrier protein homology <ACC4> F;5363-5786/Domain: acyi carrier protein homology <ACC4> F;5802-5870/Domain: acyi carrier protein homology <ACC4> F;6804-6858/Domain: acyi carrier protein homology <ACC5> F;6804-6951/Domain: acyi carrier protein homology <ACC6> F;6804-6
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Seklguchi M., Kitada C.,
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Pr
hormone) (Contains: Prolactin-releasing peptide
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Ninuma S., Habata Y., Fujii R., Kawamata Y., Hc

Kitada C., Masuo Y., Asano T., Matsumoto H., Se

Kitada C., Masuo Y., Asano T., Matsumoto H., Se

Kurokawa T., Nishimura O., Onda H., Fujino M.;

"A proiactin-releasing peptide in the brain.",

"A proiactin-releasing peptide in the brain.",

Nature 393:272-276(1998).
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Eukaryota; Metazoa: Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                               expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
TISSOE SPECIFICITY: Widely expressed, with highest levels in meduila oblongata and hypothalamus.
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Q9KGF6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
G1utamyl-trnA synthetase (EC 6.1.1.17) (Glutamate--trnA llgase)
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30-MAY 2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP)
hormone) (Contains: Prolactin-releasing pepti
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Bacteria; Firmicutes; B
Baciilus/Staphylococcus
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10; Conser
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22
53 PROLACTIN
53 PROLACTIN
53 AMIDATION
10544 MW; 08AC35Al
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Cetartlodactyla; Ruminantia; Pecora;
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83.38;
                                                                Baclllus/Clostridium
ns group; Bacillus.
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Pred. No. 0.00
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PROLACTIN-RELEASING PEPTIDE PI
AMIDATION (G-54 PROVIDE AMIDE
08AC35A13B0FA908 CRC64;
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Sekiguchi I
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PEPTIDE PRRP20.
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P00641;
21-JUL-1986
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between
the Euro
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SEQUENCE
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-!- CATALYTIC ACTIVITY: ATP + L-glutamate
                Dunn J.J., Studier F.W.;
"Nuclcotide sequence from the genetic
DNA to the beginning of gene 4.";
J. Mol. Biol. 148:303-330(1981).
                                                                                                                                                            Dunn J.J., Studier F.W.,
"Complete nucleotide sequence of ba
locations of T7 genetic elements.",
J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000924; tRNA-synt_1c.
InterPro; IPR001412; tRNA-synt_1.
Pfam; PF00749; tRNA-synt_1c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horikoshi K.; "Complete genome sequence of the alkaliphilic bacterium Bacillus "Complete genome sequence comparison with Bacillua subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami H., Nakasone
Fuji F., Nirama C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C-125 / JCM
MEDLINE-20512582; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP001507; BAB03828.1;
                                                                                               SEQUENCE FROM N.A.
MEDLINE-82078034,
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-83241725;
                                                                                                                                                                                                                                                                                                        NCB1_TaxID=10760;
                                                                                                                                                                                                                                                                                                                                                                                                             Endodeoxyribonuclease
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA
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SUBUNIT: MONOMER (BY SIMILARITY).
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54785
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Nakamura Y., O
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Last annotation update)
I (EC 3.1.21.2) (Endonuclease)
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Pred. No. 2.3;
2; Mismatches
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Y., Ogamawara N.,
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ATP (BY SIMILARITY).
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                                                                                              MAYTS W., Spieker N., Van Roy N., De Paepe A., De Boulie K., Willems P.J., Van Hul W., Versteeg R., Spieleman F.; "Refined physical mapping and genomic structure of the EXTL1 genomitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: APPEARS TO BE A TUMOR SUPPRESSOR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Type 11 membrane protein. Endoplaamic reticulum (By similarity).

-!- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97189339; PubMed-9037597; Wise C.A., Clines G.A., Massa H., Traak B.J., "Identification and localization of the gene of the multiple exostoses gene family."; Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXLI_HUMAN STANDARD; PRT; 676 AA. 092935; 15-JUL-1998 (Rei. 36, Created) 15-JUL-1998 (Rei. 36, Last sequence update) 16-OCT-2001 (Rei. 40, Last annotation update) 16-OCT-2001 (Rei. 40, Last annotation update) 16-OCT-2001 (Rei. 40, Last annotation update) 15-OCT-2001 (Rei. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iab-sib.ch).
Thia SWISS-PROT entry is copyright. It is produced through a collaboration between the Swias Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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SEQUENCE
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Homo mapiens (Numan)
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IR; S42301; S4230.

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149 AA; j
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17172 NW; D092AA28E3743BC1 CRC64;
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MEDLINE=99128221; PubMed=9929392;
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NCBI_TaxIO=55529;
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AF083624 AAD02840.1;
AF083625 AAD02840.1;
AF083626 AAD02840.1;
AF083627 AAD02840.1;
AF083628 AAD02840.1;
AF083629 AAD02840.1;
AF083631 AAD02840.1;
                                                                                                                                                                                                                                                        S.L., Liu X.-O., Douglas S.E.;
large ribosomal protein gene evolutionary
organization, sequence and evolutionary
hem. Mol. Biol. Int. 41:1035-1044(1997).
   SWISS-PROT entry
een the Swiss Ins
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    38, Last annotation
ribosomal protein L6.

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Best Local S
Matches 7
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InterPro; IPRO0238; Ribosomal_L6_1.
Pfam; PPF00347; Ribosomal_L6; 1.
PRINTS; PR00059; RIBOSOMALL6.
PRODOm; PD002236; Ribosomal_L6; 1.
PROSITE; PS00525; RIBOSOMAL_L6_1; 1.
RIBOSOMAL PRODECTION CONTROL PROSITE; PS00525; RIBOSOMAL_L6_1; 1.
RIBOSOMAL PRODECTION CONTROL PROPERTY PS00525; RIBOSOMAL_L6_1; 1.
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P07097;
01-APR-1988
01-APR-1990
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIR-ATCC 19623 / I-16-M;

MEDLINE-87083504; PubMed-2878929;

MEDDINE-8.7083504; PubMed-2878929;

Peoples O.F., Masamune S., Walsh C.T., Sinskey

"Biosynthetic thiolase from Zoogioea ramigera.

Characterization of the structural gene.";

J. Blol. Chem. 262:97-102(1987),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are use by non-profit institutions as long as its modified and this statement is not removed. Usage entitles requires a license agreement (See http://or send an email to license@isb-sib.ch).
                         This
                                                                                                                                 Palmer M.A.J., Differding E., Gamboni R., Will: Walsh C.T., Sinskey S.J., Masamune S.; Walsh C.T., Sinskey S.J., Masamune S.; Biosynthetic thiolase from Zoogloea ramigera. mechanism involving Cys-378 as the active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                              Characterization of the genes encodin acetoacetyl COA reductase.";
J. Biol. Chem. 264:15293-15297(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       РИВА
                                                                                                         J. Biol. Chem. 266:8369-8375(1991).
-!- CATALYTIC ACTIVITY: 2 acetyl-CoA -
                                                                                                                                                                                       MUTAGENESIS OF CYS-377.
MEDLINE-91217075; PubMed-1673680;
                                                                                                                                                                                                                                                                   REVISION TO 130.
MEDLINE-89359356; PubMed-2670935;
Peoples O.P., Sinskey A.J.;
"Poly-beta-hydroxybutyrate blosynthesis"
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Bacteria; Proteoba
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                              PATHWAY: FIRST STEP IN POLY-BETA-HYDROXYBUTYRATE BIOSYNTHESIS.
SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE TNIOLASE FAMILY.
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PIR; A26121; XXG2AC.
PIR; A27754, a27754
HSSP; P27796; 1AFY.
InterPro; 1PR002155; Thiolase.
Pfam; PF00108; thiolase.[].
Pfam; PF02803; thiolase.[].
PROSITE; PS00098; THIOLASE_1; 1.
PROSITE; PS00099; THIOLASE_3; 1.
PRDSITE; PS00099; THIOLASE_3; 1.
PRDSITE; PS000737; THIOLASE_3; 1.
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MUTAGEN
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-I- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
STRANDED DNA 1N AN ATP-DEPENDENT MANNER AND ALSD CATALYZES THE
INTERCONVERSION OF DITHER TOPPLOGICAL ISDMERS OF DDUBLE-STRANDED
DNA RINGS, INCLUDING CATENANES AND KNDITED RINGS.

-I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
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STRAIN-2148/89;
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01-FEB-1996 (Rel. 33, Last agence update)
01-NDV-1997 (Rel. 35, Last annotation update)
DNA gyrase subunit A (EC 5.99.1.3).
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                                                                                                                                                                                                                                                                                                                                                                     Dppegaard H., Sorum H.;
"gyrA mutations in quinolone-resistant isolates
Aeromonas salmonicida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DF 33-179 FRDM N.A. STRAIN-ATCC 14174;
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
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01-FEB-1996
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  European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed
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OF double-stranded DNA.
SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS
BREAKAGE AND READINING: THE B CHAIN CATALYZES A
ENZYME FORMS AN A2B2 TETRAMER.
                                                                 SWISS-PROT entry is copyright. It is produced through a sen the Swiss institute of Bioinformatics and the EMBI
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                                                                                                                                                                                              CHAIN
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Hypothetical protein y
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STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-STRAIN-K1 Bloch C.A., Per Blattner F.R., Plunkett G. III, Bloch C.A., Per Riley M., Collado-Vides J., Glasner J.D., Rode Gregor J., Davis N.W., Kirkpatrick H.A., Goeden Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002205; DNA_topoisoIV.
Pfam; PF00521; DNA_topoisoIV; 1.
SMART; SM00434; TDP4C; 1.
Isomerase; Topoisomerase; DNA-binding.
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EMBL; L42453; AAA87239.1;
HSSP; P09097; IAB4
                                                                                                                                                                                                                                        Hypothetical protein;
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EMBL; AE000359; AAC75799.1; ALT_INIT.
ECoGene; EG13116; ygcI.
Hypothetical protein; Signal; Complete
                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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YGCI DR B2757
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P46228;
01-NOV-1995
SEQUENCE FROM N.A.

MEDLING-97061201; PubMed-8905231;

Kaneko T., Sato S., Kotanl H., Tanaka A., Asamizu E., Nakamura Miyajina N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchl T., Matsuno A., Murakl A., Nakazaki N., Naruo K.,
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P73530;
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MEDLINE-95166170; Pt
Suglta M., Suglta C
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P05055; 1SRO.
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"Sequence analysis of the genome of the unicellular cyanobacterlum Synechocystls sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."

DNA Res. 3.109-136(1996).
                                                        annotation
reveals 17
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Yamada M
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PubMed=9799793;
                                                                                                                                                                                                                  "Molecular cloning of transferrin receptor transferrin receptor-like family."; J. Blol. Chem. 274:20826-20832(1999).
                                                                                                                                                                                                                                                                                               MEDLINE-99340005; Pubb
Kawabata H., Yang R.,
                                                                                                                                                                                                                                                                                                      TISSUE-Erythroleukemia, and Myeloid leukemia MEDLINE-99340005; PubMed-10409623; Kawabata H. Yan-
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Mammalla; Eutheria;
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204 RGIKPYGAF 212
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receptor protein 2 (TfR2).
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Isogai T., Ota T., Hsyashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nsgai K., Sugano S., Shiratori A., Sudo H., Wagstsumb M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara h Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S Watanabe S., Kimura K., Muraksmi K., Ishii S., Rawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Nakamura Y., Nagahari K., Wasuho Y., NEDO human cDNA sequencing project.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by snd for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send sn email to license@isb-sib.ch).
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Carells M., Majorano N., Tota
"The gene TFR2 1s mutated in
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                                                                                                                                      EMBL; AF067864; AAD45561.I;
EMBL; AF053356; AAC78796.I:
EMBL; AK022002; BABI3951.1;
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"The gene TFR2 is
7q22.";
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                                              InterPro; IPR003137; PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Mediates cellular uptake of transferrin-bound non-iron dependent menner. May be involved in iron metal hepatocyte function and erythrocyte differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEDUS: The variant lys-172 found in hereditary hemochromatosis type III affects the putative initiation the beta isoform thus preventing its translation. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamms; are produced by alternative splicing.
TISSUE SPECIFICITY: predominantly expressed in liver, while the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lacks the transmembrane domain and is probably intracellular. ALTERHATIVE PRODUCTS: 3 isoforms; alpha (shown here), beta and
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BUBCELLULAR LOCATION: Type II membrane
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                                                                    604250;
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PA; 1.
Glycoprotein;
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Hayashi K.,
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Receptor;
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)., Camaschella C.;
sferrin 2 in hemochromatosis
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  Signal-anchor;
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VARSPLIC
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                                                                                This SWISS-PRDT entry is copyright. It is produced through a colial between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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01-DCT-1996 (Ref.
16-DCT-2001 (Ref.
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                            EMBL; D30714; BA
MEROPS; S33.001;
                                                             or send an
                                                                                                                                                                                                                                        J. Blochem. I16:818-825(I994).
                                                                                                                                                                                                                                                            Kitazono A., Kitano A., Tsuru D., Yoshimoto T.; "Isolation and characterization of the prolyI aminopeptidase gene (Pap) from Aeromonas sobria: comparison with the Bacillus coagular
                                                                                                                                                                                                                                                                                          SEQUENCE FROM H.A., AND PARTIAL SEQUENCE MEDLINE-95189781; PubMed-7883756;
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                        P46547;
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                                                                                                                                            peptide.
SUBUNIT: HDWOTETRAMER.
SUBCELLULAR LOCATION: Cytoplasmic.
SUBCELLULAR LOCATION: PEPTIDASE FAMILY S33.
                                                                                                                                                                                             CATALYTIC
                                                                                                                                                                                                       FUHCTION: HIGHER ACTIVITY TOWARD LONG PEPTIDES. HYDRDXYPROLINE BETA-HAPHTHYLAMIDE WITH ALMOST A AS OH PROLINE BETA-NAPHTHYLAMIDE.
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                                                           requires a license sgreement (S
sn email to license@isb-sib.ch).
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Pred. No. 40;
1; Mismatches
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R -> RIPLSAQV (IH F
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INTERCHAIN (POTENTIAL)
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InterPro;

IPR000073; IPR000379; IPR002410;

Abhydrolase.
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P50336;
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INIT_MET
ACT_SITE
                                                                                                                                                                              Meissner P.N., Dailey T.A., Hift R.J., Ziman M., Corrigall A.V., Roberts A.G., Meissner D.M., Kirsch R.E., Dailey H.A.; "A R59W mutation in human protoporphyringen oxidase results in decreased enzyme activity and is prevalent in South Africans wit variegate porphyria.; htt. Genet. 13:95-97(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95229621; pubMed=7713909;
Mishimura K., Takketani S., Inokuchi H.;
"Cioning of a human cDNA for protoporphyrinogen oxidase
complementation in vivo of a hemG mutant of Escherichia
J., Biol. Chem. 270:8076-8080(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPOX.
Homo sapiens (Human).
  missense mutation in the protoporphyrinogen oxidase
Arch. Dermatol. Res. 290:441-445(1998).
-1- FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF
                                        Frank J., Poh-Fitzpatrick M.B., King L.E. Jr., Christiano A.M. "The genetic basis of 'Scarsdale Gourmet Diet' variegate porph missense mutation in the protoporphyrinogen oxidase gene.";
                                                                                                            VARIANT VP CYS-152.
MEDLINE-98434271; PubMed-9763307;
                                                                                                                                                                                                                                                                                                                                                                                                  Grandchamp B., Hordmann Y.;
"Mutations in the protoporphyrinogen
variagate porphyria.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deybach J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human protoporphyrinogen oxidase: expression, purification, and characterization of the cloned enzyme."; Protein Sci. 5:98-105(1996).
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01-OCT-1996 (Rel. 34, Last seg
15-DEC-1998 (Rel. 37, Last ann
Protoporphyrinogen oxidase (EC
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MEDLINE-96367087; PubMed-8771201;
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BY SIMILARITY.
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-!- COPACTOR: CONTALHS ONE FAD PER NOWODIMER.

-!- PATHWAY: PENULTIMATE STEP IH HEME AND PORPHYRIH BIOSYNTHESIS.

-!- PATHWAY: PENULTIMATE STEP IH HEME AND PORPHYRIH BIOSYNTHESIS.

-!- SUBBURLIT: HOMODIMER.

C -!- SUBBURLIT: ROMODIMER.

C -!- SUBCELLIAR LOCATION: BOUND TO THE MITOCNONDRIAL INNER MEMBRANE

CC -!- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUHG,

CC -!- DISEASE SEELETAL MUSCLE, KIDHEY, AND PANCREAS.

CC -!- DISEASE DEFECTS IN PPOX ARE THE CAUSE OF PORPHYRIA VARIEGATA

CC (VP), A DISEASE CHARACTERIZED BY SKIN HYPERFRIGHENTATION AND HAIR

CC (YP), A DISEASE CHARACTERIZED BY SKIN HYPERFRIGHENTATION AND HAIR

CC HYPERTRICHOSIS, ASSOCIATED WITH ACUTE ATTACKS, LIKE THOSE OF ACUTE

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1: sp_archea:*

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5: ap_inverteb;

6: sp_mammanl:*

7: sp_mhc:*

8: sp_organeli;

9: sp_phage:*

10: sp_plant:*

11: sp_rodent;

12: ap_virus:*

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Q9w194 drosophila
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O54728 rattus norv
Q979a0 thermoplasm
Q9a797 caulobacteri
O50431 mycobacteri
Q9m371 arabidopsis
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Cypriniformea; Cyprinidae; Carassius.
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MEDLINE-2112554; PubMed-11222590;
MEDLINE-21125554; PubMed-11222590;
Pajunen M.I., Kiljunen S.J., Soederholm M.

"Complete genomic sequence of the lytic ba
"Complete genomic sequence of the lytic ba
Yersinia enterocolitica serotype O:3.";
J. Bacteriol. 183:1928-1937(2001).

EMBL; AJ251805, CAB65804.1; -
SEQUENCE 153 AA; 17640 MW; 211571BBDE
                                01-MAY-2000
01-MAY-2000
01-DEC-2001
CG2812 PROTE
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SUDMILTED (MAY-2001) to The EMBL/GENBANK/DDBJEMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; asDNA
T7-like phages
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01-DEC-2001
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      Drosophila
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NCBI_TaxID=1894;
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8; Conserv
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ilarity 100.0%
Conservative
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                                              Created)
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polyketide ge
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bacteriophage phiyeO3-12
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Q92NX4
Q92NX4;
01-DEC-2001
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PROSITE; PS50082; WD_REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_REGION;
Repeat; WD repeat.
SEQUENCE 348 AA; 38787 MW; B00105
                                                                                                           PRINTS: PR00320; GPROT SMART; SM00320; WD40;
                                                                                                                                    -I- SIMILARITY: CONTAINS 7 WD
EMBL; AE003462; AAF47100.1; -
FlyBase; FBgn0034931; CG2812.
InterPro; IPR001680; WD40.
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         1 YXXRGIRPVGRF
YDIRGNRPIQRE
                                Similarity
7; Conserv
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilldae; Drosophila.
                                Conservative
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266
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                                                                          38787 MW; B001050A0EF685A0 CRC64;
                                         58.3%;
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                                         Score 37;
Pred. No.
                                Mismatches
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                                                 Length 348;
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RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,

RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,

RA Butry M., Bowser L., Buhrmester J., Cadleu E., Capela D., Chain P.,

RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,

RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,

RA Hernandez-Lucas 1., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,

RA Hernandez-Lucas 1., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,

RA Kahn M.L., Kalman S., Keating D.H., Kias E., Komp C., Lelaure V.,

RA Kahn M.L., Kalman S., Keating D.H., Kias E., Komp C., Lelaure V.,

RA Kahn M.L., Kalman S., Keating D.H., Kias E., Komp C., Lelaure V.,

RA Kahn M.L., Kalman S., Keating D.H., Wong C., Lelaure V.,

RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,

Vorhoelter F.J., Weldner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;

RT *The composite genome of the legume symbiont Sinorhizobium meliloti.";

RELE: AL591789; CAc46612.1;

Complete F. Thebaute Symbiont Sinorhizobium meliloti.";
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054728;
01-JUN-1998 (TrEMBLrel. 00
01-JUN-1998 (TrEMBLrel. 00
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                        Takemori H., Zolotaryov F.N., Ting L., Urbain T., Komataubara T.,
Hatano T., Dhamoto M., Tojo H.;
"Identification of functional domains of rat intestinal phospholipaae
B/lipase. Ita cDNA cloning, expression, and tissue distribution.";
J. Biol. Chem. 273:222-2231(1998).
EMBL; D63648; BAA73813.1;
-InterPro; IPRO1087; Lipase_GDSL.
pfam; PF00657; Lipase_GDSL.
pram; PF00657; Lipase_GDSL.
SEQUENCE 1450 AA; 161088 MW; 4555898C8FD91F45 CRC64;
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                                                                                                                                                                                                                                                                                                   STRAIN-SD; TISSUE-SMALL INTESTINE;
MEDLINE-98113187; PubMed-9442065;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCB1_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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YQARQLKPlGKF
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41.7%;
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54.5%;
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Pred. No. 1.5e
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86;
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1.5e+02;
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Q9A7W7;
01-JUN-2001 (TrEMBLrel. 17, G1
01-JUN-2001 (TrEMBLrel. 17, La
01-DEC-2001 (TrEMBLrel. 19, La
HYDDIHETICAL PROTEIN CC1602.
                                        Nierman W.C., Feidbiyum T.V., Laub M.T., Paulsen I.T., Neison K. Elsen J., Heidelberg J.F., Alley M.R., Ditha N., Maddock J.R., Potocka I., Neison W.C., Newton A., Stephens C., Phadke N.D., El DeBoy R.T., Dodaon R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry Utterback T., Tran K., Wolf A., Venathevan J., Ermolaeva M., Whi Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome aequence of Caulobacter crescentus."; "Complete genome aequence of Caulobacter crescentus."; "Embit, AE005835, AAK23361.1; "."

TIGR, CC1602, "."
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STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDLINE-20570466; PubMed-11121031;

MEDLINE-20570466; PubMed-11121031;

Kawashima T., Amano N., Koike H., Makino S.-1., Higuchi S.,

Kawashima T., Watanabe K., Yamazaki M., Kanehori K., Ka

Munoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q979S0
Q979S0;
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01-0CT-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
TVG1120468 PRDTEIN.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FRDM N.A.
STRAIN-ATCC 19089
MEDLINE-21173698;
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InterPro; IPRO02035; vWFA.
Pfam; PF01882; DUF58; 1.
SMART; SM00327; VWA; 1.
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Archaea; Euryarchaeota;
Hypothetical protein; Complete SEQUENCE 545 AA; 60175 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
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AREDLINE-98295987; PubMed=9634230;
AREDLINE-98295987; PubMed=9634230;
AREDCOCK S. F. Berosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
AREDCOCK K., Basham D., Brown D., Chillingworth T., Connor R.,
AREDCOCK K., Basham D., Brown D., Chillingworth T., Connor R.,
AREDCOCK K., Devlin K., Feltwell T., Gentles S., Hamlin N., Hoiroyd S.,
AREDCOCK S., Devlin K., Feltwell T., Gentles S., Murphy L.,
AREDCOCK S., Jagels K., Krogh A., McLean J., Moute S., Murphy L.,
AREDCOCK S., Seeger K., Skelton S., Squares S., Squares R.,
AREDCOCK S., Whitehead S., Barrell B.G.,
AREDCOCK S., WHITEHEAD, WALLEY S., WHITEHEAD, 
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Best Local S
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01-001-1998 (TrEMBLrel. 06, Crea
01-JUN-1998 (TrEMBLrel. 06, Last
01-DEC-2001 (TrEMBLrel. 19, Last
2,4-DIENOYL-COA REDUCTASE.
FADN QR RV1175C OR MTV005.11C.
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SEQUENCE
                                                              O9M371 PRELIMINARY; PRT; O9M371, O1-OCT-2000 (TrEMBLrel. 15, Created) O1-OCT-2000 (TrEMBLrel. 15, Last seq O1-DEC-2001 (TrEMBLrel. 19, Last ann HYPOTHETICAL 87.4 KDA PROTEIN. F15G16.60.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Virldiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
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STRAIN-H37RV;
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Bacteria; Firmicutes; Actlnobacteria; Actinobacteridae;
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PROSITE; PS00225; CRYSTALLIN_BETAGAMMA;
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pred. No. 1e+02;
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              Nlnomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodairs Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara Katsuta M., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irle Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saico K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyam Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai
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01-DEC-2001 (TIEMBLIE1. 19, Last sequence update)
01-DEC-2001 (TIEMBLIE1. 19, Last annotation update)
01-DEC-2001 (TIEMBLIE1. 19, Last annotation update)
CDNA FLJ32096 FIS, CLONE OCBBF2001075.
Homo sapiens (Numan).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrate Mammalla; Eutheria; Primates; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO56559; Bab71243.1: -
SEQUENCE 144 AA; 15589 MW; 9CCD9EAE7F735881 CRC64;
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EU Arabldopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL132959; CAB71097.1;
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De Haan M., Maarse A.C., Gri
Mayer K.F.X., Quetier F., Sa
Submitted (NOV-1999) to the
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NCBI_TaxID=3702;
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Catarrhini; Hominidae;
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A Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
A Durkin A.S., Gwinn M., Kolonay J.F., Melson W.C., Peterson J.D.,
A Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
A Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hanson C.L.,
A McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
A Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
A Dougherty B.A., Morrison O.A., Hollingshead S.K., Fraser C.M.;
Tomplete genome sequence of a virulent isolate of Streptococcus
T pncumoniae.;
Science 293:498-506(2001).
R EMBL; AE007336; AAK74405.1; -.
R TIGR; SP0225; -.
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042924;
01-JAN-1999
01-JAN-1999
01-JUN-2001
                                                                                                                WOOD V., Rajandream M.A., Barrell B.G., Beck A., Reinhardt Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. EMBL; ALO21748; CAAL6870.1; -. InterPro; IPR001005; Myb_DMA_bind. PROSITE; PS00037; MYB_1; UNKNOWN_1. Hypothetical Protein. BFE0EB29217107A8 CRC64; SEQUEMCE 272 AA; 30901 MW; 8FE0EB29217107A8 CRC64;
                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.
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InterPro; IPR002358; Rlbosomal_L6_1.
Pfam; PF00347; Rlbosomal_L6; 1.
PRINTS; PR00059; RIBOSOMALL6.
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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STRAIN-MAFF303099;
MEDLINE-21082930; PubMed=11214968;
Kaneko T., Makamura Y., Sato S., Asamizu I
Kaneko T., Makamura Y., Ishikawa A., Kaww
Watanabe A., Idesawa K., Ishikawa A., Kaww
Kishida Y., Kiyokawa C., Kohara M., Matsum
Mochizuki Y., Nakayama S., Makazaki M., Si
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                       MEDINE-98295987; PubMed=9634230;
MEDINE-98295987; PubMed=9634230;
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Moule S., Murphy
Oliver S., Jagels K., Kroph A., McLean J., Moule S., Murphy
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
              *Deciphering the blology of Mycobacterium tuberculosis from complete genome sequence.*;
Nature 393:537-544(1998)
-I- SIMILARITY: TO PROKARYOTE SEMSORY TRAMSDUCTIOM PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O53895, PRELIMIMARY, PRT;
O53895, O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequ
O1-DEC-2001 (TrEMBLrel. 19, Last anno
PUTATIVE TRO-COMPOMENT SENSOR.
RV0982 OR MTV044.10.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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DMA Res 7:331-338(2000).
EMBL; AP003015; BAB54606.1; -.
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01-0CT-2001 (TrembLrel.
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MLR9222 PROTEIM.
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A., Kawashima K., Kimura
Matsumoto M., Matsuno
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DR InterPro: IPR003660; HAMP.

DR InterPro: IPR003661; His_Kin.

DR InterPro: IPR003661; His_Kin.

DR InterPro: IPR003661; His_Kin.

DR InterPro: IPR00361; His_Kin.

DR InterPro: IPR00361; His_Kin.

DR Pfam; pP00512; HAMPse_c; 1.

DR Pfam; pP00512; HAMP; 1.

DR SMART: SM00387; HATPase_c; 1.

DR SMART: SM00381; Hiska; 1.

Complete proteome; Kinase: Phosphorylation; Sensory transduction;

KW Transferase.

SMART: SM00381; Hiska; 1.

Complete proteome; Kinase: Phosphorylation; Sensory transduction;

KW Transferase.

GO SEQUENCE 504 AA; 54407 MW: 26792A71AC432232 CRC64;

Query Match

Best Local Similarity 85.7%: Pred. No. 1.2e+02:

Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Hatches 6; Conservative 1; Mismatches 0; Gaps 0;

DB 188 GLRPVGR 11

Db 188 GLRPVGR 194

Search completed: September 13, 2002, 09:29:23

Job time: 1068 sec
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ine G pr	ē	Human type G prote		releasing	Bovine CRH releasi	Human oxytocin sec	ytocin secr	oxytocin	Bovine pitultary-d	an 19P2	l ligand po	ğ	pe G p	o o	ic G prote	н			rele	CRH releasing prot	Human CRH releasin	releasing	ne ČRH r	ligand	iigand	Íga	ln secret	n oxytocl	yrocin secr	oxytocin s	pitultary-	e pituitary	Human type ligand	

## ALIGNMENTS

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WPT; 1999-009423/01.		Fukugumi S, Hinuma S;	(inte ) intern them int eit.	CHARGO ANNOUN CHO THO		28-1007. 07th-010007/		27-APR-1998; 98WO-JP01923.		05-NOV-1998		WO9849295-A1.		Mus sp.		gene therapy; transgenic animal; epitope.	secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;	Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;	Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;	tissue; screen; therapeutlc; blnding; senile dementia; ligand; murine;	GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;	Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;		Murine pituitary-derived ligand polypeptide antigenic epitope.		10-MAR-1999 (first entry)		AAW95178;		AAW95178 standard; Protein; 10 AA.	AAW95178	T.T. 1

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PIXAX PRESENTATION OF THE 
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CC antibody.
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Fujii R,
Kawamata
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Fukusumi S,
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This peptide contains the partial C-terminal sequence of the synthetic citiand polypeptide 19p2-13i which is capable of binding to a G protein-coupled receptor protein. This peptide Is used as an antigen to protein-coupled receptor protein. This peptide Is used as an antigen to CC prepare rabbit anti-bovine 19p2-131 antibodies which are used in binding consays. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This itgand could have specific craphications as a prophylactic or therapeutic agent for dementla, complications as a prophylactic or therapeutic agent for dementla, complications as a prophylactic or therapeutic agent for dementla, complications, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, typer-and polyphagia, hyperlipidaemia, hypercholesterolaemia, compersiyeeridaemia, hypercholesterolaemia, compersiyeeridaemia, hypercholesterolaemia, compersiyeeridaemia, hypercholesterolaemia, compersiyeeridaemia, hypercholesterolaemia, compensiyeeridaemia, hypercholesterolaemia, compensiyeeridaemia, bone fracture, trauma, atopic dermatitis, osteoporosis and compensions because can allocate and compensions and accuration and a compensions of the compensions and a c
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Fujii R,

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ion or placental function, e.g. for treating menopausal
me, tumours, autoimmune disease or abnormal pregnancy
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y mechanism; centrai nervous system; pancreat
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        The Invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or derivative. The antibodies can be used in diagnosis or to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY49295 standard;
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                                                   Disclosure; Page 26;
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                                                                                                                                                                        21-MAY-1998;
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                                                                        monoclonal antibodies, dying diseases related
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central nervous system; pancreat
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                                                                                The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of projectin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                           Disciosure; Page 27; 73pp; Japanese.
                                                                                                                                                                                                                                   New monoclonal antibodies, studying diseases related t
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                                                                                                                                                                                                                                                                                                                                              21-MAY-1998;
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9; Conservative
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regulatory mechanism; central nervous system; pancreat
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100.08; Pr
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Pred. No.
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0.0082;
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syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipideamia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatold arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebeilar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
                                                                                                                                                                                                ligand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic prophylactic or therapeutic agent for dementia, depression, hyperkinetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; pro
 Sequence
                                                                                                                                                                                                                                                                                                           This sequence represents a peptide fragment from a novel
                                                                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                          function
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Y, Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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  central nervous system, pancreas and pituitary gland
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RESULT
AAW31387
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                                                                                                                                      CC This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 33 to 52 of the CC sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC hyperilpiddemia, hypercholesteroldemia, hyper-and polyphagia, CC hyperilpiddemia, hypercholesteroldemia, hypergiyceridaemia, for the hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC transient brain ischæmia, epilepsy, amylotrophic lateral sclerosis, CC coute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or collegosatetia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
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Kawamata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand poptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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DB: AAV02424.
RGIRPVGRF
                               h 94.1%; Similarity 100.0%; 19; Conservative 0;
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/, Kitada C;
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                               %; Score 48; DB
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0; Mismatches
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                                                DB 18;
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12

r9irpvgrf

20

3 RGIRPVGRF 11

Matches

Conservative

0

Mismatches

0

Indels

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Gaps

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RESULT
AAW31374
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                                                                                                  CC This sequence represents a peptide fragment of a novel bovine pituitary CC derived ligand corresponding to amino acid residues 34 to 53 of the Sequence in AAW31368 and is used in an assay to monitor ligand binding CC to the G protein-coupled receptor protein. Pharmaceutical compositions CC central nervous system modulator or a pancreatic function modulator. a CC central nervous system modulator or a pancreatic function modulator. CC This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, CC disturbance secretory disease, hyper-and polyphagia, cC hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia, hyperglyceridaemia, hypertipidaemia, hyperprotactinamia, diabetes, cancer, pancreatitis, renal disease, hyperprotactinamia, diabetes, cancer, pancreatitis, spinal injury, CC transient brain ischaemia, amylotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, CC trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility cand/or oilgogalactia, Asaays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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modulator; pituitary; central nervous system; pancreas; prophylactic;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic agent.
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                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligand peptide for G protein-coupled receptor - a
function in the central nervous system, pancreas
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Similarity
9; Conser
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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                94.18;
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                Score 48;
Pred. No.
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              DB 18;
0.011;
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                                                                                                                                      Query Match
Best Local
                                                                                                            Matches
                                                                                                                                                                                                                                                                                          pituitary adenomatosis, brain tumour, emmentopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, gaiactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan ayndrome or dyazoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoms, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a grottein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypometabolism. They can by used for promoting syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammai and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing prolactin secretion can be used for treating or preventing prolactin secretion can be used for treating or preventing pituitary adenomators to the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for treating or preventing of the secretion can be used for the 
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                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of G protein-coupled receptor ligands - for modulating projectin secretion or placental function, e.g. for treating menopausal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-105614/09.
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                                                      RGIRPVGRF 11
rgirpvgrf 20
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                                                                                                                                      Similarity
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                                                                                                            Conservative
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                                                                                                                                      94.18;
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                                                                                                                                      Score 48;
Pred. No.
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0.011;
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rgirpvgrf RGIRPVGRF

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RESULT 11
AAW97234
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is used in the course of the invention. The specification describes
an agent for modulating proiactin secretion which comprises a
ligand polypeptide or a salt, for a grotein-coupled receptor (GPCR)
protein. The agents for promoting proiactin secretion can be used for
treating or preventing hypowearianism, goneryst carogenesis menopeusal
syndrome, euthyroid or hypometabolism. They can by used for promoting
lactation in a domestic manmal and as an aphrodisiac. The agents for
inhibiting prolactin secretion can be used for treating or preventing
pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
prolactinoma, infertility, impotence, amenorrhes, galactorrhes,
caromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
for briefinhibitory agents can also be used as contraceptives. The agents for
modulating pitacental function can be used for treating or preventing
choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,
abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    menopausai syndrome; euthyroid; hypometabollam; lactation; pluitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; proiactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly. Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes Albright syndrome; lymphoma; Sheehan syndrome; dyazoospermla; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometaboliam; irruption mole; abortion; unthrifty fetus; abnormal saccharometaboliam;
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                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Page 154; 241pp; English.
 Similarity
9: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-coupled receptor ligands - for modulating projectin or placental function, e.g. for treating menopausal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumours, autoimmune disease or abnormal pregnancy
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                                                                                          20
 Conservative
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                  94.1%;
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score 48; DB; Pred. No. 0.0 0; Mismatches
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                  DB 20;
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RESULT 12

AAW97236 standard;

peptide;

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Is used in the course of the invention. The specification describes

an agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a sait, for a G protein-coupled receptor (GPCR)

CC protein. The agents for promoting prolactin secretion can be used for

CC treating or preventing hypocovarianism. They can by used for promoting

CC syndrome, cuthyroid or hypometabolism. They can by used for promoting

CC inhibiting prolactin secretion can be used for treating or preventing

CC inhibiting prolactin secretion can be used for treating or preventing

CC pluitary adenomatosis, brain tumour, emmenlopathy, autolumune disease,

CC prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

CC acromegaly, Chlari-Frommel syndrome, Argonz-del Castilo syndrome,

CC acromegaly, Chlari-Frommel syndrome, Argonz-del Castilo syndrome,

CC rorbes-Albright syndrome, Sheehan syndrome or dyszoospermia.

CC The Inhibitory agenta can also be used as contraceptives. The agents for

CC modulating placental function can be used for treating or preventing

CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fettus,

CC charian saccharametabolism abnormal linidmetabolism or particular.
                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use Of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumoura, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypocvarianism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1997;
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|rgirpvgrf 20
                                    RGIRPVGRF 11
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                                                                       Similarity 100
9; Conservative
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                                                                                       Score 48;
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The invention relates to a murine pitultary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pitultary, central nervous ayatem, pancreas and other CC function can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementis, Alzheimer's, Parkinson's or Huntington's CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC disease; creutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genea, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide sequences; in receptor-binding assays; for production of Ab and CC related sequences; in receptor-binding assays; for production of Ab and CC animals. The present sequence represents a bovine genome-derived ligand CC ligand for the sequence represents a bovine genome-derived ligand collypeptide fragment which is similar to the murine ligand-polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancress, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; transgenic animal; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer'a diaeaae; Parklnaon's disease; Huntington's diaease; drug;
Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
secretion; diabetes; cancer; rheumatoid arthritla; epilepsy; vaaopressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pltultary-derived ligand polypeptide; G-protein coupled orp GPR10; UHR-1; modulator; pitultary; central nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW95191 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukugumi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1997;
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RESULT 14 AAW95175

AAW95175 atandard; Protein; 20

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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing GPR10 (human) or UHR-1 (rat) are used to produce a recombinant GC ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a GC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's GC diabetes; achizophrenia; disorders of growth hormone accretion; cancer; CC operative nutritional status and as vasopressor. Transgenic animals GC carrying the idgand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding DNA or its mutein are used to GC disease, for drug screening and as source of cell lines. The ligand CC polypeptide DNA is used as a source of probes and primers; to identify CC antispen; in receptor-binding assays; for production of Ab and CC antispen; and may also be used for the preparation of anti-iigand polypeptide con antiscre; the disease is not cancer and to develop transgenic animals. Sequences AAM95174 to AAM95178 represent antigenic canchides.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzhelmer's disease; parklnson's disease; Huntington's disease; drug; creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritia; epilepsy; vasopressor;
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 26; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide ligand for orpha-
for treating disorders of centra-
pancreas, and for drug screening
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for orphan G protein coupled receptors - of central nervous system, pituitary and
Score 48;
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DB 20;
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                                                                                                                                                    This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placents, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                             Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin aecretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow caeaarean aection; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                       Claim 5; Page 51; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-452298/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine oxytocin secretion promoting peptide SEQ ID NO:
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                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                  medicine
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ian/6B_COMB.pep:*
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-09-	-09-421-208	-08-776	-08-776-971	-776-971	-08-77	-09-172	-09-10	-09-105-678 <i>z</i>	-09-10	US-09-105-678A-9	-09-10S	-09-105	-09-	US-09-421-208-42	-09-421	-08-776-971	US-08-776-971-66
Sequence 8, Appl1	7,		Sequence 61, Appl		Sequence 5, Appli	4	4	37	Sequence 31, Appl	Sequence 9, Appli	Sequence 8, Appli					73,	Sequence 66, Appl

## ALIGNMENTS

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US-08-776-971-93
; Sequence 93, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOTTWARE: FOSTSEO for Windows Version
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: UT/09/09/03821
APPLICATION NUMBER: PCT/JP96/03821
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/241805
FILING DATE: 15-AWR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21805
APPLICATION NUMBER: JP 8/21805
APPLICATION NUMBER: JP 8/21805
                                                               NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUKUSUM1, Shoj1

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                 APPLICATION NUMBER: JP 8/246573 FILLING DATE: 18-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hlnuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
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                                              TELEFAX: 617-523-6440
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Fujii, Ryo
Fugumi, Shoji
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                                                                                                                                              US-09-105-678A-34
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                                           Query Match
Best Local Similarity 100.0%; F
Matches 9; Conservative 0;
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Best Local :
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                                                                                                                                                                                                                                           TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Fioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: pepi
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
12 RGIRPVGRF 20
                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                  3 RGIRPVGRF 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGIRPVGRF 15
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STRANDEDNESS: single
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Conservative C
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100.0%; Pred. No. 0.0
Live 0; Mismatches
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                                                            b; Score 48; DB
b; Pred. No. 0.0
0; Mismatches
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ches 0; Indeis
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Sequence 46, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCTIONERS. 52
                                                                                                                                                                                                                                                                                                                                                                       밁
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Best Local Similarity
Thes 9; Conserve
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MOLECULE TYPE:
US-09-105-678A-40
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: Sequence 40, Application US/09105678A

: Patent No. 6103882
                                                                                                                                                                                                                                                                                           RESULT 4
US-09-105-678A-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAV1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
REFERENCE/DOCKET NUMBER: 48466-342
TELEOMONICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Fioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAN NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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APPLICANT: Tanaka, Yoko
APPLICANT: Nishlmura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 130 |
CITY: Boston
                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
               COUNTRY:
                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                     12 RGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amlno acid
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MA
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                                                                130 Water Street
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100.08; Pred. No.
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                                                                                                                                      PRODUCING A 19P2 LIGAND
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Query Match
Bost Local Similarity
"~*~hes 9; Conserv
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US-08-776-971-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 1:
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 RGIRPVGRF 20
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RGIRPVGRF 11
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                        COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRATSCP for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,9718
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                   Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hinuma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                                   STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
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100.0%; Pred. No.
Live 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27,026
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0.0032;
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FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-776-971-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 문
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Patent No. 6228984
GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 8:
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FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
AFTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RGIRPVGRF 11
                                                                                                                                                                                                                  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 27,0
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi, Sboji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                 PRIOR APPLICATION DATA:
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9, Conserv
                                                                      APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
                                                                                                                                                           APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: MA
                                  APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street
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PPLICATION NUMBER: JP 8/211805
LING DATE: 12-AUG-1996
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100.0%; Pred. No. 0.0032;
Live 0; Mismatches 0;
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LENGTH: 20 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPQLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ IU NO: 50:
US-08-776-971-50
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US-08-776-971-64
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REGISTRATION NUMBER: 27,026
REFERENCE, DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEFHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ IQ NO: 50:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
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8est Local :
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            COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: UOS
SOFTWARE: FBSTS50 for Windows Version 2.0
CURRENT APPLICATION UNINER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNknown>
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DT 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/9419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/9419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/9419
FILING DATE: 11-MAR-1996
APPLICATION NUMBER: JP 8/9419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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12 RGIRPVGRF 20
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les 9; Conserv
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ATTORNEY/AGENT INFORMATION:
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COMPUTER REAUABLE FORM:
MEQIUM TYPE: Diskette
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS,
NUMBER OF SEQUENCES: 140
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STATE: MA
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Fujii, Ryo
Fukusumi, Shoji
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100.08; Pr
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SEQUENCE DESCRIPTION: SEQ ID NO: US-08-776-971-64
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GENERAL INFORMATION:
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Best Local 9
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                                                                               ATTORNEY/AGENT INFORMATION:
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
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TELECOMMUNICATION INFORMATION:
FOR EPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hinuma, Shuji
                                                                                                                          APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING QATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
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9; Conserv
                                               NAME: Conlin, David C
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109
                                                                                               APPLICATION NUMBER: JP 8/246573 FILING QATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
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Kawamata, Yuji
Hosoya, Masaki
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                                                              David G.
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0; Mismatches
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0.0032;
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids

LENGTH: 20 amino acids
TYPE: amino acid

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RESULT 9
US-09-421-208-34
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; MOLECULE TYPE:
US-09-421-208-34
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Best Local Similarity
                               Matches
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                                                          Query Match
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                                                                                                                                                                                                                   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                              NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               Local Similarity
hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
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                                                                                                                                                      STRANDEDNESS
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3 RGIRPVGRF 11
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                                                                                                                                                                      amino acid
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130 Water Street
                                                                                                                                                                                     20 amino acids
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                               Conservative
                                                                                                                       peptide
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100.0%; Pr
0;
                           94.1%; Score 48; DB 4; Length 20; 100.0%; Pred. No. 0.0032; tive 0; Mismatches 0; Indels
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Pred. No.
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0.0032;
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Query Match
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US-09-421-208-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/09421208 Patent No. 6258561
                                                                                                                                             Patent No. 625856;
                                                                                                                                                                Sequence 46, Application US/09421208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David 6.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                              GENERAL INFORMATION:
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osbmu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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CITY: Boston
STATE: MA
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12 RGIRPYGRF 20
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OPERATING SYSTEM: PC-DOS/MS-DOS
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12 RGIRPVGRF 20
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02109
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                                                                                                                                                                                                                                                                                                                                                    94.18;
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Pred. No. 0.0032;
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; MOLECULE TYPE: peptide
US-09-421-208-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09105678A Patent No. 6103882
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INFORMATION FOR SEO
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FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: US/09/105,678A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1721T8//^~
                                                                                   COMPUTER READABLE FORM:
MEDIUM TWEE: Floppy disk
COMPUTER: IBM FC-Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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APPLICATION NUMBER: US,
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ADDRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suenaga, Masat
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osa
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                  CITY: Uoston
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STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                      STREET:
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Pred. No.
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; FEATURE:
; INAME/KEY: Modified-site
; LOCATION: 21
; OTHER INFORMATION: /product- "Gly-OH or Gly-Arg" US-09-105-678A-28
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US-09-105-678A-35
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/I05,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
APTONNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27.026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/09105678A Patent No. 6103882
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ADDRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: N1shimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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LENGTH: 21 amino acids
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ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 48 PELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                      CITY: Boston
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                  48466-342
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TELEPHONE:

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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-35
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US-09-105-67BA-41
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Best Local Similarity
                                             Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRION APPLICATION DATA:
APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTONNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-640
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                       STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MORIYA, TAKEO
APPLICANT: TANAKA, YOKO
APPLICANT: NISHIMURA () SPAMU
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: Boston
                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                     LENGTH:
3 RGIRPVGRF 11
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                                               Conservative
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617-523-6440
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100.0%; Pr
                                          94.1%; Score 48;
100.0%; Pred. No.
tive 0; Mismatc
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                                             DB 3; Length 21; 0.0034; hes 0; Indels
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US-09-105-678A-47; Sequence 47, Apj; Patent No. 6103
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Best Local Similarity
----hes 9; Conserve
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; MOLECULE TYPE: peptide
US-09-105-678A-47
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Search completed: September 13, 2002, 09:20:58 Job time: 623 sec
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: 27,004
REPERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODOCING A 19P2 LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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STATE: MA
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S16594	G70749	A72658	D83573	T51126	AG3444	G70947	T29118	AD0883	C70643	G95926	T50932	T43770	S76104	T34825	S09872	
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## ALIGNMENTS

prolactin-releasing peptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence\_revision 30

30-Jun-2001 #text\_change 30-Jun-2001

T.; Ishizuka, T.; Hosoya

RESULT JC7607

C;Genetics: A;Gene: PrRP A;Introns: 33/1 probable oxidoreductase (EC 1.5.99.-) - Mycobacterium tuberculosis (strain H37RV) C.Species: Mycobacterium tuberculosis C.Jun-2000 C.Accession: G70875
R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gor, Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holrx, Connor, R.; Davies, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
A.\*Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.\*Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.\*Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.\*Authors: G70875
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A.\*Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.\*Accession: G70875
A.\*Accession: G70875 A; Molecule type: DNA
A; Residues: 1-674 <COL>
A; Residues: 1-674 <COL>
A; Cross-references: GB:AL010186; GB:AL123456; NID:93261493; PIDN:CAA15852.1; PID:9269
A; Experimental source: strain H37Rv
C; GenetLcs:
A; Gene: fadH A;Molecule type: DNA A;Residues: 1-83 </ANA A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid release, and stimulation of ACTH secretion from t C;Accession: JC7607
C;Accession: JC7607 밁 S Query Match Best Local S Matches 9 44 w N RGIRPVGRF RGIRPVGRF 11 Similarity 9: Conserv Conservative 52 94.18; Score 48; 0; Mismatches DB 2; . 0.016; the pituitary. metabolite release 0 Length 83 Inde19 0 from Gaps rat anterior ö Holroyd, Gordon

9eno

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R;Peoples, O.P.; Masamune, S.; Walsh, C.T.; Sinskey, A.J.
J. Biol. Chem. 262, 97-102, 1987
A;Title: Biosynthetic thiolase from Zoogloea ramigera. III. Isolation and capacities and service of the servic
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                                                                                                                                         C/Superfamily: acetyl-CoA acetyltransferase
C/Keywords: acyltransferase; coenzyme A; homotetramer; ketone body metabolism;
F/2-391/Product: acetyl-CoA acetyltransferase *status predicted <MAT>
F/89/Activo site: Cys *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - Zoogloea ramigera
N;Altornate names: acetoacetyl-CoA thiolase; biosynthetic thiolase; thiolase
C;Species: Zoogloea ramigera
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 05-May-2000
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C:Radandream, M.A.;
R:Wood, V.: Radandream, M.A.;
Submitted to the EMBL Data Lib
A:Reference number: Z21862
A:Accession: T39533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SPBC16A3.19 - fission yeast (Schlzosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A; Introns: 53/1;
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A;Molecule type: DNA
A;Residues: 1-272 < KNOO>
A;Cross-references: EMBL:AL021748;
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                                                                                    RESULT
E82221
DNA gyrase, chain A VC1258 [imported] - Vlbrio cholerae (strain N16961 serogroup OI) C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C; Genetlcs:
A; Gene: Rv0982
C; Superfamily:
                                                                                                                                                                                                                          R;James, K.D.; Parknii, ...
R;James, K.D.; Parknii, ...
submitted to the EMBL Data
submitted to number: 222967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
A;Accession: B70821
                                                                                                                                                                         A; Note: MLCB373.27
C; Superfamily: envi
                                                                                                                                                                                                                                                                                                                                                                                                                              probable two-component system sensor [Imported] - Mycobacterium
C;Specles: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Rv0982 - Mycobacterium tuberculosis (strain H37RV) C; Species: Mycobacterium tuberculosis C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-C; Accession: B70821
                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T45447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL021999; GB:AL123456;
A;Experimental source: strain H37RV
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                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from
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                                                                             Query Match
Best Local s
Matches 6
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Best Local Similarity 85.,
"--hes 6; Conservative
                                                                                                                                                                                                                  Genetics:
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266 RGIQPLGR 273
  188
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                                      4 G1RPVGR 10
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T:[||||
GLRPVGR 194
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6; Conserv
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he EMBL Data Library, February 1998
                                                                                                                                                                           envz protein; sensor histidine kinase homology
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                                                                               Conservative
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85.7%;
                                                                                                68.6%;
85.7%;
                                                                           Score 35; DB
Pred. No. 44;
1; Mismatches
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Pred. No.
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44;
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20-Aug-2000 #text\_change 02-Feb-2001

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A; Residues: 1-1056 <SIM>
A; Residues: 1-1056 <SIM>
A; Residues: 1-1056 <SIM>
A; Residues: 1-1056 <SIM>
A; Residues: GB:AE004053; GB:AE003849; MID:g9107631; PIDM:AAF85244.1; GSPDB:GM00; A; Experimental source: Strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abrcu, F.A.; Acencio, M.; Alvarenga, R.; Jarwheto, E.; Ducena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, larmeto, E.; Ducena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lalg; Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.; Marino, C.L.; Marques, M.Y.; Martins, I.A.; Madeira, A.M.; Mathors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C.Y.
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C.Y.
C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Dilveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Roirigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasai
A; Authors: de Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei, M.; Tsuhako, M.H.; Valiada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
B82557
hypothetical protein XF2445 [imported] - Xylella faatidiosa (strain C:Species: Xyleija fastidiosa revision 20-Aug-2000 #text_change 20-/
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R;Heldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.: Baas, S.; Din, H.; Dragoi, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                        A;Contents: annotation C;Genetics: A;Gene: XF2445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The genome sequence of the plant pathogen Xylella fast1diosa. A:Reference number: A82515; MUID:20365717
A;Note: for a complete list of authora aee reference number A59328 below A;Accession: B82557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Xyleila fastidioaa
C:Dato: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: B82557
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A;Moiecule type: DMA
A;Residues: 1-894 <HEI>
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A; Residues: 1-1056 <:
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C; Superfamily: |
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                                                                                                          Duery Match
Best Local S
Matches 6
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Best Local
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1047 GLRPVGR 1053
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                                                                                                          Local Similarity
nes 6; Conser
                            4 GIRPVGR 10
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5; Conserv
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62.5%;
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Pred. No. 92;
1; Miamatches
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3; Mismatches
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Pred. No.
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ribosomal protein S1 - Synéchococcus ap

C:Specias: Synéchococcus sp.

A:Variety: PCC 6301

C:Date: 15-Jul-1995 #sequence_revision

C:Accession: S51485
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A; Residues: 1-226 <BLAT>
A; Residues: 1-226 <BLAT>
A; Construction of the control of the
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hypothetical protein b2757 - Eacherichia coll (strain K-12)
C:Species: Escherichia coll
C:Date: 12-Sep-1997 *sequence_revision 17-Sep-1997 *text_change 08-Dct-1999
C:Accession: A65057
                                                                                           A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision
C; Accession: S77236
R; Kaneko, T.; Sato, S.; Kotani, H.; Tan
                                                                                                                                                                                                                     ribosomai protein S1 - Synechocyatia
N;Aiternate names: protein siri356
C;Speciea: Synechocystis sp.
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C; Keywords:
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A;Title: The complete genome sequence of Eacherichia coli K-12. A;Reference number: A64720; MUID:97426617
A;Accession: A65057
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A; Residues: 1-307 <SUG>
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A;Accesaion: S51485
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                R:; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Nasamizu, Rs: 3, 109-136, 1996
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-343 <KUR>
A; Gross-references: GB:BA000019; PIDN:BAB77660.1; PID:gl7l35114; GSPDB:GN00179
A; Gross-references: Strain PCC 7120
                                                                                                                           A;Reference number: A97359; PMID:11743194
A;Accession: F97646
A;Starum:
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A; Residues: 1-328 <KAN>
A; Cross-references: EMBL: D90907; GB: AB001339;
A; Note: the nucleotidc sequence was submitted
C; Genetics:
                                                                                                                                                                            R;Goodner, B.; Hinkie, G.; Gsttung, S.; Milier, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrob
                                                                                                                                                                                                                                                              C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: F97646
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C;Species: Agrobacterium tumefaclens
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C;Superfamily:
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DNA Res. 8, 205-213, 2001
A;Tille: Complete Genomic Sequence of the Filamentous Nitrogen-flxing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AN1823
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A; Accession: S77236
A; Map
                                                      A;Cross-references: GB:AE007869; PIDN:AAK88127.1; PID:g15157563; GSPDB:GN00169
                                                                             A; Molecule type: DNA
A; Residues: 1-290 <KUR>
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                    Gene: AGR_C_4335
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14-Dec-2001 #text_change 11-Jan-2002
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R; Barnett, M. J.; Elsher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.; Kalman, S.; Keating, D.H.; Palm, C., Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A; Title: Nucleotide sequence and predicted functions of the entire Slnorhlzobium mell A; Reference number: A95262; MUID:21396509; PMID:11481432

A; Reference number: A95262; MUID:21396509; PMID:11481432

A; Residues: pellminary
A; Molecule type: DNA
A; Residues: 1-313 <KUR>
A; Cross-references: GB:AE006469; PIDN:AAK65372.1; PID:g14523833; GSPDB:GN00165
A; Experimental source: strain 1021, megapiasmid pSymA
A; Residues: 1-313 <KUR>
A; Experimental source: strain 1021, megapiasmid pSymA
A; Experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VlrB6 type IV secretion protein [imported] - Sinorhizoblum meliloti (strain 1021)
C;Species: Sinorhizoblum meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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B95351
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A; Map position:
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A; Contents: annotation
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A;Residues: 1-290 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43378.l; PID:g17740875; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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Kitada C., Masuo Y., Asano T., Matsumoto H., Si
Kurokawa T., Nishimura O., Onda H., Fujino M.,
"A prolactin-releasing peptide in the brain.";
Nature 393;272-276(1998).
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90-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
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Sekiguchi M., Kitada C.,
Sumino Y., Fujino M.;
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Mammalia; Eutheria;
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PROLACTIN-RELEASING PEPTIDE PR
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T., Nishimura O., Or
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing Prolactin-releasing peptide PrRP31; Prolactin-releasing Prolactin-releasing peptide PrRP31; Prolactin-releasing Prolactin-rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of prolactin through its receptor GPRIO. May lactotrophs directly to secrete PRL.

-!- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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SEQUENCE FROM N.A.
STRAIN-ATCC 19623
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Pred. No. 0.0
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PROLACTIN-RELEASING PERTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35A13B0FA908 CRC64;
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0.0048;
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cora; Bovoidea;
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GYALAS

ID GYRALA

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AC P48369

DT 01-FEB

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DE DNA 97

GN GYRA. 97

GN Bacter

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Best Local :
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P48369;
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DNA 9yrase subunit
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Biosynthetic thiolase from zoogloea ramigera. Evidence for a mechanism involving Cys-378 as the active site base.";
J. Biol., Chem. 266:8369-8375(1991).
-I- CATALYTIC ACTIVITY: 2 acetyl-CoA - CoA + acetoacetyl-CoA.
-I- PARHWAY: FIRST STEP IN POLY-BETA-HYDROXYBUTYRATE BIOSYNTHESIS.
-I- SUBCELULIAR LOCATION: Cytoplasmic.
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PIR; A
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Characterization of the genes encoding beta-ketothiolase and 
aceroaceryl-CoA reductase ":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR002I55; Thiolage Pfam; PF00108; thiolage; 1. Pfam; PF02803; thiolage_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetoacetyl-CoA reductase
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                Aeromonas salmonicida
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                                         FEB-1996 (Rel. 33, Created)
FEB-1996 (Rel. 33, Last sequence up
FEB-1997 (Rel. 35, Last annotation
OV-1997 (Rel. 35, Last annotation
OV-1997 (Rel. 35, Last annotation)
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A26121; XXCGAC.
A27754; A27754.
; P27796; LAEY.
                                                                                                                                                                                                                                                                                                                                                                                02803; thiolase_C; 1.
02803; thiolase_C; 1.
PS000096; THIOLASE_1; 1.
PS00099; THIOLASE_3; 1.
PS00737; THIOLASE_2; 1.
PS00737; THIOLASE_2; PHB biosynthesis.
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6; Conserv
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 Proteobacteria;
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377
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gamma
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Pred. No.
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BASE.
C->G: LOSS OF ACT1
                                                                                                                     PRT;
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6D2351A1BC0E4EDD CRC64,
 subdivision;
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                                                         update)
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amlgera. III. Isolation and
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1.3;
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 Aeromonadaceae;
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=K12 / MGI655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A.,
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., RC
Riley M., Collado-Vides J., RC
Riley M., Collado-Vides RC
Riley M., Collado-Vides
                                                                                                                                                                                                                                                                                                       16-OCT-2001 ()
16-OCT-2001 ()
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Hypothetical
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"gyrA mutations in quinolone-resistant isolates

Aeromonas salmonicida.";
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Submitted (OCT-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isomerase; Topoisomerase: DNA-binding.
ACT_SITE 122 122 DNA CLEAVAGE (BY SIMILARITY).
SEQUENCE 922 AA; 101333 MW; 8894965DC4217077 CRC64;
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                                                                                                                                                                                                                                                          Escherichia coli
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Q46898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro; IPR002205; DNA_topoisoIV.
pfam; PF00521; DNA_topoisoIV; 1.
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                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                     Escherichia.
                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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NCBI_TaxID=645;
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CATALTYIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING, THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
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L42453; AAA87239.1;
P09097; LAB4.
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                   A., Perna N.T., Burland
, Rode C.K., Mayhew G.F.
Goeden M.A., Rose D.J.,
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Matches 6; Conser
                                                            Ribosomal
INIT_MET
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AE000359; AAC75799.1; ALT_INIT.
ECOGENO; EG13116; ygc1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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                                                                                                                                                                                      EMBL; D287S2; BAA05946.1;
HSSP; P05055; 1SRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE-95166170; PubMed-7862084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechococcus sp. (strain PCC 6301) (An
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32,
01-FEB-1996 (Rel. 33,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P46228;
01-NOV-1995
                                           DOMAIN
                                                                                                        PROSITE;
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'TE; PSS0126; S1; 3.
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224 AA;
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25209 MW;
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Pred. No. 8.5;
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MOTIF
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les; Synechococcus.
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RESULT 8
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RESULT 9
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Best Local s
Matches
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                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Sato S., Kotani H., Taneka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain pcC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

-I- SUNILARITY: BELONGS TO THE SIP FAMILY OF RIDOSOMAL PROTEINS.
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P73530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/snnounce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcal
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30s ribosomal
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
al_protein S1 homolog A.
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SI MOTIF 1.
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DC3FF9BlE5A40619 C
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Pred. No. 12;
1; Mismatches
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PubMed-10802645;
Camaschella C., Roetto
Careila M., Majorano i
"The gene TFR2 is muta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Large scale analysis of two regions in human chromosome 7g22: annotation of 650 kb of genomic aequence around the EPO and CU reveals 17 genes."; Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol.
[2]
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last seguence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           Biood
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NIEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
chhmitted (AUG-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo aapiena (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gloeckner G., Scherer
Tsui L.-C., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of transferrin receptor transferrin receptor-like family.": J. Biol. Chem. 274:20826-20832(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS ALPHA I TISSUE-Erythroleukemia, and Myeloid MEDLINE-99340005; PubMed-10409623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roetto A., Totaro A., Piperno A., P
Cail A., De Gobbi M., Gasparini P.,
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gamma; are produced by alternative spitcing.

TISSUE SPECIFICITY: Predominantly expressed in liver. While the alpha form is also expressed in apieen, lung, muscle, prostate an peripheral blood mononuclear ceils, the beta form is expressed in all tissues tested, aibelt weakly.

DISEASE: Defects in TFR2 are a cause of hereditary hemochromatosi type III (HFE3). HFE3 is a disorder of iron hemostasis resulting in iron overload and has a phenotype indistinguishable from that of hereditary hemochromatosis (HH). HH is characterized by abnormai intestinal iron absorption and progressive increase of
                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type II membrane protein. The b lacks the transmembrane domain and is probably intracal alternarive PRODUCTS: 3 isoforms; alpha (ahown here).
                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                      FUNCTION: Mediates cellular uptake of transferrin-bound iron i non-iron dependent manner. May be involved in iron metabolism, hepatocyte function and erythrocyte differentiation.
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ini P., Camaachella C.;
tranaferrin 2 in hemoch
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                                        Homo aapiena (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; AK000421; I
MEROPS; M28.973;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          total body iron, which results in midlife in clinical complications including cirrhosis, cardiopathy, diabetes, complications including cirrhosis, cardiopathy, and susceptibility to endocrine dysfunctions, arthropathy, and susceptibility to cancer. Since the disease complications can be effectively prevented by regular phiebotomies, early diagnosis is most important to provide a normal life expectancy to the affect
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en oxidase (EC
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                                          Chordata;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM BETA).
MISSING (IN ISOFORM GAMMA).
M -> K (IN HFE3).
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Pred.
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R -> RIPLSAQV (IN REF. 2)
; D3D3082BA835413A CRC64;
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INTERCHAIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                        Craniata; Vo
Catarrhini;
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red. No. 31;
Mismatches
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3.4) (PPO)
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                                                            Vertebrata; Euteleostom1;
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                                          Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frank J., Poh-Fitzpatrick M.B., King L.E. Jr., Christiano A.M.;
"The genetic basis of 'Scarsdadie Gourmet Diet' variegate porphyria:
missense mutation in the protoporphyrinogen oxidase gene.";
Arch. Dermatoi. Res. 290:441-445(1998).
Arch. Dermatoi. Res. 290:441-445(1998).
IF FUNCTION: CANTALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPHYRINOG
IX TO FORM PROTOPORPHYRIN IX

-1- CATALYTIC ACTIVITY: Protoporphyrinogen-IX + O(2) = protoporphyri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meissner P.N., Dailey T.A., Hift R.J., Ziman M., Corrigall A. Roberte A.G., Meissner D.M., Kirsch R.E., Dailey N.A.;
"A R59W mutation in human protoporphyrinosen oxidase results decreased enzyme activity and is prevalent in South Africans variegate porphyria.";
Nat. Genet. 13:95-97(1996).
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                                                                                                                                                                                                     EMBL; D38537; BAA07538.1; -. EMBL; U26446; AAA67690.1; -.
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MEDLINE-98434271; PubMed-9763307;
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MEDLINE-96241580; F
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[3]
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                                        Fiavoprotein;
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97005368; PubMed=8852667;
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N1shimura K., Taketani S., Inokuchi N.,
                                                                                                            Porphyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPACTOR: CONTAINS ONE FAD PER HOMODIMER.

PATHWAY: PENULTIMATE STEP IN HEME AND PORPNYRIN BIOSYNTNESIS.

SUBGUIT: NOMODIMER.

SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRANE
WITN ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG,
LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.

LIVER SKELETAL MUSCLE, KIDNEY, AND PANCREAS.

LIVER SKELETAL MUSCLE, KIDNEY, AND PANCREAS.

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LIVE THOSE OF ACID MUSCLE AND PANCRESS.

LIVE THOSE OF ACID MUSCLE AND PANCRESS.
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esis, Name biosynthesis; Oxidored
Mitochondrion; Disease mutation;
i4 FAD (POTENTIAL).
59 R -> W (IN VP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             is produced through a collaboration -
                                                                                                      Oxidoreductase;
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Best Local S
Matches 6
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PDOX_MOUSE STANDARD,
P51175; p97344;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                              J. B101.
                       This
                                   J. B101. Chem. 263:3835-3839(1988).

1. FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPI IX TO FORM PROTOPORPHYRIN IX.

1. CATALYTIC ACTIVITY: PROTOPORPHYRINGEN.

1. CATALYTIC ACTIVITY: PROTOPORPHYRINGEN.

1. CATALYTIC ACTIVITY: PROTOPORPHYRINGEN.

1. CATALYTIC ACTIVITY: PROTOPORPHYRINGEN.

1. CATALYTIC ACTIVE STEP IN HEME AND PORPHYRIN BIOSYNTHE.

1. SUBCULILAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER ME

WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE.

1. SIMILARITY: BELONGS TO THE PROTOPORPHYRINGEN OXIDASE FAM.
                                                                                                                                                                                   "Organization of the terminal two enzymes of the heme biosynthetic pathway. Orientation of protoporphyrinogen oxidase and evidence for membrane complex.";
                                                                                                                                                                                                                                                                               Nishimura K., Inokuchi N.;
"Induction of terminal enzymes for heme biosynthesis differentiation of mouse erythroleukemia ceils.";
Eur. J. Blochem. 230:760-765(1995).
                                                                                                                                                                                                                                                                                                                                       TISSUE-Erythroieukemia;
MEDLINE-95331315; PubMed-7607249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                        <u>:</u>
                                                                                                                                                                                                                                  MEDLINE-88153682; PubMed-3346226;
                                                                                                                                                                                                                                                  TISSUE-Liver
                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION
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Mammalia; Eutheria;
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Dailey T.A., Dailey H.A., Meissne
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        SW1SS-PROT entry is copyright. It is produced through seen the Swiss institute of Bioinformatics and the EM
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6; Conserv
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85.7%;
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N.,
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mouse protoporphyrinogen
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/ Murinae; Mus
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Bacteris; Firmicutes; Bacillus/Clostridium
"--"'llus/Staphylococcus group; Bacillus.
                  EMBL; AP001507; BAB03828.1; -.
InterPro; IPR000924; tRNA-synt_lc.
InterPro; IPR001412; tRNA-synt_l; 1.
Pfam; PF00749; tRNA-syntHCLU.
PROSITE; PR00987; TRNASYNTHCLU.
PROSITE; PS00178; AA_TRNA_LIGASE_l; 1.
Aminoacyl-tRNA synthetsse; Protein biosynthssis; Ligase; ATP-binding;
                                                                                                                                                                                                  the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions ss long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce, or send an emsil to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               halodursns snd genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).

1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = ANP +
diphosphate + L-glutamyl-tRAA(Glu).

1- SUBUNIT: MONOMER (BY SIMILARITY).

1- SUBCELLULAR LOCATION: Cytoplasmic.

1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horikoshi K.;
"Complete genome sequence of the alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takami H., Nakasone K., Takaki Y.
Fuji F., Hirama C., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C-125 / JCM 9153;
MEDLING-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-C-125 / JCM
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NCBl_TaxID-86665;
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                                          Q55578;
15-DEC-1998;
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16-OCT-2001
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01-AUG-1990
01-FEB-1991
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MEDILINE-90269039; PubMed-2161319;
Chee M.S., Bankisr A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
Horsnell T., Hutchison C.A. Ill, Kouzarides T., Martignetti J.A.,
Preddie E., Satchwell S.C., Tomiinson P., Weston K.M., sarrell B.(
"Analysis of the protein-coding content of the sequence of human
cytomegalovirus strain AD169.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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                                                                                                                                                                                                                                                             PIR; S09872; S09872.
Hypothetical protein
CARBOHYD 144 1
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           Synechocystis sp.
                       Hypothetical SLR0361.
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NCB1_TaxID=10360;
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Viruses; dsDNA viruses, no RNA stage;
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kDa protein slr0361.
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AR72_HUMAN STANDARY,
043488; 075749;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aflatoxin Bl aldehyde reductase 1 (EC 1.-.-)
                                                                                                                                                                                                                                                       MEDIINE-98244807; PubMed-9576847; Ireland L.S., Harrison D.J., Weal G.E., Hayes J.D.; "Molecular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin 81-aldehyde reductase."; Blochem. J. 332:21-34(1998).
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InterPro: iPR000748; Psi_RSU.
InterPro: iPR002942; 94.
InterPro: iPR002942; 94.
InterPro: iPR002942; 94.
InterPro: iPR002942; 94.
InterPro: iPR0049; Pseudou_synth_2; 1.
Pfam; PF01479; 84; 1.
SMART; SM00363; S4; 1.
SMART; SM00363; S4; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
SEQUENCE 249 AA; 28228 MW; 315F208030180326 CRC64:
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"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
MEDLINE-99040634; PubMed-9823300;
Praml C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-
1p36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
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Mammalla; Eutherla; Primates;
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TISSUE-Brain;
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MIM; 603418;
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EMBL; Y16675; CAA76347.1; -.
EMBL; AL035413; CAB72321.1; -.
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FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHVDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOCENIC
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
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SIMILARITY: BELONGS TO THE ALDO/KE
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Copyright (c) 1993 - 2000 Compugen Ltd
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01-DEC-2001
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09W624;
01-NOV-1999
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                                                                                                                                                                                                                                                                                                               Carassius auratus (Goldfish).

Bukaryota; Metazoa; Chordata; Craniata;

Actinopterygii; Neopterygii; Teleostei;

Cypriniformes; Cyprinidae; Carassius.

NCBI_TaxID-7957;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUE-BRAIN;
Satake H., Minakata H., Fujimoto M.;
Satake H., Minakata H., Fujimoto M.;
Carassius Resmide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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Contain-GSS1 / DSW 4299 / JCM 9571;

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01-DEC-2001 (TrembLrel.
TVG1120468 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 426 AA;
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.

A Gordon S.V., Elgimeler K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davles R., Devlin K., Feltwell T., Gentles S., Hamilin N., Holroyd S.

A Davles R., Devlin K., Feltwell T., Gentles S., Hamilin N., Holroyd S.

A Davles R., Dagels K., Krogh A., McLean J., Woule S., Murphy L.,

A Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J.,

A Nutrer S., Seeger K., Skelton S., Squares S., Squares R.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Sulston J.E., Taylor K., Whitchead S., Barrell B.G.;

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Wood V., Rajandream M.A., Barrell B.G., Beck A.,
Wood V., Rajandream M.A., Barrell B.G., Eeck A.,
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ dat
EMBL; AL021748; CAA16870.1;
InterPro; TRR001005; Myb_DNA_bind.
PROSITE: PS00037; Myb_TDNA_bind.
PROSITE: PS00037; Myb_TINNOWN_1.

Hypothetical protein.
SEQUENCE 272 AA; 30901 MM; 8FE0EB29217107A8 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                   O42924 PRELIMINARY; PRT; 272 AA.
042924;
01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 30.9 KDA PROTEIN C16A3.19 IN CHROMOSOME
SPBC16A3.19.
                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TremBLrel. 19, La 2,4-DIENOXL-COA REDUCTASE. FADH OR RV1175C OR MTV005.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterlum tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
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  Similarity 85.7%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteome.
674 AA;
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PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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Score 35; DB
Pred. No. 45;
1; M1smatches
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Pred. No. 75;
1; Mismatches
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                                                                                                                    8FE0EB29217107A8
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75,
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                                             Length 272;
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PRELIMATIVA.....
O53895;
O53895;
O1.JUN-1998 (TrEMBLrei. 06, Last sequence update)
O1.JUN-1998 (TrEMBLrei. 19, Last annotation update)
O1.DEC-2001 (TrEMBLrei. 19, Last annotation update)
PUTATIVE TWO-COMPONENT SENSOR.
RV9982 OR MTV044.10.
Mycobacterium tubercuiosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Mycobacteridae;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
MEDLINE-9895987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown O., Chilingworth T., Connor R.,
Badcock K., Basham D., Brown O., Chilingworth T., Connor R.,
Davles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hoiroyd Hornsby T., Jageis K., Kroph A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Ouali M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeper K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (TIE
01-OCT-2001 (TIE
01-OCT-2001 (TIE
01-OCT-2001 (TIE
MLR9222 PROTEIN
MLR9222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome structure of the nitrogen-flxing symblotic bacterium Mesorhizobium 10t1.";
DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54606.1; -.
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MEDLINE-21082930; PubMed-11214968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phyliobacterlaceae; NCBI_TaxID=381;
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5; Conserv
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(TrEMBLIE1. 18,
(TrEMBLIE1. 18,
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; 42385 MW;
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Pred. No. 63;
2; Mismatches
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Last sequence up
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Best L
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Leproma: ML0175; -.; InterPro; IPR004358; InterPro; IPR003560; InterPro; IPR003594; InterPro; IPR003661; InterPro; IPR003661; InterPro; IPR004359; InterPro; IPR004359; Pfam; PF00572; HAMP; IPfam; PF02518; HATPass
                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDECTION
EMBL; AL035500; CAB36699.1; -.
EMBL; AL583917; CAC29683.1; -.
                                                                                                                                                                                   Coie S.T., Eiglmeier K., Parkhili J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungail K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devin K., Duthoy S., Feitwell T., Fraser A., Hamlin N. Holroyd S., Hornsby T., Jagels K., Lacroix C., Maciean J., Moule S., Murphy L., Oliver K., Quali M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09Z5G7;
01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence up
01-DEC-2001 (TIEMBLIEL 19, Last annotation
PUTATIVE TWO-COMPONENT SYSTEM SENSOR KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
Bacteria; Firmicutes;
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                                                                                                                                                                            Squares S., S
Barreil B.G.,
                                                                                                                                                                                                                                                                                                                                         Harris D., Taylor K.;
Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Harris D., Taylor
                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ML0175 OR MLCB373.27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 393:537-544(
                                                                                                                                                                                                                                                                                         MEDLINE-21128732; PubMed-11234002;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piam,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
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m; PF00672; HAMP; 1.
m; PF002318; HATPase_c; 1.
pF00512; signal; 1.
RT; SM00304; HAMP; 1.
RT; SM00387; HAMP; 1.
RT; SM00388; H1SKA; 1.
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P02933; 1E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                    IBXD.
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  HATPase_c;
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                                                                                                                                                                                                                                                                                                                                                                                                       utes; Actinobacteria; Actinobacteridae;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                       HATPase_C.
H1s_k1nA.
HIS_KIN_S1g.
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His_kinA.
HIS_KIN_sig.
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85.7%;
                                                                           BCTRLSENSOR
                                                                 HAMP
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Pred. No.
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RESULT
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Q1-MAY-2000 (TrEMBLrel. 1
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STRAIN-EI TOR H16961 / SEROTYPE 01;

MEDLINE-20406833 pubmed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Omayam L.A.,

Gill S.R., Heison K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Hierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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Q9KSJ8;
01-0CT-2000
01-0CT-2000
01-DEC-2001
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PRIHTS; PR00344; BCTRLSEHSOR.
SMART; SM00304; HAMAP; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; H1SKA; 1.
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SEQUEHCE 894 AA;
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EMBL, AE004205; AAF94417.1;
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HSSP, P09097; IAB4
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RESULT
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Adams D.D. Celariker S.E. Holt R.A. Evans C.A. Gocayne J.D.,
Adams M.D. Celariker S.E. Holt R.A. Bokkins R.A. Galle R.F.,
RA Amanatides P.G., Scherer S.E., Holt R.A. Ashburner M., Henderson S.H.,
RA George R.A., Levis S.E. R.C. Hald R.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxen E.G., Helt G., Nelson C.R., Miklog G.L.G.,
RA Abril J.F., Apbayani A., An H.-J., Andrews Pfannkoch C. Beadewin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dletz S.N.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dletz S.N.,
RA de Pablos B., Deltelan A.E., Garzy N.S., Gelbart M.M., Glasser K.,
RA dolek A., Gong F., Gorreil J.H., Gu Z., Guan P., Harris M.,
RA Goldek A., Gong F., Gorreil J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibogwam C.,
Jaiali M., Ralush F., Karpen G.H., Karvitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
RA Kerkulov G., Wilshina N.V., Mobary C., Morris J., Woshereil A.,
RA Neckulov G., Wilshina N.V., Mobary C., Morris J., Woshereil A.,
RA Nelson D.R., Nelson K.A., Sunpon M.P., Welsend D.R., Pacleb J.M.,
RA Abuent S.M., Mydn M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stopski M.P., Smith T.,
RA Sylish R.-Y., Wassarman D.A., Weissenbach J.,
RA Sylish R.-Y., Bands F.-Y., Zhon M., Shao Q., Zheng L.,
Then G. D., Shang S., Dondox S., Zhu X., Smith H.O.,
RA Shee B.-Y., Shang M., Shang S., Shang S., Shang S., Shan
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Matches 6
  Q9PAQ0
Q9PAQ0;
01-OCT-2000
01-OCT-2000
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Tnsecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
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SMART; SM00239; C2;
PR0SITE; PS50004; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome sequence of Drosophila melanogastar.";
Science 287:2185-2195(2000)
EMBL, AE003559; AAF50589.1; .
HSSP; P21707; 1BYN
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InterPro; IPR000008; C2.
Pfam; PF00168; C2; 1.
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| 130 RGVRGLGRF 138
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6; Conserv
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    (TrEMBLrel.
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  15,
Created)
Last sequence update)
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Pred. Ho. 1.8e+02;
2; Nismatches 1
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DR EMBL, AEO04053, AAF65244.i. -
DR InterPro, IPR00192; HAR, dim. .

DR Hypotheticsi protein; Compiete proteome.
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Best Local :
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O9VU79, O1-MAY-2000 (TIEMBLIEL 1
O1-MAY-2000 (TIEMBLIEL 1
O1-DEC-3001 (TIEMBLIEL 1
CG1073B PROTEIN.
                                                                                      Drosophila meianogaster (Frult fiy).
Eukaryota; Metazoa; Arthropoda; Trscheats; Hexapods; Insecta;
Pterygota; Neoptera; Endopteryots; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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1047 GLRPVGR 1053
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STRAIN-BERKELEY;
MEDLINE-20196006;
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                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conserv
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 PubMed-10731132
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85.7%;
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RESULT 13
Q9HJR7
ID Q9RJR7
AC Q9HJR7
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DT 01-MAY
DT 01-MAY
DT 04-DEC
DE PUTATI
GN SCF51.
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchakov S.,
RA Bockova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler N., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dshike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dshike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dshike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dshike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dshike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dshike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dshike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dshike C., Bayrar R.C.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rochs S., Dunkov B.C.,
Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rochs S., Dunkov B.C.,
Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rochs S., Dunkov B.C.,
Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Lisny Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Lisny Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Poilard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Poilard J., Puri V., Reese M.G.,
RA Palazzolo M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Syler B., Pacleb J.M., Simpson M., Stong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yang Z. P., Wassarman D.A., Welnstock G.M.,
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Best Local
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclsse.
Pfam; PF01094; ANE_receptor; 2.
Pfam; PF00211; guanylste_cyc; 1.
Pfam; PF00069; pkinase; 1.
SMART; SM00044; CYCC; 1.
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PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
PROSITE; PS50111; PROTEIN_KINASE_DOM; 1
ATP-binding; Lyase; Transferase.

ATP-binding; Lyase; Transferase.
OSRJR7 PRELIMINARY; PRT;
OSRJR7; OTTEMBLTel. 13, Created)
O1-MAY-2000 (TTEMBLTel. 13, Last sequ
O1-DEC-2001 (TTEMBLTel. 19, Last and
PUTATIVE ZINC-BINDING OXIDOREDUCTASE.
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Scherer S.E., Ll P.W., Hosh
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75.0%;
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Best Local S
Matches 7
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SEQUENCE FROM N.A.

Jeong M.-J., Park S.-C.;

*Cloning of the Catalase gene fr

*Cloning of the Catalase gene fr

*Cloning of the Catalase in the EMBL

EMBL; AF286097; AAK15159.1; -.

HSSP; P15302; 1A4E.

InterPro; IPR002226; Catalase. 1.

PRAINTS; PR00199; Catalase; 1.

PROSITE; PR00067; CATALASE.; 1.

PROSITE; PS000437; CATALASE.; 1.

PROSITE; PS00438; CATALASE.; 1.

PROSITE; PS00438; CATALASE.]; 1.

PROSITE; PS00438; CATALASE.]; 1.
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MEDLINE-9700351; PubMed-8843436;
MEDLINE-9700351; PubMed-8843436;
Redenbach M., Kleear H.M., Denapaite D., Eichner A., Cullum J.,
Rinashi H., Nopwood D.A.;
Kinashi H., Nopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map
"A set of ordered cosmids and a detailed genetic and physical map
"A set of ordered cosmids and a detailed genetic and physical map
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01-JUN-2001 (TrEMBLrel. 17, Last sequer
01-DEC-2001 (TrEMBLrel. 19, Last annote
HEAT-INDUCED CATALASE.
Pleurotus sajor-caju (Oyster mushroom)
Eukaryota; Fung1; Basidiomycota; Hymen-
Agaricales; Pleurotaceae; Pleurotus.
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Submitted (FEB-2000) to the
[3]
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Mol. Microbiol. 21:77-96(1996).
EMBL: AL132707; CAB59716.1; -.
InterPro: IPR002085; Adh_zn_fam11y.
Pfam; PF00107; adh_zinc; 1.
SEQUENCE 329 AA; 34155 MW; SDCAD4FB
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Seeger K.J., Harris |
Submitted (OCT-1999)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales, Streptomycineae, Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
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298
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e EMBL/GenBank/DDBJ databases.
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Pred. No. 1.5e
2; Mismatches
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A432BE6445B6AC13 CRC64;
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Search completed: September 13, Job time: 1068 sec
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SEQUENCE
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EMBL; ACOO
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Kadner K., Mijuel T., Miller
Subramanian S., Martin C.N.;
"Sequencing of human chromosom
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                             "Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System."; Comparison JUNN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005178; AAC24489.1; -.
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5 RGIRPFGK 302
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58017 MW;
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Primates;
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Catarrhini; Nominidae;
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Pollard M.,
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ACCOMPAND DESCRIPTION OF STATEMENT OF STATEM

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Post-processing: Minimum Match 0%
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A_Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
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3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
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3.057 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Rat type ligand po	Bovine pitultary-d	Bovine G protein-c	Rat type G protein	Human type G prote	19P2 ligand peptid	ligand	19P2 ligand peptid	C-terminal iigand	Synthetic ligand 1	Murine pituitary-d	Description

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Rat type G protein Bovine G protein-c	CRH	Bovine CRH rejeasi	Rat oxytocin secre		Manumarian 1922 11g Bovine pituitary-d	Partial ligand pol		0 0 0	Synthetic G protei		Prolactin releasin		Projactin releasin	CRH releasing prot	OI	Rat CRH releasing	ne CRH I	ligand	ligand	19F2 ligand pertid	Oxytocin secretion	an oxytoci	~			Pitu	Human type ligand

## ALIGNMENTS

RESULT AAW95178 AAW95178; AAW95178 standard; Protein; i0-MAR-1999 (first entry) μ 10 Ä

Murine pitultary-derived ligand poiypeptide antigenic epitope.

Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; epitope.

Mus sp.

WO9849295-Al.

05-NOV-1998.

27-APR-1998; 98WO-JP01923.

28-APR-1997;

97JP-0109974

(TAKE ) TAKEDA CHEM IND LTD

WPI; 1999-009423/01. Fukusumi S, Hinuma S;

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PIL X PAR PRESENTATION OF THE PRESENTATION OF 
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cc transgenic animals. Sequences ANM95174 to ANM95178 represent antigenic epiotpes which can be used for the preparation of anti-ligand polypeptide enotypeptide.
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Matches 9
                                                                                                                                          18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
Fujii R,
Kawamata
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                                                                                     (TAKE ) TAKEDA CHEM IND LTD
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treating disorders
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Fukusuml S, Y, Kitada C;
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95JP-0343371,
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96JP-0211805.
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100,0%; Pred. No. 0.0
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                           Hinuma
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                           Hosoya
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Matchea 9
                                                                                                                                                                                                                                               G protein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; pituitary adenomatoals; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; eorbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocla; prolactin secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                   C-terminal ligand polypeptide derived antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97230 standard; Peptide;
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                                                                       23-JUN-1997;
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                                                                                                                                                                                                                   Synthetic.
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7 rgirpvgrf 15
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100.0%; Pr
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Hinuma

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Matches 9
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                 WPI;
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                                                                                                                                                                                                                                                                                                                      pituitary;
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or derivative. The antibodies can be used in diagnosis or to treat opprevent diseases associated with abnormality in the pituitary fund
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                                                                                  The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of projectin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 1992 ligand.
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                                                                        ilgand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for demontia, depression, hyperkinetic prophylactic or therapeutic agent for demontia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagia, hyperprolactinaemia, hypercholesterolaemia, hyperolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyper-lipidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hypersent brain ischaemia, epilepsy, amylotrophic lateral scierosis, acute myocardial infarction, infertility, spinocerebaliar degeneration, clipogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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modulator; pituitary; central nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                    protein-coupled
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m; pancreas; pro
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RESULT
AAW31387
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                                                                                                                                       CC ligand polypeptids corresponding to amino acid residues 31 to 52 of the C sequence represented in AAW3183 and is used in an assay to monitor CC idgand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a modulator. This ligand could have specific applications as a cc prophylactic or therappeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, crauma, growth hormone secretory disease, hyper- and polyphagia, for hyperipidaemia, hyperchoiestcrolaemia, hyperglyceridaemia, for consciousness and polyphagia, cc translent brain ischaemia, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, cc translent brain ischaemia, epilepsy, amyiotrophic lateral sclerosis, according to accuratility, spinocerebellar degeneration, CC constends and consciousness and/or collegalantia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting cc activation of the G protein-coupled rsceptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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7, Kitada C;
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                                                                                        cc derived ligand corresponding to amino acid residues 34 to 53 of the sequence in AAW31368 and is used in an assay to monitor ligand binding to the groteln-coupled receptor protsin. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. CC this ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, cc disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, cc growth hormone secretory disease, hyper- and polyphagia, hypercholesterolaemia, hyperglyceridaemia, hyperflipidaemia, hypersprolactinemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinemia, diabetes, cancer, pancreatitis, renal disease, transient brain ischaemia, amylotrophic lateral scierosis, acute myocardial infarction, spinocerebeilar degeneration, bone fracture, ctrauma, atopic dermatitis, osteoporosis, asthma, epilapsy, infertiity candyor oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus account of the grotein-coupled receptor protein.
             Query Match
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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N-PSDB; AAV02397.
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                                                                                                                                                                                                                                                                                                                                                                                                          Ligand peptide for G protein-coupied receptor - function in the central nervous system, pancreas
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                                                                    Sequence
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 9; Conserv
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 Conservative
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RESULT 10
AAW97232
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    menopausai syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; contruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syndrome, tumours,
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                                                                                                                                                                              Sequence
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                                       RGIRPVGRF 10
rgirpvgrf 20
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9; Conserv
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The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a g protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, caromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, acromegaly, Chiari-Frommel, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal inpidmetabolism or oxytocia.
Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disense; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; chorlocarcinoma; hydatid mole; curtivity; outhrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of G protein-coupled receptor ligands - for modulating projectin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-coupled receptor; GPCR; hypoovarianism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-105614/09
Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             24lpp; English.
                 96.0%;
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                 Score 48;
Pred. No.
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                 DB 20:
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RESULT 12

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                                                                                                                                                                                                                                             The present sequence represents a human type ligand fragment. It

Clear agent for modulating prolactin secretion which comprises a

nagent for modulating prolactin secretion which comprises a

clear agent for modulating prolactin secretion can be used for

protein. The agents for promoting prolactin secretion can be used for

tresting or preventing hypowearianism, gonecyst cacogenesis, menopausai

syndrome, euthyroid or hypometabolism. They can by used for promoting

lactation in a domestic mammal and as an aphrodistac. The agents for

inhibiting prolactin secretion can be used for treating or preventing

pituitary adenomatosia, brain tumour, emmentopathy, autoimmune disease,

prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

cromegaly, Chiari-Frommel syndrome, Argonz-del Castilo ayndrome,

The inhibitory agents can also be used as contraceptives. The agents for

modulating placental function can be used for treating or preventing

choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

can absorbed the proper contraction of the contraction of th
                                                                                       Query Match
Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat type 11gand; modulation; prolactin secretion;
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RGIRPVGRF 10
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                                                                                          Similarity 100
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-coupled receptor ligands - for modulating prolactin
n or placental function, e.g. for treating menopausal
, tumoura, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinuma S,
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                                                                                                             96.0%;
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                                                                                   J.0%;
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                                                                                       Score 48; DB
; Pred. No. 0.0
0; Mismatches
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CC which is a ligand for the protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cella transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC function of the pituitary, central nervous system, pancreas and other CC ellypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; polsoning by heavy metals or drugs; CC diseases; creutzfeld-Jakob disease; and many others, also to improve post-CC operative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC enlated sequences; in receptor-binding assays; for production of Ab and CC animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide 11gand for orphan G protein coupled receptors -
for treating disorders of central nervous system, pituitary and
pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-009423/01.
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Sequence
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RGIRPVGRF

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Score 48; DB; Pred. No. 0.0

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RESULT 14
AAW95175
                                                                              The invention relates to a murine pituitary-derived ligsnd polypeptide CC which is s ligand for the G-protein coupled orphan receptor designated CC GPRID (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC function of the pituitary, central nervous system, pancreas and other CC fusues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the smount of receptor in a CC sample and to rsise sntibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disesse; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disesse; poisoning by heavy metals or drugs; CC disease; Schizophrenia; disorders of growth hormone secretion; cancer; CC coperative nutritional status and ss vssopressor. Transgenic snimals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC related sequences; in receptor-binding assays; for production of Ab and CC related sequences; in receptor-binding assays; for production of Ab and CC renthody. Sequences and primers; to identify cellulates which can be used for the preparation of snti-ligand polypeptide encoding assays; for production of Ab and CC antisers; which can be used for the preparation of snti-ligand polypeptide.
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW95175 standard;
                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide ligand
for treating disorders
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96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           screening
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Score 48;
Pred. No.
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DB 20;
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                  20;
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                                                                                                                                                                This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before snd after expulsion of placenta, uterine recovery failure, csesaresn section, stoppage of artificial fertilization or galactostasis and is slso applicable in veterinary medicine for promoting milk production in cow, goat and plg. This sequence represents a bovine peptide which acts ss an oxytocin secretio
                                                                                                                                                                                                                                                                                                                                          Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as injugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine; oxytocin secretion promoter; G protein-coupled receptor protain; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                         Claim 5;
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8	7,	Sequence 97, Appl	Sequence 61, Appl	Sequence 47, Appl	Sequence 5, Appl1	Sequence 4, Appli	_	Sequence 37, Appl	Sequence 31, Appl	Sequence 9, Appli	Sequence 8, Appli	Sequence 7, Appll	Sequence 48, Appl	Sequence 42, App1	Sequence 36, Appl	Sequence 73, Appl	Sequence 66, Appl

ALIGNMENTS

#### RESULT 1 US-08-776-971-93 Sequence 93, Appllcat1 Patent No. 6228984 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996 APPLICATION NUMBER: P 7/343371 FILING DATE: 28-DEC-1995 APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996 APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-AUG-1996 APPLICATION NUMBER: JP 8/24573 FILING DATE: 18-SEP-1996 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 27,026 REGISTRATION INFORMATION: TELEPHONE: 617-523-3400 TELEPHONE: 617-523-6440 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown> Fujli, Ryo Fukusumi, Shoji Kitada, Chieko TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140 CORRESPONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP APPLICANT: Hinuma, Shuji Habata, Yugo Kawamata, Yuji Hogoya, Masaki SEQUENCE CHARACTERISTICS ZIP: CITY: Boston STATE: MA COUNTRY: STREET: Application US/087769718 130 Water Street USA for Windows Version

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STRANDEDNESS: single
TOPOLOGY: linear
HOLECIDE TYPE: protein
FRACMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-08-776-971-93
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Patent No. 6103882
                                                                                                                                                                                                                                                                            TELEPHONE: 617-523-34
TELEFAX: 617-523-6440
INPORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G.
REGISTRATION NDMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TOPOLOGY: Tinear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Maraka, Yoko
APPLICANT: Mishimura, Osamu
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 1992 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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                                  2 RGIRPVGRF 10
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-40
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US-09-105-678A-40
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GENERAL INFORMATION:
                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                        Sequence 46, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/105,678A ETLING DATE: 26-7UN-1998
PRIOR APPLICATION DATA: APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-7UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
                                                                                          APPLICANT: MOriya, Takeo
APPLICANT: Manaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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100.0%; Pred. No. 0.0032;
tive 0; Mismatches (
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                                                                               ROBERTS & CUSHMAN, LLP
                                                                                                                                   PRODUCING
                                                                                                                                   A 19P2 LIGAND
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US-08-776-971-B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTMARE: PATENTIA Release #1.0, Vers
SOFTMARE: PATENTIAN Release #1.0, Vers
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON111, David G.
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                     COMPUTER: IBN compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILLING DATE: 06-Feb-1997
CLASSIFICATION CURRON>
PRIOR APPLICATION UNBER: PCT/JP96/03821
FILLING DATE: 28-DEC-1996
FILLING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBN PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 9; Conserv
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TOPOLOGY: 11
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                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIIN TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ninuma, Shuji
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                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CDSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08776971B
       APPLICATION NUMBER: JP 7/34337I FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Fujii, Ryo
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Kawamata, Yuji
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Best Local :
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                                                                                                                                                   COMPUTER: IBN compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNMAER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 RGIRPVGRF 20
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APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGNENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
NEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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Habata, Yugo
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APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
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STATE: MA
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STRANDEDNESS: single
TOPOLOGY: linear
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REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   CODNTRY: USA
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                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
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Nosoya, Masaki
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IOO.0%; Pred. No. 0.1
Live O; Mismatches
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US-08-776-971-64

Sequence 64, Sepplication US/08776971B

Patent NO. 628898

GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTN: 20 amino acids
TYPE: amino acid
STARNDEDNESS: single
COMPUTER: IBH COMPATIBLE
COMPUTER: IBH COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 11-NGCNAATION:
NAME: Conlin, David G.
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukusum1, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, TNEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nosoya, Masaki
Fujii, Ryo
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Habata, Yugo
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Fred. No. 0.0032;
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GENERAL INFORMATION:
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Best Local :
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12 RGIRPVGRF 20
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                                                                                                                                                                                                                                                                                                                  SOPTWARE: FastSEQ for Windows Vers.
CURRENT APPLICATION DATA:
APPLICATION UNUMER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIXE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
FRAGMENT TYPE:
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                         APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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9: Conserv
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                      NAME: Conin, David (
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 20 amino acids
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100.0%; Pred. No. 0.
Live 0; Mismatches
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ita, Yuji
                                                                          David G
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Best Local Similarity
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                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-34
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                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER; US 09/103,070
APPLICATION NUMBER; US 09/103,070
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
PILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1075-23-3400
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GENERAL INFORMATION:
                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA:
05.09/105,678
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ADDRESSEE: DIKE, BRO
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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                              Local Similarity
hes 9; Conserv
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ZIP: 02109
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2 RGIRPVGRF 10
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                                                                                                                                                                          amino acid
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                                Conservative
                       96.0%; >--
100.0%; Pr
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                            ; Score 48; DB
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0; Mismatches
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Pred. No.
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                       DB 4;
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RESULT 10
US-09-421-208-40
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Best Local Similarity 100.
Conservative
                                                                                                                         Sequence 46, Application US/09421208 Patent No. 6258561 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
APPLICATION NUMBER: JP 172118/1997
APPLICATION NUMBER: 27-JUN-1997
APPLICATION NUMBER: 27-JUN-1997
APPLICATION NUMBER: 27-026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
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APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METNOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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CITY: Boston
STATE: MA
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Pred. No.
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RESULT 12
US-09-105-678A-28
; Sequence 28, Application US/09105678A
"Arant No. 613882
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; MOLECULE TYPE: peptide
US-09-421-208-46
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TELEPHONE: 617-523-6400
TELEPAX: 617-523-640
INFORMATION FOR SEQ 1D NO: 46:
                                                            MEOTUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION OATA:
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OPERATING SYSTEM: PC-OOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                COMPUTER READABLE FORM: MEOIUM TYPE: Floppy
                                                                                                                                                                                                                                                  CORRESPONDENCE ADORESS:
AODRESSEE: DIKE, BRC
                                                                                                                                                                                                                                                                                       APPLICANT: Suenaga, Masato
APPLICANT: Moriya. Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishlmura, Osamu
TITLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGAND
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy dlsk
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                              APPLICATION NUMBER: US/09/105,678A FILING OATE: 26-JUN-1998
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STREET: 130 Water
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JP 172118/1997
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Pred. No.
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; OTHER INFORMATION: /product=
US-09-105-678A-28
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US-09-105-678A-35
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Patent No. 6
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                          APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION OATA:
                                                                                                                                                                                              COMPUTER READABLE FORM: MEOIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADORESSEE: OIKE, BRO
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Moriya, Ta.
APPLICANT: Tanaka, Yo.
APPLICANT: Nishimura,
TITLE OF INVENTION: M.
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TOPOLOGY: 11
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TYPE: amino acid
              NAME: Conlln, David G. REGISTRATION NUMBER: 2
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OTHER INFORMATION: /product-
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REFERENCE/DOCKET NUMBER:
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les 9; Conserv
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Tanaka, Yoko
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            27,026
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48466-342
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; TOPDLOGY: linear
; MDLECULE TYPE: peptide
US-09-105-678A-41
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                      Query Match
Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DDS
SDETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION ORDER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONITY DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41, Application US/09105678A Patent No. 6103882
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Best Local S
                                                                                                                                                                                                                   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID ND:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHDNE: 617-523-3400
TELEPAX: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishamura Desamu
TITLE DF INVENTION: METHOD DF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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STATE: MA
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617-523-6440
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100.0%; Pr
                                          96.0%; Score 48; DB 3; Length 21; 100.0%; Pred. No. 0.0034; 110e 0; Mismatches 0; Indels
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Pred. No. 0.0034;
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
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                                                                                            D
                                                                                                                                                                                                                                                                 ; TOPDLOGY: linear; MOLECOLE TYPE: peptide US-09-105-678A-47
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                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                        Matches
                                                                                                                                                                                                       Query Match
                                                                                                                                                                    Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFDRMATION:
NAME: CON110, DAVId G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
DPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRDNSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Takeo
APPLICANT: Tanaka, Tokeo
APPLICANT: Nishimura, Dsamu
TITLE DF INVENTIDN: METHOD DF PRDDUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 130 W
CITY: Boston
STATE: MA
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                                                                                                                                                                Score 48; DB 3; Length 21; pred. No. 0.0034; 0; Mismatches 0; Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                                                          283138 seqs, 96089334 residues
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                                                                                                                                                                                                                                                                                                 1 XRGIRPVGRFX 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                             ; Search time 172.41 Seconds
(without alignments)
6.131 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greator than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	Φ	տ	4	w	2	ų	:	Result
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AH2262	I35055	F75393	G87485	T40334	E83663	A56449	\$65684	868367	T35893	C70365	C70502	E70655	T36845	B95351	AD2870	F97646	AH1823	877236	S51485	A65057	B82557	E82221	T45447	B70821	XXGZAC	T39533	G70875	JC7607		In
hypoth	MHC cl	hypoth	hypoth	hypoth	91utan	protor	protop	protop	FAD-de	twitch	hypoth	hypot	probak	VirB6	ABC tr	probat	30S r1	r1bosomal	ribosomal	hypoth	hypoth	DNA 9y	probat	hypoth	acetyl	hypoth	probat	prolac	1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Description
cal				_	lutamy1-tRNA synt	protoporphyrinogen	protoporphyrinogen	protoporphyrinogen	FAD-dependent oxid	-		hypothetical prote	probable membrane	VirB6 type IV secr	transporter, m	probable aliphatic	$^{\circ}$		pro	_	hypothetical prote	rase, chain		hypothetical prote	1	hypothetical prote	probable oxidoredu	prolactin-releasin	- Port-Cit	2

A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barreii, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A:Reference number: A70500; MUID:98295987
A:Accession: G70875
A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA
A:Residues: 1-674 <COL>
A:COLS
A:Cross-references: GB:AL1010186; GB:AL123456; NID:g3261493; PIDN:CAA15852.1; PID:g269
A:Experimental source: strain H37Rv
C:Genetics:

probable oxidoreductase (EC 1.5.99.-) - Mycobacterium tubercuiosis (strain H37RV)
C;Species: Mycobacterium tubercuiosis
C;Species: Mycobacterium tubercuiosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000
C;Accession: G70875
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Gentles, S.; Hamiln, N.; Hoiroyd, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeiton, S.; Squares, S.
Nature 393, S37-544, 1998

45	44	43	42	41	40	39	38	37	36	35	34	w w	32	31	30	
32	32	32	32	32	32	32	32	32	32	32	32	<u>3</u> 2	32	32	32	
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562	492	435	410	409	388	374	309	307	299	292	285	266	249	154	150	
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	
S16594	G70749	A72658	D83573	T51126	AG3444	G70947	T29118	AD0883	C70643	G95926	T50932	T43770	S76104	T34825	809872	
regulatory protein	probable hyce prot	probable isocitrat	tŘNA nucleotidyí t	hypothetical prote		hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	probable saccharid	short-chain dehydr .	ribosomai protein	hypothetical prote	hypotheticai prote	hypotheticai prote	

## ALIGNMENTS

RGIRPVGRF 10         RGIRPVGRF 52	C:GenetLos: A:Gene: PTRP A:Introns: 33/1  A:Introns: 33/1  Query Match 96.0%; Score 48; DB 2; Length 83;  Query Match Best Local Similarity 100.0%; Pred. No. 0.016;  Best Local Similarity 100.0%; Pred. No. 0.16;  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A; Contents: Spleen A; Accession: JC7607 A; Molecule type: DNA A; Residues: 1-83 < YAM> A; Residues: 1-83 < YAM> A; Cross-references: DDBJ:AB040612; DDBJ:AB040613 A; Cross-references: DDBJ:AB040612; DDBJ:AB040613 C; Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.	R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hoshida, T.; Ishizuka, T.; Hosoya, Biochem. Biophys. Res. Commun. 281, 53-56, 2001 A;Title: Isolation and characterization of the rat prolactin releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959	JC7607  prolactin-releasing peptide - rat prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7607
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x;rcopies, Q.P.; Masamune, S.; Walsh, C.T.; Sinskey, A.J.
J. Blol. Chem. 262, 97-102, 1987
A;Titie: Biosynthetic thiolase from Zoogloea ramigera. III. Isoiation and characterizati A;Reference number: A26121; MUID:87083504
A;Accession: A26121
A;Moleculo: A26121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SPBC16A3.19 - fission yeast (Schizosaccharomyces C, Species: Schizosaccharomyces pombe C, Date: 03-Dec: 1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec C, Accession: T39533 R, Wood, V., Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R. submitted to the EMBL Data Library, February 1998 A, Reference number: $21862 A, Accession: T39533
                                                                                                    C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A; homotetramer; ketone body metabolism;
E;2-391/Product: acetyl-CoA acetyltransferase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                           acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - Zoogloem ramigera N;Alternate names: acetomeetyl-CoA thlohase; blosynthetic thiola C;Species: Zoogloem ramigera C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change C;Accession: A26121
R;Pcoples, Q.P.; Massmune, S.; Walsh, C.T.; Sinskey, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: Methylophilus methylotrophus W3A1 trimethylamine C;Keywords: 4Fe-4S; metalloprotein; oxidoreductase F;337,340,344,356/Binding site: 4Fe-4S cluster (Cys) (covalent)
                                                                                                                                                                                                 A;Cross-references: EMBL:J02631; NID:g155617; PIDN:AAA27706.1; PID:g155618 A;Experimental source: strain I-16-M, AFCC 19923 C:Comment: The active enzyme, a tetramer of identical chains, catalyzes the hes1s, and poiy-beta-hydroxybutyrate biosynthes1s.
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                                                                                                                                                                                C; Genetics:
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A; Introns: 53/1;
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A:Experimental source: strain 972h-;
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-; cosmid c16A3
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DNA gyrase, chain A VC1258 [Imported] - Vibrio cholerae (strain N16961 serogroup Q1) C:Specles: Vibrio cholerae C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; James, K.D.; Parkhill, J.; submitted to the EMBL Data L: A; Reference number: Z22967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable two-component system sensor [imported] - Mycobacterium
C:Species: Mycobacterium ieprae
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change
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C; Superfamlly:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Titie: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: B70821
                                                                                                                                                                                                                                                                                                                    A; Note: MLCB373.27
C; Superfamily: env
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from A;Holecule type: DNA A;Residues: 1-519 <JAM>
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C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-
                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: cosmid C; Genetics:
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A; Residues: 1-504 <COL>
A; Cross-references: GB;
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                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
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85.7%;
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Library, February 1998
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1; Mismatc
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Pred. No.
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A; Status: prediminary
A; Madetus: prediminary
A; Molecule type: DNA
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A; Molecule type:
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A:Accession: E82221
A:Status: preliminary
A:Molecule type: DNA
A:RCSiducs: 1-894 (HEI)
A:Cross-references: GB:AE004205; GB:AE003852; NID:g965574
A:Experimental source: aerogroup O1; strain N16961; bloty
C:Genetics:
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C;Accessaion: E82221

R;Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.N.

Nature 406, 477-483, 2000
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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A83515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
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C; Superfamily: DNA topoisomerase
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Ol; strain N16961; biotype
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Pred. No.
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R;Blattner, F.R.; Piunkett III, G.; Bloch, C.A.; Perna, N.T.; B.A.; Rose, D.J.; Nau, B.; ShBO, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; NUID:97426617
A;Accession: A65057
                                                           C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S77235

C;Accession: S77235

C;Accession: S77236

C;Acces
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S77236
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A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: Escherichia coli hypothetical protein b2757
A;Title: Sequence analysis of the genome of the uniceilular cyanobacterium Synechocys {\mathfrak s}.
                                                                                                                                                                                                                                                                                                      ribosomal protein Si - Synechocystis
N;Alternate names: protein slri356
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C; Keywords: pro
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C;Genetics:
A;Gene: rpsl
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A; Accession: S51485
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C; Date: 15-Jui-1995 #sequence_revision
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A; Residues: 1-226 <BLAT>
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C;Specles: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Scp-1997 #text_change 08-Oct-1999
C;Acceasion: A65057
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Best Local :
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6; Conserv
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0; N1smatches
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Pred. No.
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Yamada, N.; Ya
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C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AN1823 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; 1rigu: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 R;Kaneko of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: Ab1807; MUID:21595285; PMID:11759840 A;Accession: AN1823
                                                                                                                                                          R;Goodner, B.; Ninkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Llu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
A;Accession: F97646
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C:Superfamily: Synechocystis ribosomal protein
C:Keywords: protein biosynthesis; ribosome
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A:Residues: 1-328 <KAN>
A:Cross-references: EMBL:D90907; GB:AB001339; NID:91652618; PIDN:BAA17570.1; PID:9165265
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
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A;Accession: S77236
A;Status: nucleic acid sequence not shown
                                               A;Cross-references: GB:AE007869; PIDN:AAK88127.1; PID:g15157563; GSPDB:GN00169
C;Genetics:
                                                                                            A;Status: preliminary
A;Molecuie type: DNA
A;Residues: 1-290 <KUR>
                                                                                                                                                                                                                                                                                                                           probable aliphatic sulfonateS transport permease protein ssuc AGR_C_4335 [imported] -
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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Best Local Similarity
""**ches 6; Conserv
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C;Superfamily: Synechocystis ribosomal
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A;Genc: AGR_C_4335
A;Map position: ci
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A; Residues: 1-343 <KUR>
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Best Local S
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  position: circular chromosome
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Pred. No. 46;
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A;Cross references: GB.AE006469; PIDN:AAK65372.1; PID:g14523833; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Baric
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisi
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.N.; Kiss, E.; Komp, C.;
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meillotil.
A;Reference number: A96039; MUID:21368234; PMID:il474104
                                                                                                                                                                                                                                                      R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.; Katnan, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.N.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A;Reference number: A95262; NUID:21396509; PMID:11481432

A;Accession: B95311
A;Status: preliminary
A;Moiecule type: DNA
A;Residues: 1-313 <KURN
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C;Accession: B95351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VirB6 type IV secretion protein [imported] - Sinorhizobium meiiloti (strain 1021) mag C; Species: Sinorhizobium meiiloti
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A; Hap position: circular chromosome
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A; Residues: 1-290 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gllet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, F.; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
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Scoring table:

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## SUMMARIES

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30-MAY-2000 (Rei. 39. Last sequence update)
01-MAY-2022 (Rei. 41. Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; prolactin-
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Hinuma S., Habata Y., Fujii R., Kawamata Y., Ho
Kitada C., Masuo Y., Asano T., Matsumoto N., Se
Kitada C., Nishimura O., Onda N., Fujino M.;
Kurokawa T., Nishimura O., Onda N., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
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PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Ve
Catarrhini;
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T., Nishimura O., On
                                             DB 1; Le
0.0042;
hes 0:
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1; Hominidae; Nomo.
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0.004;
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                                                                                                                                                                                                                                                                                                                                                                                       peptide (PrRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sekiguchi M., Fu
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                                                                    Length 87
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RESULT 3
PRRP_BOVIN
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Best Local S
Matches 9
                                                                                                            01-APR-1988
01-APR-1990
01-OCT-1996
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PEPTIDE
MOD_RES
SEQUENCE
                                                                                                                                                  TNIL_ZOORA
P07097;
                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hinuma S., Habata Y., Fujii R., Kawamata Y., Nosoya M., Fukusum Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin-releasing peptide in the brain."; "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).

-I- FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPRIO. May Sti actotrophs directly to secrete PRL.

-I- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND NYPOTNALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP)
hormone) [Contains: Prolactin-releasing peptide]
SEQUENCE FROM
STRAIN-ATCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as ion as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       PNBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa:
Mammalia; Eutheria;
                                                            Zoogloea ramigera.
Bacteria; Proteobacteria:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                   Zoogloea.
NCBI_TaxID=350;
                                                                                                  Acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB015417; BAA29025.1;
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9; Conserv
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0 (Rel. 14, Last sequence update)
6 (Rel. 34, Last annotation update)
acetyltransferase (EC 2.3.1.9) (Ac
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Pred. No.
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PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35Al3B0FA908 CRC64;
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0.0048;
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PEPTIDE PRRP20.
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Best Local :
                                        GYRA_AERSA
P48369;
01-FEB-1996
01-FEB-1996
01-NOV-1997
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SEQUENCE
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Pfam; PF00108; thiolase_C; 1.

Pfom; PF02803; thiolase_C; 1.

PROSITE: PS00098; THIOLASE_1; 1.

PROSITE: PS00099; THIOLASE_3; 1.

PROSITE: PS00737; THIOLASE_2; 1.

Transferase; Acyltransferase; PHB blosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-87083504; PubMed-2878929;
Peoples O.P., Masamune S., Waish C.T., Sinskey
"Biosynthetic thiolase from Zoogloea ramigera.
Characterization of the structural gene.";
J. Biol. Chem. 262:97-102(1987).
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ACT_SITE
ACT_SITE
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PIR; /
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   Bacteria;
             Aeromonas
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A26121; XXGZAC.

A27754; AX7754.

P27796; IAFY.
                               gyrase
                                                                                                                                            RGIRPVGR
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                                                                                                                                                                       Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long a d and this statement is not removed. s requires a license agreement (See h an email to license@isb-sib.ch).
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 salmonicida.
Proteobacteria;
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(Re1.
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                                                                                 STANDARD;
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Last
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                                                             Created)
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  gamma
                               sequence update) annotation updat .99.1.3).
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Pred. No. 9.3;
2; Mismatches
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C->G: LOSS OF ACTIVITY
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   subdivision;
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                                        update)
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   Aeromonadaceae;
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TII. Isolation a
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
Hypothetical protei
YGCI OR 82757.
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EMBL; L42453; AAA87239.1; -.
HSSP; P09997; 1AB4.
InterPro; IPR002205; DNA_topo1soIV.
Pfam; PF00521; DNA_topo1soIV; 1.
SMART; SM00434; TOP4c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as ion as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (OCT-1995) to
Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Giasner J.D., R Gregor J., Davis N.W., Kirkpatrick H.A., Go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isomerase; Topoisomcrase; DNA-binding.
ACT_SITE I22 122 DNA CLEAVAGE (BY SIMILARITY).
SEQUENCE 922 AA; 101333 MW; 8894965DC4217077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95142596; PubMed-7840589; Oppegaard H., Sorum H.;
                                             STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                        Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                             046898;
16-0CT-2001
                                                                                                                                                                                                                                                                            ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrob. Agents Chemother. 38:2460-2464(1994).
-1- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gyrA mutations in quincione-resistant isolates 
Aeromonas salmonicida.";
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NCBI_TaxID=645;
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                    Escherichia coli
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STRAIN-ATCC 14174;
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CATALTYIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
ENZYME FORMS AN A2B2 TETRAMER.
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STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
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protein ygcI precursor.
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62
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                                                                                                                                     gamma subdivision; Enterobacteriaceae;
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Pred. No.
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22;
   Goeden
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              , Perna N.T., Burland V
Rode C.K., Mayhew G.F.,
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Best Local S
Matches 6
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"The complete genome sequence of Escherichia coli K-12.",
"Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                Sugita M., Sugita C., Sugitra M.;

Structure and expression of the gene encoding ribosomal protein from the cyanobacterium Synechococcus sp. strain PCC 6301: striki sequence similarity to the chloroplast ribosomal protein CS1.";

Hoi. Gen. Genet. 246:142-147(1995).
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 INIT_MET
DOMAIN
DOMAIN
DOMAIN
                                                          Pfam; PF00575; S1; 3.
SMART; SM00316; S1; 3.
PROSITE; PS50126; S1; 3.
                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                              Synechococcus sp. (strain PCC 6301) (Anacystis niduians). Bacteria; Cyanobacteria; Chroococcales; Synechococcus. NCBI_TaxID-1139;
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P46228;
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01-FEB-1996 (Rel. 33,
16-OCT-2001 (Rel. 40,
305 ribosomal protein
                                                                                                          EMBL; D28752; BAA05946.1;
HSSP; P05055; 1SRO.
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MEDLINE-95166170; P
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                                                                                              InterPro; IPR003029; S1.
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                                                 Ribosomal
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AE000359; AAC75799.1; ALT_INIT.
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protein CS1.";
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Nosouchi T., Matsuno ...,
Nosouchi T., Matsuno ...,
Nosouchi T., Matsuno ...,
Nosouchi T., Matsuno ...,
Nokumura S., Shimpo S., Takeuchi C., waua ...,
Yasuda M., Yasuda M., Tabata S.;
Yamada M., Yasuda M., Tabata S.;
Sequence analysis of the genome of the uniceilular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions."
DNA Res. 3:109-136(1996).
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P73530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Sato S., Kotani H., Tanaka A., Agamizu E., Naka
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Nosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                      Interpro; IPR003029; S1.
Pfam; PF00575; S1; 3.
SMART; SM00316; S1; 3.
PROSITE; PS50126; S1; 3.
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HSSP; P05055;
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MEDLINE-97061201; PubMed-8905231;
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66.7%;
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annotation updat
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                                                                                                              Score 34; DB
Pred. No. 12;
1; Mismatches
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Pred.
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Mismatches
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O9UP52; O75422; (
01-MAR-2002 (Rel
01-MAR-2002 (Rel
01-MAR-2002 (Rel
-I-SUBURIT: Homodimer.
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-I-SUBURIT: Homodimer.
-I-SUBURIT: Homodimer.
-I-SUBURIT: Homodimer.
-I-SUBURIT: Homodimer.
-I-SUBURIT: Homodimer.
-I-ALTERNATIVE PRODUCTS: 3 lacforms: Alpha (shown here), beta and gamma; are produced by alternative splicing.
-I-TISSUE SPECIFICITY: Predominantly expressed in liver. While the alpha form is also expressed in splicen, lung, muscle, prostate and peripheral blood mononuclear cells, the beta form is expressed in all tissues tested, albeit weakly.
-I-DISEASE: Defects in TFR2 are a cause of hereditary hemochromatosis type III (HFE3), HFE3 is a disorder of iron hemostasis resulting in iron everload and has a phenotype indistinguishable from that of hereditary hemochromatosis (HH). HH is characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Carcinoma, and Embryo;
Isogal T., Ota T., Hayashi K., Sugano T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara t
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi t
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A.,
Ninomlya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databasea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gloeckner G., Scherer S., Schaltevoy N., Pragon S., Rosenthal A.;
"Large scale analysis of two regions in human chromosome 7q22:
"Large scale analysis of genomic sequence around the EPO and CU
                                                                                                                                                                                                                                                                                                                                                                       Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11313241;
Roetto A., Totar
Cali A., De Gobb
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PubMed=9799793;
Gloeckner G., Scherer S., Schattevo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koeffler H.P.;
"Molecular cloning of transferrin receptor transferrin receptor-like family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS ALPHA AND TISSUE-ETYTHTOLEUKEMLE, and Myelotd LeumenLine-99340005; PubMed-10409623; Kawabata H., Yang R., Hirama T., Yuong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiena (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                               A., Totaro A., Piperno A., Piga A., Longo
., De Gobbi M., Gasparini P., Camaschella
uatations inactivating transferrin 2 in he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 genes.";
Res. 8:1060-1073(1998).
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"Atazoa; Chordata; (
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Gasparini P.;
type of haemochromatosis mapping
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                                                                          of hereditary hemochromatosis
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Protoporphyrinogen
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                                                                                                              PFOX_HUMAN
P50336;
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                    Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalla; Eutheria;
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Pfam; PF02225; PA; 1.
Transmembrane; Glycoprotein;
NCBI_TaxID-9606;
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MISCELLANEOUS: The variant 199-172 found in hereditar
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AK000421;
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; Primates;
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annotation
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INTERCHAIN (POTENTIAL).

INTERCHAIN (POTENTIAL).

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N-LINKED (GLCNAC...) (POTENTIAL).

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N-LINKED (GLCNAC...) (POTENTIAL).

MISSING (IN ISOFORM BETA).

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MISSING (IN ISOFORM GAMMA).
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SIGNAL-ANCHOR (TYPE-II MEMBRANE
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R -> RIPLSAQV (IN REF. 2)
D3D3082BA835413A CRC64;
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                     Craniata; Vertebrata; Catarrhini; Hominidae;
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Meissner P.N., Dalley T.A., Hift R.J., Ziman M., Corrigall A. Roberts A.G., Meissner D.M., Kirsch R.E., Dalley H.A.; "A R59W mutation in human protoporphyrinogen oxidase results decreased enzyme activity and is prevalent in South Africans variegate porphyria."; Nat. Genet. 13:95-97(1996).
                                                                                                                                                                                                                entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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*The genetic basis of 'Scarsdale Gournet Diet' variegate porphy
missense mutation in the protoporphyrinogen oxidase gene.";

Arch. Dermatol. Res. 290:441-445(1998).

-I- EUNCTION: CATALYES THE 6-ELECTRON OXIDATION OF PROTOPORPHY
                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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MEDLINE-98434271; PubMed-9763307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein Sci. 5:98-105(1996).
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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"Cioning of a human cona for protoporphyrinogen oxidase complementation in vivo of a heme mutant of Escherichia J. Biol. Chem. 270:8076-8080(1995),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT VP TRP-59, AND VARIANT CYS-168.
MEDLINE-96241580; PubMed-8673113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deybach J.-C.,
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                                                         Flavoprotein;
                                                                                  Porphyrin biosynthesis;
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Nishimura K., Taketani S., Inokuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER
SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRANE
WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LDNG,
LIVER, SKELETAL MUSCLE, KIDNEY, AND PRACERAS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISEASE: DEFECTS IN PPOX ARE THE CAUSE OF PORPHYRIA VARIEGATA (VP), A DISEASE CHARACTERIZED BY SKIN HYPERRIGMENTATION AND HYPERREICHOSIS, ASSOCIATED WITH ACUTE ATTACKS, LIKE THOSE OF INTERMITTENT PORPHYRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: PENULTIMATE
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Genet. 5:40
                                                         FAD;
                                                                                                                                                            BAA07538.1;
AAA67690.1;
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PENULTIMATE STEP IN HEME AND POI
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Mitochondrion; Disease mutation;
14 FAD (POTEMTIAL).
59 R -> W (IN VP).
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                                                                                  Heme
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P51175; P97
                            This
                                                                                                                                                                              Ferreira G.C., Andrew T.L., Karr S.W., Dailey H.A.;
"Organization of the terminal two enzymes of the heme blosynthetic
pathway. Orientation of protoporphyrinogen oxidase and evidence for
membrane complex.";
J. Biol. Chem. 263:3835-3839(1988).
-!- FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPHYRIM
                                                                                                                                                                                                                                                                                                            TISSUE-Erythroleukemia;
MEDLINE-9531315; PubMed-7607249;
MEDLINE-9531315; PubMed-7607249;
Taketeni S., Yoshinaga T., Furukawa T., Kohno H., Tok
Mishimura K., Inokuchi H.;
"Induction of terminal enzymes for heme blosynthesis
differentiation of mouse erythroleukemia ceils.";
Eur. J. Blochem. 230:760-765(1995).
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01-OCT-1996 (Rei. 34, Last squence
15-DEC-1998 (Rei. 37, Last annotation
Protoporphyrinogen oxidase (EC 1.3.:
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                             IX + H(2)0(2).

COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMILARITY).

COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMILARITY).

PATHMAY: PENULTIMATE STEP IM HEME AND PORPMYRIM BIOSYNTHESIS.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRA

WITH ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE.

INDUCTION: DURING ERYTHROID DIFFERENTIATION.

SIMILARITY: BELONGS TO THE PROTOPORPHYRINGCEN OXIDASE FAMILY.
                                                                                                                                                      CATALYTIC ACTIVITY: Protoporphyrinogen-IX + O(2)
                                                                                                                                                                     IX TO FORM PROTOPORPHYRIN IX.
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 SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no restr
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Bacillus halodurans.

Bacteria: Firmicutes; Bacillus/Clostridium

Bacillus/Staphylococcus group: Bacillus.
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QSKGF6;

QSKGF6;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

GLULAMYI-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA 11gase)
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                                Pfam; PF00749: tRNA-synt_1c: 1.
PRINTS: PR00987; TRNASYNTHGLU.
PROSITE: PS00178: AA_TRNA_LIGASE_I:
                                                                                            EMBL: AP001507; BAB03828.1; -. InterPro; IPR000924: tRNA-synt_lc. InterPro; IPR001412: tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                      haiodurans and genomic sequence comparison w
Nucleic Acids Res. 28:4317-4331(2000).
-1- CATALYTIC ACTIVITY: ATP + L-giutamate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takami H., Nakasone K., Takaki Y., Maeno G.
Fuji F., Hirama C., Nakamura Y., Ogasawara
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MEDLINE-20512582; PubMed
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01-AUG-1990 (
01-FEB-1991 (
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MEDILINE-90269039: PubMed-2161319;

MEDILINE-90269039: PubMed-2161319;

Chee M.S., Bankler A.T., Beck S., Bohnl R., Brown C.M., Cerny R.,

HOTSNeil T., Butchison C.A. III. Kouzarides T., Martignetti J.A.,

HOTSNeil T., Butchison C.A. Tomlinson P., Weston K.M., Barreil B.

Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barreil B.

Analysis of the protein-coding content of the sequence of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae: Cytomegalovirus.
                         Hypothetlcal
SLR0361.
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Synechocystis sp. (strain PCC 6803). Bacteria: Cyanobacteria; Chroococcaies:
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PIR; S09872; S09872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                cytomegalovirus strain AD169.";
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04348B: 075749;
15-JUL 1999 (Rel. 38, Created)
16-CCT-3001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Aflatoxin B1 aldehyde reductase 1 (EC 1.-.-.) (AFB1-AR 1)
                                                                                                                                                                                                                                                                                                                       MEDLINE-98244807; PubMed-9576847; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; "Molccular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin B1-aidehyde reductase."; B1ochem. J. 332:21-34(1998).
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InterPro; IPR000613; PseudoU_synth.
InterPro; IPR000748; Psi_RSU.
InterPro; IPR002942; S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordota;
Mammalia; Eutheria; Primates;
MC8I_TaxID=9606;
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PROSITE; PS01149; PSI_RSU; 1.
Hypothetical protein; Complete
SEQUENCE 249 AA; 28228 MW;
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Pram1 C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-
1p36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
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or send an email to license@isb-sib.ch).
                                                                                                                                                              MEDLINE-99040634; PubMed-9823300;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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MEDLINE-96127529;
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A., Sato S., Kotani H.,
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFBL) PROTEIN-BINDING
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFBL) PROTEIN-BINDING AFBL DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINGENIC
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [3]
SEQUENCE
Hall R.;
                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        InterPro; IPR001395; Aldo_ket_red.
Pfam; PF00248; aldo_ket_red; 1.
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EMBL; Y16675; CAA76347.1; -.
EMBL; AL033413; CAB72321.1; -.
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215 GKQPYGRF
                             3 GIRPVGRF 10
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                                                          Similarity
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330 AA;
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Search completed: September 13, 2002, 09:30:48 Job time: 1138 sec

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1: sp_archea:*
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3: sp_fung1:*
4: sp_human:*
5: sp_inverteb:
6: sp_mamma1:*
7: sp_mhc:*
8: sp_organe1:
9: sp_plant:*
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(without alignments)
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12, 19,

Last sequence update)
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9			773		О.	Φ	œ			Q964n4 caenorhabdi	O	deinococcu	Q99yp5 streptococc		Q9a718 caulobacter	schi	Q99m34 mus musculu	O50531 streptomyce	aquifex ae		P96221 mycobacteri	O88067 streptomyce	092yz8 rhizobium m		096tc9 homo sapien		1e1sh	Q9up52 homo sapien

### ALIGNMENTS

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  093L27
093L27;
01-DEC-2001
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Eukaryota; Metažoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
NCB1_TaxID=7957;
                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUE-BRAIN;
TISSUE-BRAIN;
Satake H., Minakata H., Fujlmoto M.;
Satake H., Minakata H., Fujlmoto M.;
"Carcassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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77 88;
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C STRAIN-GSS1 / DSM 4299 / JCM 9571;

C STRAIN-GSS1 / DSM 4299 / JCM 9571;

X MEDLINE-20570466; PubMed-11121031;

X Kawashima T., Amano N., Koike N., Makino S.-I., Niguchi S.,

X Mawashima T., Amano N., Xolke N., Yamazaki M., Kawamo N., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

**Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.*;

**T "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.*;

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01-OCT-2001 (TrEMBLrel. 1
01-OCT-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
TYG1120468 PROTEIN.
                                         050431;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY033994; AAK61719.1; -.
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
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                                                                                                                                                             304 GIRPAGKE
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Pred, No. 1.7;
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sequence update)
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polyketide gene ciuster
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Nature 393:537-544 (1998).
EMBL; ALO10186; CAA15852.1; -.
Tuberculist; Rvi175c; -.
TuterPro; IPR001064; Crystailin.
InterPro; IPR001327; FAD_byr_redox.
InterPro; IPR001327; FAD_binding.
InterPro; IPR00135; Oxidored_FMN.
Pfam; PP00724; Oxidored_FMN; 1.
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                                                                   Wood V., Rajandream M.A., Barrell B.G., 8eck A submitted (FEB-1998) to the EMBL/GenBank/DDBJ EMBL; AL021748; CAA16670.1; -. InterPro; IPR001005; Myb_DNA_bind. PROSITE; PS00037; MYB_1; UNKNOWN_1. Hypothetical protein. SEQUENCE 272 AA; 30901 MW; 8FE0EB29217107A
                                                                                                                                                                                                                                                                               01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 30.9 KDA PROTEIN C16A3.19 IN CHROMOSOME
SPBC16A3.19.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.
Bavies R., Devlin K., Feitwell T., Gentles S., Hamlin N., Ho
Nornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy
Oliver S., Osborne J., Quali M.A., Kogers J.
Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barreil B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-972;
Wood V., Rajandrea
                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetaceae;
                                                                                                                                                                                                            Schizosaccharomyces.
NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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2,4-DIENOYL-COA REDUCTASE.
FADH OR RV1175C OR MTV005.11C.
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PF00070; pyr_redox; 1.
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PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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           70.0%;
85.7%;
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Score 35; DB
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Mismatches
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%/DDBJ databases.
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                             Length 272;
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RA Cole S.T., Brosch R., Psrkhiil J., Garnier T., Churcher C., Harris D.,

RA Cole S.T., Brosch R., Frithill Tekais F.,

RA Gordon S.V., Eigimeier K., Gas S., Barry C.E. III, Tekais F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

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RA Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,

RA Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Qusil M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehesd S., Barreli B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

re complete genome sequence.";
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01-0CT-2001 (TrEMBLrel. 1
01-0CT-2001 (TrEMBLrel. 1
MLR9222 PROTEIN.
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Mycobacterium tuberculosis.
Mycobacterius; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteris; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriscese; Mycobacterium.
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HCBI_TsxID=1773;
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STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
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Phyllobacteriaceae; Mesorl
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Best Local !
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InterPro; IPR003561; His_kin
InterPro; IPR004359; HIS_KIN
InterPro; IPR004359; HIS_KIN
Pfam; PF00572; HAMP; 1
Pfam; PF00512; HAMP; 1
SMART; SM00304; HAPP; 1
SMART; SM00308; HAPP; 1
SMART; SM00388; HASKA; 1
HSSP; P02933; IBXD.
Leproma; ML0175; ...
InterPro; IPR004358; E
InterPro; IPR003660; E
InterPro; IPR003594; E
InterPro; IPR00361; E
InterPro; IPR00361; E
InterPro; IPR004359; E
Pfam; PF00572; HAMP; J
Pfam; PF02518; HATPBse
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01-MAY-1999 (TREMBLREL. 10, Last sequence updste)
01-DEC-2001 (TREMBLREL. 19, Last annotation updste)
01-DEC-2001 (TREMBLREL. 19, Last annotation updste)
PUTATIVE TWO-COMPONENT SYSTEM SENSOR KIHASE.
MLO175 OR MLCB373.27.
MYCOBacterium leprae.
Bscteria: Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobscterisco
                                                                                                           Cole S.T., Eiglmeier K., Psrkhill J., Jsmes K.D., Thomson N.R., Wheeler P.R., Honore N., Gsrnier T., Churcher C., Harris D., Wingall K., Bssham D., Brown D., Chiliingworth T., Connor R., Davies R.M., Deviin K., Duthoy S., Feitwell T., Fraser A., Hamlin Holroyd S., Hornsby T., Jagels K., Lacroix C., Maciean J., Moule Murphy L., Oliver K., Ouail M.A., Rajandresm M.A., Rutherford K.M. Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares S., Stevens K., Taylor K., Whitehesd S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM H.A. HSTRIS D., Taylor K.; Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculist; Rv0982;
InterPro; IPR003660;
                                                                                                                                                                             Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                           STRAIN-TH;
MEDLINE-21128732; PubMed-11234002;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM H.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q925G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1769;
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L; AL021999;
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AL583917;
P02933; 1E
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 HATPase_c;
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                       HATPASC_C.
His_kinA.
His_KIN_sig.
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His_kinA.
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85.7%;
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Pred. No.
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                   O9VS40, PRELIMINARY;
O9VS40, TrEMBLrel. i
01-MAY-2000 (TrEMBLrel. i
01-MAY-2000 (TrEMBLrel. i
01-DEC-2001 (TrEMBLrel. i
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01-OCT-2000 (
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DNA GYRASE, (
                                                                                                                                                                                                                                 SEQUENCE
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833 PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Ciayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Seliers P.,

McDonald L., Dtterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRUSENSOR.
SMART; SM00304; HATPASE_C; 1.
SMART; SM0038; HATPASE_C; 1.
 CG8608 PROTEIN.
UNC-13-4A OR CG
                                                                                                                                                                                                                                                    InterPro; IPR002205; DNA_topolsoIV Pfam; PF00521; DNA_topolsoIV; 1. SMART; SM00434; TOP4c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VC1258.
Vibrio cholerae
                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000).
EMBL; AE004205; AAF94417.1;
HSSP; P09097; LAB4.
TIGR; VC1258; -
                                                                                                                                                                                                                                                                                                                                     cholerae.
                                                                                                                                                                                                                                                                                                                                       "DNA sequence of both chromosomes cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-666;
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 CG8608
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Pred. No. 1.6et
3; Mismatches
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Last
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Last annotation update)
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                     annotation update)
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                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00360; C2D0
SMART; SM00239; C2; C2; PROSITE; PS50004; C2; SEQUENCE 1000 AA;
   09PAQ0;
09PAQ0;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003559; AAF50589.1; HSSP; P21707; 1BYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glibbs R.A., myself
"The genome sequence of Drosopi
Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophiia melanogaster (Fruit fiy).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00168; C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0035756; unc-13-4A.
InterPro; IPR000008; C2.
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6; Conserv
   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                            PRELIMINARY;
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A; 114286 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                        70.0%;
   15,
Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 5;
Pred. No. 1.8e+02;
2; Mismatches 1
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDF14F05A55696A2 CRC64;
                                                                                                  1056 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1000;
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RA Alvarenga R., Aives L.M.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Aives L.M.C., Arruda P., Bala G.S., Baptista C.S.,
RA Barros M.N., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto M.R.P., Cammargo A.A., Camrargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.C.R.,
RA Coulinho L.L., Cristofani M., Dias-Neto E., Docena C., Ei-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Frags J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kursmae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.P., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Menok C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitoreilo C.B.,
RA Menok C.P.M., Miracca E.C., Niyaki C.Y., Monteiro-Vitoreilo C.B.,
RA Menok C.P.M., Mogal M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA de Oliveira M.C., de Oliveira R.C., Pathieri D.A., Paris A.,
RA de Oliveira G.A.G., Pereira H.M. Jr., Pesquero J.B.,
RA de Suza A.P., Tercozi M.F., Truffi D., Tsai S.M., Jr.,
RA de Silva A.C., da Silva A.M., da Silva F.V., Savasaki H.E.,
RA de Souza A.P., Tercozi M.F., Truffi D., Tsai S.M., Tshako M.N.,
RA Alada B., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Gago M.A., Zatz M., Meldanis J., Setubal J.C.,
RH., Alada B., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RH., Chan Shuys M.A., Verjovski-Almeida S., Vettore A.L.,
RH., Sepones sequence of the plant pathogen Xylella fastidiosa.",
RM Hypothetical protein; Complete proteome.
Sequence 1055 AA; 118471 MW; 361CF2S10BDFFC10 CRC54;
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                                                                                                                                                         O9VU79 PRELIMINARY;
O9VU79;
O1-MAY-2000 (TIEMBLIE1. 1
O1-MAY-2000 (TIEMBLIE1. 1
O1-DEC-2001 (TIEMBLIE1. 1
CG10738 PROTEIN.
                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso:
Ephydroidea; Drosophilldae; Drosophila.
NCBI_TaxID=7327;
SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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1047 GLRPYGR 1053
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6; Conserv
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13,
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Last sequence update)
Last annotation update)
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Pred. No. 1.9e+02;
l; Mismatches 0
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                                                                                                       Brachycera; Muscomorpha;
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RESULT
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RA Beeson K.Y. Bends P.V., Berman B.P. Bhandari D., Bolshakov S.,
RA Beeson K.Y. Bends P.V., Berman B.P. Brokstein P., Bolshakov S.,
RA Cherry J.M. Bottchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pieischmann W.,
RA Fosier C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorreli J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Nowland T.J., Wei M.-H., Dogwam C.,
RA Hostin D., Houston K.A., Nowland T.J., Wei M.-H., Dogwam C.,
RA Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi D.L.,
RA Reinert K., Remlngton K., Saunders R.D.C., Scheeler F., Shen N.,
RA Reinert K., Remlngton K., Saunders R.D.C., Scheeler F., Shen N.,
RA Reinert E., Spradling A.C., Stapleton M., Skropsh A.H., Wang X.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodsey R.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhon M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhon M., Shoodse J.M., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhon M., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhon G., Zheo Q.A.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhon G., Zheo Q.A.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhon G., Zheo Q.A.,
RA Zheng X.H., Zhong S.J., Rubin G.M., Venter J.C.,
RA Zheng X.H., Xhang R.S., Pan M., Zhong S.J.,
RA Zheng X.H., Zhong R.S., Shihh M.,
                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
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InterPro; IPR001828; ANF_receptor.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR001054; Guanylt_cyclase.

Pfam; PF001094; ANF_receptor; 2.

Pfam; PF000211; guanylate_cyc; 1.

Pfam; PF00069; pkinase; 1.

SMART; SM00044; CYCC; 1.
O9RJR7 PRELIMINARY; PRT, 329 AA. 09RJR7, 01-MAY-2000 (TrembLrel. 13, Created) 01-MAY-2000 (TrembLrel. 13, Last sequence up 01-DEC-2001 (TrembLrel. 19, Last annotation putative ZinC-BINDING OXIDOREDUCTASE. SCF51.18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMO0044; CYCC: 1.
PROSITE; PS00452; GUNNYLATE_CYCLASES_1;
PROSITE; PS50125; GUNNYLATE_CYCLASES_2;
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-bindlng, Lyase; Transferase.
SEQUENCE 1172 AA; 131992 MW;
                                                                                                                                                                                                                                                          434 GLRPVGTF 441
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                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 5;
Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C6450931F82A6D5S CRC64;
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                                              update)
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Matches 5
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Best Loc
Matches
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Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cul
Kinsshi H., Kopwood D.A.;

**A set of ordered cosmids and a detailed genetic and phy
the 8 Mb Streptomyces coelicolor A3(2) chromosome.**;

MOL. Microbiol. 21:77-96(1996).

EMBL; ALI32707; CAB59716.1; -.

InterPro; IPR002085; Adh_zn_family.

Pfam; PF00107; adh_zlnc; i.

SEQUENCE 329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64;
                                                                                                                        InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRNTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; UN
PROSITE; PS00438; CATALASE 2; UN
SEQUENCE 529 AA; 59791 MW; #
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Jeong M.-J., Park S.-C.;
Jeong M.-J., Park S.-C.;
*Cloning of the catalase gene
submitted (JUL-2000) to the E
EMBL; AF286097; AAK15159.1;
NSSP; P15202; 1A4E.
                                                                                                                                                                                                                                                                                                                            Q9CIM8 PRELIMINARY; PRT; 529 AA.
Q9CIM8;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEAT-INDUCED CATALASE.
Pleurotus sajor-caju (Oyster mushroom).
Eukaryota; Pingi; Basidiomycota; Hymenomycetes; Nomobasidiomycetes;
Agaricales; Pieurotaceae; Pleurotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
Cerdeno A.M., Parkhill J.,
Submitted (FEB-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
Seeger K.J., Narris I
Submitted (OCT-1999)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycinese; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                         NCBI_Tax1D-50053;
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298
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LRPIGRE 304
                        1RPVGRF 10
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                                                   Similarity
5; Conserv
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87
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                                                                                                                                                                                                                                                    gene from Pleurotus sajor-caju.";
he EMBL/GenBank/DDBJ databases.
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e EMBL/GenBank/DDBJ databases,
                                                   Score 34; DB
Pred. No. 1.5e
2; Mismatches
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Pred.
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A432BE6445B6AC13
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О
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1.5e+02;
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Search
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Best Local Similarity 75.
Matches 6; Conservative
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075230;
01-NOV-1998 (TrEMBLrel. (
01-NOV-1998 (TrEMBLrel. (
01-NOV-1998 (TrEMBLrel. (
N53_GS1 (FRAGMENT)).
   time:
                                                                                                                                                          EMBL; ACO
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Kimmarly W., Bondoc M., Cheng J., Connolly K.S.

Kadmer K., Miguel T., Miller C., Pitluck S., F

Kadmer K., Miguel T., Miller C., Pitluck S., F

Subramanian S., Martin C.H.;

*Sequencing of human chromosome 5.*;

*Sequencing of human chromosome 5.*;

*Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Primates;
NCBl_TaxID=9606;
                                                                                                                                                                                          "Large Scale Sequence Analysis and Annotation Comparison Analysis (SCAN) System."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AC005178; AAC24489.1; -.
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## ALIGNMENTS

RESULT AAW95178 Pituitary-derived ligand polypeptide; 6-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheiner's disease; Parkinson's disease; Huntington's disease; drug; creutzfeld-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene WPI; 1999-009423/01. Fukusumi S, WO9849295-A1. Mus Murine pituitary-derived ligand polypeptide antigenic epitope. 10-MAR-1999 AAW95178; AAW95178 standard; (TAKE ) TAKEDA CHEM IND LTD 28-APR-1997; 27-APR-1998; 05-NOV-1998. therapy; Hinuma S; (first entry) transgenic animal; epitope. 97JP-0109974 98WO-JP01923. Protein; 10 ₹

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RESULT
AAW31400
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                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                      modulator;
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pdulator; pituitary; central nervous system; pancreas; pro
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95JP-0343371.
96JP-0059419.
96JP-0211805.
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100.0%; Pred. No.
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which are capable of altering the binding activity of the ligand
affecting activation of the G protein-coupled receptor protein.
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100.0%; Pr
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Pred. No.
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0.0082;
hes 0;
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modulation;
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RESULT
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AC AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97229-31 represent a ligand polypeptide derived fragments used to produce antibodles. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a grotein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing thypocovarianism, gonecyst cacegenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing prolacting secretion can be used for treating or preventing prolacting secretion can be used for treating or preventing prolactinomal, infertility, impotence, amenorrhea, galactorrhea, acromegaly, chiari-frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright Syndrome, Sheehan syndrome or dyszoospermia. The inhibitory cylentate can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing unthrifty chertagolism. Abnormal saccharometabolism.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of G protein-coupled receptor iigands - for modulating prolactin secretion or placental function, e.g. for treating menopausal
                                                                      (TAKE
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                                           Matsumoto H,
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100.0%; Pr
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Query Match
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Matches 9
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7 rgirpygrf 15
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                                                                                                                                                                                                                                                                                                                                                    antibody; 19P2 ligand; diagnosis; prolactin secretion;
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o ligand abnormallty
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or derlyative. The antibodies can be used in diagnosis or to treat or prevent diseases sssociated with abnormality in the pitultary func

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RESULT
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                                                                                   The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences ANY49290-302 represent peptide fragments of the 1992 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivativ sequences ANY49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                               Disclosure; Page 27; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY49296 standard;
                                                               Sequence
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studying diseases related
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98.0%; Score 48; DB 21;
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                                              CC This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the Sequence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-Coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC acute myocardial infarction, infertility, spinocerebellar degeneration, CC acute myocardial infarction, infertility, spinocerebellar degeneration, CC conspinactia, Assays can also be developed to screen compounds which are CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic agent.
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| rgirpvgrf 15
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m; pancreas; pro
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RESULT
AAW31387
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                                             Query Match
Best Local Similarity
Matches 9; Conserv
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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Y, Kitada
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                                             Mismatches
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Local Similarity

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                      CC derived ligand corresponding to amino acid residues 34 to 53 of the CC sequence in AAN31368 and 18 used in an assay to monitor ligand binding CC to the G protein-coupled receptor protein. Pharmaceutical compositions CC central nervous system modulator or a pancreatic function modulator. a CC central nervous system modulator or a pancreatic function modulator. CC This ligand could have specific applications as a probplactic or CC therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, CC typercholesterolaemia, hyperglyceridaemia, hyperlipidaemia, hyperglyceridaemia, hyperlipidaemia, for the hormone secretory disease, hyper- and polyphagia, acute CC hyperprolactinemia, disbetes, cancer, pancreatitis, renal disease, hyperprolactinemia, diabetes, cancer, pancreatitis, spinal injury, CC transient brain ischaemia, amylotrophic lateral scierosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertillty CC and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulator;
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pdulator; pituitary; central nervous system; pancreas; prophylactic;
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Y, Kitada C,
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Bovine pituitary-derived llgand polypeptide fragment.

06-MAY-1999

(first entry)

AAW97232 standard; peptide;

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                                                                                                                                                                                            fragment. It is used in the course of the invention. The specification classribes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a sait, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, enthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodislat. The agents for inhibiting prolactin secretion can be used for treating or preventing pluitary adenomatosis, brain tumour, emmenipathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, carcomegaly, Chiari-frommel syndrome, Argonz-del Castilo syndrome, for modulating placental function can be used for treating or preventing chalbitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing chalbitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing chalbitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing chalbitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing chalbits.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a bovine pitultary-derived ligand fragment. It is used in the course of the invention. The specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3;
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rglrpvgrf 20
                                                                                  9; Conserv
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Pred. No.
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The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes a rate of the invention. The specification describes a can agent for modulating prolactin secretion which comprises a comprise a sait, for a g protein-coupied receptor (GPCR) comprises. The spents for promoting prolactin secretion can be used for creating or preventing hypowerianism, gonecyst cacogenesis, menopausal conditions, eathyroid or hypometabolism. They can by used for promoting contestion in a domestic mammal and as an aphrodisia. The agents for conditions in a domestic mammal and as an aphrodisia. The agents for conditions in a domestic mammal and as an aphrodisia. The agents for conditions, infertility, impotence, amenorabea, autolumnne disease, corposes-Albright syndrome, lymphoma, sheehan syndrome or dyszoospermia. The inhibitory agents can also be used for treating or preventing conditions ting placental function can be used for treating or preventing conditions, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyrold; hypometabolism; lactation, pituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; chorlocarcinoma; hydatid mole; inruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                       Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypoovarianism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal ayndrome, tumoura, autoimmune disease or abnormal pregnancy
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                                                                                                                                                                                                                                                      aaccharometabolism,
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CC which is a ligand for the e-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the CC polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimes's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Schizophrenia; disorders of growth hormone secretion: cancer; CC rhemmatol arthritia, epilepsy and many others, also to improve post-CC operative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of CC study the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide DNA is used as a source of cell lines. The ligand CC animals. The present sequence represents a bovine genome-derived ligand colypeptide fragment which is similar to the murine ligand-polypeptide.
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for treating disorders
pancreas, and for drug
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1997;
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                                                                                                The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of CC the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementie; Alzheimer's, Parkinson's or Huntington's CC diseases: Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases: Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; schizophrenia; disorders of growth hormone secretion; cancer; CC crarying the ligand polypeptide encoding DNA or its mutein animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC cantisers; in drug development; for gene therapy and to develop continued as a force of probes and primers; to identify continued as which can be used for the preparation of anti-ligand polypeptide cantisers; in sequences and states and primers and polypeptide cantisers; to identify continued as a source of cell lines. The ligand continued as a source of cell lines. The ligand continued as a source of cell lines are discussed to continue the sequences and states and primers; to identify continued as a source of cell lines. The ligand continued to development and sequences and sequences and sequences and sequences and sequences and sequences and sequences and sequences and sequences and sequences and sequences and 
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    98.0%;
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                                                                                                                                              This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its sait for the 6 protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and plg. This sequence represents a bowlne paptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                           Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine oxytocin
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                                                                                                             Sequence
                                                                                                                                      promoter
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                                                                                                                                                                                                                                                                                                    medicine
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd
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        24425594 residues
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| US-09-421-208-8   | -421-208 | -08-776-97        | US-08-776-971-61  | US-08-776-971-47 | -08-776-971 | US-09-172-353-4 | US-09-105-678A-43 | US-09-105-678A-37 | -09-10 | 678A              | -09-105 | 678A-             | ځ  | US-09-421-208-42 | ώ                 | US-08-776-971-73 | us-08-776-971-66  |
| Sequence 8, Appl: | 7,       | Sequence 97, Appl | Sequence 61, Appl | 47               | رتا<br>د    | 4               | Sequence 43, Appl | 37,               | 31     | Sequence 9, Appli | œ       | Sequence 7, Appli | 8  | •                | Sequence 36, Appl | •                | Sequence 66, Appl |

## ALIGNMENTS

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US-08-776-971-93
  Sequence 93, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
TELEPNONE: 617-523-340
TELEPAX: 617-523-6440
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                ATTOKNEL/ ATTOKNEL/ ATTOKNEL/ ATTOKNEL/ ANAME: CONIIN, DAVIG U. NAME: CONIIN NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
  COMPUTER READABLE FORM:
MEDIN TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wind
CURRENT APPLICATION DATA:
   NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
  Fujli, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS,
NUMBER OF SEQUENCES: 140
  PRIOR APPLICATION DATA:
  APPLICANT: Ninuma, Shujl
   APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28 DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28 DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
   APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <Unknown>
   CITY: Boston
STATE: MA
   ZIP: 02109
  COUNTRY:
   Habata, Yugo
Kawamata, Yuji
Nosoya, Masaki
  130 Water Street
  USA
  BRONSTEIN,
  for Windows Version
  ROBERTS & CUSHMAN, LLP
  THEIR PRODUCTION AND USE
  2.0
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  ; SEQUENCE DESCRIPTION: SE0 ID NO: 93: US-08-776-971-93
  US-09-105-678A-34
  US-09-105-678A-34
  S
  Query Match
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Matches 9
   Best Loc
Matches
   sequence 34, Applicat Patent No. 6103882 GENERAL INFORMATION:
   Query Match
   TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
  NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENGE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & GUSHMAN, LLP
  STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
   APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
   GOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION OATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compati
  SEQUENCE CHARACTERISTIGS
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  TYPE:
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   LENGTH:
   COUNTRY:
   STREET:
   Local Similarity
les 9; Conserv
                              1 RGIRPVGRF 9
  1 RGIRPVGRF 9
   MOLECULE TYPE: protein FRAGMENT TYPE: internal
RGIRPVGRF 20
   RGIRPVGRF 15
   02109
  amino acid
  Boston
  ¥
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   Application US/09105678A
  130 Water Street
   20 amino acids
   OSA
  98.0%; Score 48; OB 4; Initiatity 100.0%; Pred. No. 0.0024; Conservative 0; Mismatches 0;
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  98.0%; Score 48;
100.0%; Pred. No.
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   34:
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; LENGTH: 20 amino acids
; TYPE: mmino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-40
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US-09-105-678A-40
  US-09-105-678A-46
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ANTORNEY AGENT INFORMATION:
NAME: CON11h, David G.
REGISTRATION NUMBER: 27.026
REFERENCE/DOCKET NUMBER: 48466-342
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TELEPHONE: 617-523-440
INFORMATION FOR SEQ ID NO: 40:
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   Patent No.
   Sequence 40,
   GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Toko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PI
NUMBER OF SEQUENCES: 52
  GENERAL INFORMATION:
  GOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTMARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105.678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ENTITY OF THE TOR
   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
   CORRESPONDENCE ADORESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
   STREET: 130 W:
CITY: Boston
STATE: MA
               STATE: N
  COUNTRY: U
  CITY: Boston
   STREET:
   12 RGIRPVGRF
  1 RGIRPVGRF 9
   0, Application US/09105678A
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   130 Water Street
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   ASD
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  98.0%; Score 48; DB 3; 100.0%; Pred. No. 0.0032
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US-08-776-971-8
; Sequence 8, Application US/08776971B
; Patent No. 6228984
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APPLICANT: Hinums, Shuji
  US-09-105-678A-46
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   NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
TELEFAN: 617-523-6440
  INFORMATION FOR SEQ ID NO: 46;
  FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 20 amino acids
  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION ODATA:
APPLICATION NUMBER: UT/09/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DT/JP96/03821
FILING DATE: 28-DEC-1995
APPLICATION UMBER: DT/J443371
FILING DATE: 28-DEC-1995
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  STRANDEDNESS
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  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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   MEDIUM TYPE: Floppy disk
   1 RGIRPVGRF 9
   CDRRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
   FURUSUMI, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, TNEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
  RGIRPVGRF 20
   amino acid
   COUNTRY: USA
2IP: 02I09
  STATE: MA
  CITY: Boston
   Conservative
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   Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
  Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
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Pred. No.
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   Length 20
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US-08-776-971-50
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US-08-776-971-8
  Sequence 50, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
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Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
   1 RGIRPVGRF 9
   COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
OF THE COMPANY OF THE COMPANY OF THE CASE OF 
  Fukusumi, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
   REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
TELEFAX: 617-523-6440
   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
  APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: TP 8/59419
   CITY: Boston
STATE: MA
  TYPE: amino acid
  COUNTRY: USA
  STREET:
   TOPOLOGY: linear
  STRANDEDNESS: single
  APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
  APPLICATION NUMBER: JP 8/59419 FILING DATE: 15-MAR-1996
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   98. V. 100. 08; F1
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100.0%; Pred. No.
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TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996
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  Local Similarity
   LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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  APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G,
REGISTRATION NUMBER: 27,026
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CDSHMAN, LLP
STREET: 130 Water Street
  Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Fukusumi, Shoji
Kitada, Chieko
TITLE DF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND DSE
NUMBER DF SEQUENCES: 140
   APPLICANT:
  COMPUTER: IBM compatible
OPERATING SYSTEM; DDS
SOFTWARE: FastSED for Windows Version 2.0
   STATE: MA
   CITY: Boston
   CLASSIFICATION: <Unknown>
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  COUNTRY: USA
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Kawamata, Yuji
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INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
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   1 RGIRPVGRF 9
  CDMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOSTWARE: FESTESO for Wir
CURRENT APPLICATION DATA:
   Fukusumi, Shoji

Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND DSE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
  REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
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  ATTORNEY/AGENT INFORMATION:
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FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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  TYPE: amino acid
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  CITY: Boston
  STREET:
   LENGTH: 20 amino acids
  DDRESSEE: DIKE, BRONSTEIN, RDBERTS & CUSHMAN, LLP
TREET: 130 Water Street
   Application US/08776971B
  Conservative
   Kawamata, Yuj.
Kawamata, Yuj.
Hosoya, Masaki
Fujii, Ryo
Fujii, Shoji
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TOPOLOGY: linear
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US-09-421-208-34
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APPLICATION NUMBER: US 09/105,678
ETIING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
APPLICATION DATE: 27-JUN-1997
  Sequence 34, Application US/09421208 Patent No. 6258561
  TELEFAX: 617-523-5440
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   APPLICANT: Suenaga, Masato
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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REFERENCE/DOCKET NUMBER: 48466-342
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: CODILD, DAVIG G.
   CORRESPONDENCE ADDRESS:
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  12 RGIRPVGRF 20
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130 Water Street
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PRIOR APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: 26-JUN-1998
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ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVId G.
NAME: CONLIN, DAVId G.
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   Sequence 46, Application US/09421208 Patent No. 6258561
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GENERAL INFORMATION:
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APPLICANT: Suenaga Masato
APPLICANT: MOTiya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Alshimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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MEDIUM TYPE: Floppy disk
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TELEPHONE: 617-523-3400
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  12 RGIRPVGRF 20
  TELEPHONE:
   ADDRESSEE:
  LENGTH:
   Boston
   0, Application US/09421208 6258561
   amino acid
  ¥
  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
  20 amino acids
   Moriya, Takeo
Tanaka, Yoko
   Conservative
   Suenaga,
   98.0%; Sc.
100.0%; Pr
  Masato
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  TELEPHONE: 617-523-3400
  FILING OATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
  COMPUTER READABLE FORM:
   APPLICANT: Nishimura, Osamu
T1TLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGANO
NUMBER OF SEQUENCES: 52
   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
  TYPE.
STRANOEONESS:
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  NAME: Conlin, Oavid G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
  CITY: Boston
STATE: MA
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  FILING DATE:
  ZIP: 02109
  CITY: Boston
  LENGTH:
   ADORESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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 NUMBER:
   98.0%; 5rr
100.0%; Prr
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   APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGANO
NUMBER OF SEQUENCES: 52
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ADDRESSEE: OIKE, BRONSTEIN, ROBERTS & CUSRMAN, LLP
                            APPLICATION NUMBER: JF 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAYIG G.
REGISTRATION NUMBER: 27,026
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   21 amino acids
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FILING DATE: 26-JUN-1998
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APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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  GENERAL INFORMATION:
  APPLICANT: Suenaga, Masato
APPLICANT: Morlya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
  NAME: CON11n, Dav1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-523-3400
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  COMPUTER READABLE FORM:
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STATE: MA
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Job time: 624 sec
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PRIOR APPLICATION DATA:
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FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION: INFORMATION:
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  TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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LENGTH: 21 amino acids
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APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NOMBER OF SEQUENCES: 52
  TOPOLOGY: linear MOLECULE TYPE: peptide
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STREET: 130 Water Street
   12 RGIRPVGRF 20
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein protein search, using sw model

Run

September 13, 2002, 09:24:03 ; Search time 172.41 Seconds
(without alignments)
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cell updates/sec

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Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB pag pag length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

Database PIR\_71:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 32        | 32     | E<br>E | E)     | 33                 | E                  | 33                 | 33                 | 33                 | 33                 | 33     | 33     | 33                 | 33     | 33                 | 33                 | 33                 | 34     | 34                | 34     | 34     | 35     | 35                | 35     | 35                 | 35     | 35                 | 36                 | 48        | score       | ,      |
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| 149       | 57     | 1940   | 589    | 511                | 485                | 477                | 477                | 477                | 445                | 366    | 353    | 335                | 319    | 313                | 290                | 290                | 343    | 328               | 307    | 226    | 1056   | 894               | 519    | 504                | 391    | 272                | 674                | 6.3       | rengen I    |        |
| 2         | N      | N      |        |                    | 2                  |                    |                    |                    |                    | _      | _      |                    |        |                    |                    |                    |        |                   |        |        |        | N                 | N      |                    |        |                    |                    |           | <br>DR      |        |
| AH2262    | I35055 | F75393 | G87485 | T40334             | E83663             | A56449             | S65684             | 568367             | T35893             | C70365 | C70502 | E70655             | T36845 | B95351             | AD2870             | F97646             | AH1823 | S77236            | S51485 | A65057 | B62557 | E82221            | T45447 | B70821             | XXGZAC | T39533             | G70875             | JC7607    | TD          | 1      |
| othetical |        |        |        | hypothetical prote | glutamyl-tRNA synt | protoporphyrinogen | protoporphyrinogen | protoporphyrinogen | FAD-dependent oxid | ~      | prot   | hypothetical prote |        | VirB6 type IV secr | ABC transporter, m | probable aliphatic | 0      | ribosomal protein | 0      |        | cal    | DNA gyrase, chain |        | hypothetical prote |        | hypothetical prote | probable oxidoredu | in-releas | Description |        |

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|   | 562                | 492                | 435                | 410                | 409                | 388                | 374                | 309                | 307    | 299                | 292                | 285                | 266               | 249                | 154                | 150                |
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|   | regulatory protein | probable hyce prot | probable isocitrat | tRNA nucleotidyi t | hypothetical prote | transporter BMEI15 | hypothetical prote | hypothetical prote |        | hypothetical prote | probable saccharld | short-chain dehydr | ribosomal protein | hypothetical prote | hypothetical prote | hypothetical prote |

## ALIGNMENTS

JC7607

prolactin-releasing peptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C;Accession: JC7607
R;Yamada, M; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 201, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Accession: JC7607

A; Molecule type: DNA A; Residues: 1-83 < YAM>

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.

C;Genetics: A;Gene: PrRP A;Introns: 33/1

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probable oxidoreductase (EC 1.5.99.-) - Mycobacterium tuberculosis (strain H37RV) (;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000 C;Accession: G70875

R.Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.: Connor, R.: Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.: Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Decliphering the biology of Mycobacterium tuberculosis from the complet A; Reference number: A70500; MUID:98295987
A;Accession: G70875
A;Status: preliminary; nucleic acid sequence not shown: translation not shown Holroyd,

Whitehead, S.; Barrell, B.G. tuberculosis from the complete

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Barrell, B.G

geno

D.; Gordon

Holroyd

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J. Biol. Chem. 262, 97-102, 1987
A;Title: Biosynthetic thiolase from Zoogloea ramigera. III
A;Accession: A26121
A;Molecule turn
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A:Experimental source: strain I-16-M, ATCC 19623
C:Comment: The active enzyme, a tetramer of identical chains, catalyzes the hesis, and poly-beta-hydroxybutyrate biosynthesis.
   acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - Zoogloea ram1gera N.Alternate names: acetoacetyl-CoA thiolase; biosynthetic thiolase; thiolase
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  R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, submitted to the EMBL Data Library, February 1998
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l; Mismatches
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   30-Jun-1991 #text_change
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   05-May-2000
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Darrell, B. Ca;Title: Deciphering the biology of Mycobacterium tuberculosis from the complex A; Reference number: A70500; MUID:98295987

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ebruary 1998
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R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.: Ermolaeva, M.D.: Vamathevan, J.: Bass, S.; Qln, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
   A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: E82221
  hypothetical protein XF2445 [Imported] - Xylella fastidiosa (strain 9a5c) C;Specias: Xylella fastidiosa (C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C:Accession: B82557
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  A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82315; MUID:20365717 A:Note: for a complete list of authors see reference number A59328 below A:Accession: B82557
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   밁
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A, ROSE, D. J.; MBN, B.: Shao, Y.

Science 277, 1453-1462, 1997

A,Title: The complete genome sequence of Escherichia coii K-12.
A,Reference number: A64720; MUID:97426617
A,Refession: A65057
A,Reference number: A64720; MUID:97426617
  ribosomal protein S1 - Synechocystis sp. N;Alternate names: protein s1r1356 C;Species: Synechocystis sp. A: Variety: PCC 6803 C:Date: 25-Apr-1997 #scquence_revision C:Accession: S77236 R;Kaneko, T.; Sato, S.; Kotani, H.; Tan
  hypothetical protein b2757 - Escherichia coli (strain K-12)
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C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: A65057
R;Kaneko, T.; Sato, S.; Kotani, H.; Taneka, A.; Asamizu, E.; Nakamura. Y.; Miyajlma, o, K.: Dkumura, S.; Shimpo, S.: Takeuchi, C.; Wada, T.; Watanabe, A.: Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unlcellular cyanobacterium Synechocys s.
   C:Species: Synechococous ap.
A:Variety: PCC 6301
C:Date: 15-Jul-1995 #sequence_revision
C:Accession: S51485
C:Accession: S51485
R;Sugita, M.; Sugita, C.; Sugita, M.
Moi. Gen. Genet. 246, 142-147, 1995
   A;Cross-references: GB:AE000359: GB:U00096; NID:g1789110: A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: Eacherichia coli hypothetical protein b275;
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75.08:
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrob A;Reference number: A97359; PMID:11743194
  Nakazaki, N.: Shimpo, S.: Sugimoto, M.; Takazawa, M.: Yamada, M.: Yasuda, M.; Tabata, (DNA Res. B, 205-213, 2001
A:Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Superfamily: Synechocystls r1bosomal protein
   C:Racession: AH1823
C:Accession: AH1823
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.: Sasamoto, :
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A;Molecule type: DNA
A;Residues: 1-290 <KUR>
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  A: Molccule type: DNA
A: Residues: 1-343 < KDR>
   무
   Ś
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A; Accession: S77236
  A; Accession: F97646
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   Os ribosomal protein s1 [imported] - Anabaena sp. (strain PCC 7120)
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K; Barnett, M.J.: Fisher, R.F.: Jones, T.; Komp, C.: Abola, A.P.: Barloy-Hubler, F.; B.; Kalman. S.; Keating, D.H.; Palm, C.; Peck, M.C.: Surzycki. R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-988. 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A; Reference number: A95262: MUID:21396509: PMID:11481432

A;Accession: B95351
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L.: Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh,
A;Titla: The composite genome of the legume symblont Sinorhizoblum meliioti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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A:Title: The Genome of the Natural Genetic
A:Reference number: AB2577; PMID:11743193
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Science 294, 2317-2323, 2001
A:Authors: Yoo, H.: Tao, Y.; Biddle, P.: Jung, M.: Krespan, W.: Perry, M.; Gordon-Kam
  ABC transporter, membrane spanning protein Atu2390 [Imported] - Agrobacterlum C:Species: Agrobacterlum tumefaciens C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:30:48; Search time 80.21 Seconds (without alignments) 4.827 Million cell updates/sec

Titie: Perfect score: Sequence: US-09-446-543A-73\_COPY\_12\_21 1 RGIRPVGRFX 10

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 105224

105224 seqs, 38719550 rcsidues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| 3331<br>331                                                  | 328<br>3098                           | 26<br>27                     | 225                                      | 2 2 2 E      | 20         | 18      | 16                       | 114        | 15                 | 10                                       | ်ဖွ                | p ~1       | <b>σ</b> , υ                             | 1 4-       | ω <b>κ</b>        |          | Reguit         |
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| 3333                                                         | 322                                   | 31<br>11                     | <u> </u>                                 | <u> </u>     | 225        | 2 2 2   | <br>                     | 32         |                    | <u>ယ မ</u>                               | <b>3</b>           | υ<br>4     | 3 L<br>2 C                               | 35         | 4 ¢               | 48       | Score          |
| 5555<br>                                                     | 55.5                                  | $\omega \omega$              |                                          |              | 55.5       | ωι      | າເກະ                     | 155        | າ ∵່               | 67.3                                     | 9:                 | 69.4       | 69.4                                     | ٠:-        | 98.0              |          | Query<br>Match |
| 625<br>631                                                   | 430<br>433<br>463                     | 372<br>413                   | 364<br>367                               | 233          | 207        | 130     | 331                      | 249        | 285<br>284         | 477                                      | 801                | 306<br>308 | 224                                      | 391        | 98                | 38       | Length         |
|                                                              |                                       |                              | ,                                        |              |            |         |                          | , p.,      | <u>- 1</u>         |                                          | μ,                 | ىر د       | <b>~</b> ~                               | μ,         | <b>-</b>          | μ.       | 8              |
| DHGL_DROME DHGL_DROPS DNAK_THERO                             | PYRC_MYCTU<br>ZUO1_YEAST<br>K10 DROME | KK11_HUMAN<br>CSD_THEMA      | MR11_MOUSE                               | PYRE_PASMU   | YDQ5_SCHPO | RL3_PIG | AR74_HUMAN<br>AR73_HUMAN | Y361_SYNY3 | SYE_BACHD          | PPOX_HUMAN PPOX_HOUSE                    | TFR2_HUMAN         | RS1_SYNP6  | YGCI_ECOL1                               | THIL_ZOORA | PRRP_BOVIN        | PRRP_RAT | ID             |
| P18173 drosophila<br>P18172 drosophila<br>P96133 thermomicro | 70                                    | 9 homo sapie<br>1 thermotoga | Q9wuii mus musculu<br>Q10376 mycobacteri | 1 pasteurell |            |         | homo                     | synec      | Q9k9f6 bacillus ha | P50336 homo sapien<br>P51175 mus musculu | Q9up52 homo sapien | 0 0        | P48369 aeromonas s<br>Q46898 escherichia | 2009       | PB1264 bos taurus | rattu    | Description    |

| 45         | 44         | 43         | 42        | 41         | 40        | 39         | 38        | 37        | 36        | 35          | 34         |
|------------|------------|------------|-----------|------------|-----------|------------|-----------|-----------|-----------|-------------|------------|
| 30         | 30         | 30         | 30        | 30         | 32        | 31         | 31        | <u> </u>  | 3         | 3           | 31         |
| 61.2       | 61.2       | 61.2       | 61.2      | 61.2       | 63.3      | 63.3       | 63.3      | 63.3      | 63.3      | 63.3        | 63.3       |
| 376        | 36B        | 292        | 179       | 116        | 1565      | 1561       | 1416      | 1056      | 1056      | 908         | 719        |
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| MPK5_ARATH | YG3Y_YEAST | CNTB_HUMAN | RK6_GU1TH | RL34_HUMAN | PAC_STRMU | SPAP_STRMU | BLM_MOUSE | POL_BIV27 | POL_BIV06 | ACON_BACSU  | NRP1_YEAST |
| Q39025     |            |            |           | P49207     |           |            |           |           |           | P09339      | P32770     |
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## ALIGNMENTS

| CCC<br>CCC<br>CCC<br>CCC<br>CCC<br>CCC<br>CCC<br>CCC<br>CCC<br>CC | 488888888888                                                                                                                                                                                                                                                                                                                                                                                                           | REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE | PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESULT PRESUL |
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  Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
Sumino Y., Fujino M.;
*Tissue distribution of p
   TISSUE SPECIFICITY.
PubMed=10498338;
  MEDLINE-98268781; PubMed-9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fu Kitada C., Masuo Y., Aaano T., Mataumoto H., Sekiguchi M., Kurokawa T., Niahimura O., Onda H., Eujino M.;
*A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
   30-MAY-2000 (Rei. 39, Created)
30-MAY-2000 (Rei. 39, Last sequence update)
01-MAR-2002 (Rei. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
  PEPTIOE
   SEQUENCE FROM N.A.
   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
  PRRP_HUMAN
P81277;
   SEQUENCE
   Homo sapiens
  releasing peptide
   4
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                       н
   FUNCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPR10. May lactotrophs directly to secrete PRL. TISSUE SPECIFICITY: MEDULIA OBLONGATA AND HYPOTHALAMUS.
   ; AB015419; BAA29027.I; 602663; -.
                      RGIRPVGRF 9
  RGIRPVGRF 9
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  Pept. 83:1-10(1999).
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   Score Pred.
   BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIQE AMIDE GROUP

229A2F3F50CF981B CRC64;
  Craniata; Vertebrata; |
Catarrhini; Hominidae;
   Mismatches
   Mismatches
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T., Nishimura
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Accetyl-CoA acetyltransferase (Recounty of the company of the com
   PRRP_BOVIN
P81264;
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01-MAR-2002
  BOVIN 3
  Hormone;
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   MOD_RES
   MEDLINE-98268781; PubMed-9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Ho
Kitada C., Maauo Y., Aaano T., Matsumoto H., So
Kurokawa T., Nishimura O., Onda H., Fujino M., So
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998)
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SEQUENCE FROM
STRAIN-ATCC 1
   Bacteria;
  PHBA.
  Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last aequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PRRP)
hormone) [Contains: Prolactin-releasing peptireleasing peptide PRRP20].
  Zoogloea ramigera
   EMBL; AB015417; BAA29025.1;
  SEQUENCE FROM N.A.,
   NCBI_TaxID=9913;
   Bos taurus (Bovine).
   NCBI_TaxID=350;
   $
   1 RGIRPVGRF 9
   FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPRIO. May stimulate lactotropha directly to secrete PRL.

TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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  Score 48;
Pred. No.
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   subdlviaion; Rhodocyclua
  Mismatches
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   PrRP) (Prolactin-releasing
peptide PrRP31; Prolactin-
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RESULT 5
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ID GYRA_AERSA
AC P48369;
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DT 01-PEB-1997
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Matches 6
   Palmer M.A.J., Differding E., Gamboni R., Williams S. Walsh C.T., Sinskey S.J., Masamune S.;
Biosynthetic thiolase from Zoogloea ramigera Eviden mechanism involving Cys-378 as the active site base. The Biol. Chem. 266:8369-8375 (1991).

I. Biol. Chem. 266:8369-8375 (1991).

I. CAPALYTIC ACTIVITY: 2 acetyl-COA - COA + acetoace - PATHMAY: FIRST STEP IN POLY-BETA-HYDROXYBUTYRATE - SUBUNIT: NOMOTETRAMER.

I. SUBCELLULAR LOCATION: Cytoplasmic.
   MEDLINE-87083504; PubMed-2878929;
Peoples O.P., Masamune S., Walsh C.T., Sinskey
"BioSynthetic thiolase from Zoogloea ramigera.
characterization of the structural gene.";
J. Biol. Chem. 262:97-102(1987).
   ACT_SITE
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  Peoples O.P., Sinskey A.J.; "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus Characterization of the genes encoding beta-ketothiolase and
  Pfam;
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   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Biolicormatics and the Exthe European Biolinformatics Institute. There are no restruce by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of the long as its content use of long 
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   acetoacetyl-CoA reductase."
J. Biol. Chem. 264:15293-15
   MEDLINE-89359356; PubMed-2670935; Peoples O.P., Sinskey A.J.;
  SEQUENCE
   Pfam;
   InterPro; IPR002155; Thiolase.
   MUTAGENESIS OF
   REVISION TO 130.
  PROSITE;
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  I; PF00108; thiolase; 1.
I; PF02803; thiolase; 2:
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IITE; PS00737; THIOLASE 2; 1
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MEDLINE=97426617; PubMed=9278503;
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  Isomerase;
ACT_SITE
SEQUENCE
  SEQUENCE OF 33-179 FROM N.A. STRAIN-ATCC 14174; MEDLINE-95142596; PubMed-7840589;
   Escherichia coii.
Bacteria, Proteobacteria;
Escherichia.
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   EMBL; L47978; AAB41037.1;
EMBL; L42453; AAB67239.1;
NSSP; P09097; LAB4
  Oppegaard N.;
Submitted (OCT-1995) to the
  SEQUENCE FROM N.A.
STRAIN-2148/89;
   Nypothetical YGCI OR B2757
  16-0CT-2001
16-0CT-2001
   <del>-</del>
  Antimicrob. Agents Chemother. 38:2460-2464(1994)
-1- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CI
  "gyrA mutations in quinolone-resistant isolates 
Aeromonas salmonicida.";
  Oppegaard N., Sorum
  Aeromonas.
NCBI_TaxID=645;
  NCBI_TaxID-562;
   YGCI_ECOLI
   InterPro;
   758 KGVRPMGR
  1 RGIRPVGR
   DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
SUBUNIT: MADE UP OF TWO CNAINS. THE A CHAIN IS RESPONSIBLE FOR DN BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
   FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
  ENZYME FORMS AN A2B2 TETRAMER.
   PF00521; DNA_topoisoIV; SM00434; TOP4c; 1.
  Similarity
5; Conser
  IPR002205; DNA_topoisoIV. 0521; DNA_topoisoIV; 1.
  Topoisomerase; DNA-binding.
122 122 DNA CLEAV
922 AA; 101333 MW; 889496
  coii.
   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
protein ygcI precursor.
  Conservative
   STANDARD;
   2
  71.48; 62.5%;
   gamma subdivision;
   EMBL/GenBank/DDBJ
   Score 35; DB
Pred. No. 22;
3; Mismatches
  'n
  DNA CLEAVAGE (BY SIMILARITY). 8894965DC4217077 CRC64;
   PRT;
   Bioch C.A.,
   224
   update)
   DB
22;
                         Goeden
   ζ
   Rode C.K., Mayhew
  ::
   Enterobacteriaceae;
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   databases
  Length 922:
   Q.
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   fish pathogen
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   Gaps
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RESULT 7
  S
   SOFT AND THE COCCOCCA COCCA COCA COCCA COC
   밁
   Query Match
Best Local
Matches
  Suglta M., Suglta C., Suglura M.;

*Structure and expression of the gene encoding ribosomal protein from the cyanobacterlum Synechococcus sp. strain PCC 6301: striki sequence similarity to the chloroplast ribosomal protein CS1.";

MOI. Gen. Genet. 246:142-147(1995).

-1- FUNCTION: BINDS MRNA.
Ribosomal
INIT_MET
DOMAIN
DOMAIN
DOMAIN
   Pfam; PF00575; S1; 3.
SMART; SM00316; S1; 3.
PROSITE; PS50126; S1; 3.
Ribosomal protein; Repea
   Synechococcus sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; C
   01-FEB-1996 (Rel. 33,
16-OCT-2001 (Rel. 40,
30S ribosomal protein
  RS1_SYNP6
P46228;
  use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
   Thls
   EMBL; U29579; AAA69267.1; ALT_INIT.
EMBL; AE000359; AAC75799.1; ALT_INIT.
   EMBL; D28752; BAA05946.1;
HSSP; P05055; ISRO.
   use by non-profit Institutions as long modified and this statement is not removed.
  the
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
   SEQUENCE FROM N.A., MEDLINE-95166170; F
  the European Bloinformatics Institute.
  between the
  RPSA OR RPS1.
   SEQUENCE
  Hypothetical protein; SIGNAL 1
  Sclence
  InterPro;
   23
   Match
  Ŋ
   B., Shao v.;
e complete genome sequence of
ence 277:1453-1474(1997).
  SIMILARITY: BELONGS TO THE S1P FAMILY OF SIMILARITY: CONTAINS 3 S1 MOTIF DOMAINS.
  European
   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
   GTRPTGRF
  GIRPVGRF
   Similarity
6; Conserv
  s requires a license agreement (S an emall to license@isb-sib.ch).
  EG13116; ygcI.
ical protein; Signal;
  IPR003029; S1.
   224 AA;
   (Rel. 32,
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(Rel. 40,
   Conservative
   Bioinformatics Institute. The sprofit institutions as long
   18
  9
  STANDARD;
   PubMed-7862084;
   224
25209
  100
182
264
   Repeat;
  Last sequence upon Last annotation upon S1.
   69.4%;
75.0%;
   Created)
   n PCC 6301) (Anacystis nidula
Chroococcales; Synechococcus
   Œ;
   sequence update) annotation update)
  RNA-binding.
   agreement (See http://www.lsb-sib.ch/announce/
   Score 34; DB
Pred. No. 8.5;
0; Mismatches
   HYPOTHETICAL PROTEIN YGCI.
; 1C42CC009B317D68 CRC64;
  S1 S1
   Complete proteome POTENTIAL.
  MOTIF
   MOTIF
   ဝှု
  Escherichia coli K-12.9;
   1-13.
  306
   There are no restrictions ong as its content is in
  8.5;
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RESULT 9
TFR2_HUMAN
ID TFR2_HUMAN
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   Query Match
Best Local S
Matches 6
  Matches
  Query Match
Best Local
  01-NOV-1997 (Rel. 35, 0
01-NOV-1997 (Rel. 35, 1
16-OCT-2001 (Rel. 40, 1
30S ribosomal protein 9
RPSIA OR SIR1356.
   Ribosomal protein; I
DOMAIN 31 1
DOMAIN 118
DOMAIN 196
SEQUENCE 328 AA;
  RS1A_SYNY3
P73530;
01-NOV-1997
  Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Yasuda M., Tabata S., "Sequence analysis of the genome of the uniceliular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
   Pfam; PF00575; S1; 3.
SMART; SM00316; S1; 3.
PROSITE; PS50126; S1; 3
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   SYNY3
  SEQUENCE
  EMBL; D90907; BAA17570.1; -. HSSP; P05055; 1SRO.
   or send an email to license@isb-sib.ch).
  MEDLINE-97061201;
   SEQUENCE FROM
   Bacteria; Cyanobacteria;
  Synechocystis sp. (strain PCC 6803)
  interPro;
   204
  204
   1 RGIRPVGRF
   1 RGIRPVGRF
  FUNCTION: BINDS MRNA.
SIMILARITY: BELONGS TO THE S1P FAMILY OP
SIMILARITY: CONTAINS 3 S1 MOTIF DOMAINS.
   RGIKPYGAF
   RGIKPYGAF
  similarity 66. 6; Conservative
   similarity
6; Conserv
  3:109-136(1996).
  IPR003029; S1.
   306
  31
118
196
328 /
  Conservative
   ø
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   STANDARD;
  PubMed=8905231;
  Repeat;
   182
264
36570
   34492 MW;
   69.4%;
66.7%;
  69.4%;
  Last sequence up
Last annotation
Si homolog A.
  Created)
  Chroococcales;
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:
   RNA-binding;
S1 MOTIF 1.
S1 MOTIF 2.
S1 MOTIF 3.
   Pred. No. 12;
1; Mismatches
  Score 34;
Pred. No.
   PRT;
   82D4A2EBE69B97CE CRC64;
  SIP FAMILY OF
  DC3FF9B1E5A40619
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  Synechocystis
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   Length 306
  Length 328
   proteome.
  Indels
  PROTEINS
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STANDARD;

PRT;

108

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SEQUENCE OF 1-158 AND 37D-8D1 FROM N.A.

TISSUB-Carcinoma, and Embryo;
IBogai T., Ota T., Haysahi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo N.,
Wagatsuma M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara
Wagatsuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
  "Large scale analysis of two annotation of 650 kb of genom reveals 17 genes.";
Genome Res. 8:1060-1073(1998)
  09UP52: 075422; Q9HA99; Q9NX67;
01-MAR-2002 (Rei. 41, Created)
01-MAR-2002 (Rei. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Transferrin receptor protein 2 (TfR2).
  Camaschella C., Roeti
Carella M., Majorano
The gene TFR2 is mui
  Gloeckner G., Scherer
Tsui L.-C., Rosenthai
  "Molecular cloning of transferrin receptor transferrin receptor-like family."; J. Biol. Chem. 274:20826-20832(1999).
  SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA). TISSUE-Erythroleukemia, and Myeloid leukemia MEDLINE-99340005; PubMed-10409623;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   BLood
  Roetto A., Totaro A., Plperno A., P
Caii A., De Gobbl M., Gasparinl P.,
   PubMed-10802645;
  Submitted
  PubMed-9799793;
   SEQUENCE
  Kawabata H.,
Koeffler H.P.
   Kawabata
   Homo sapiens
   FUNCTION: Mediates cellular uptake of transferrin-bound non-iron dependent manner. May be involved in iron metal hepatocyte function and erythrocyte differentiation.
   gene TFR2
   mustations insctivating
  Genet.
  97:2555-2560(2001).
  11313241;
  FROM
   (AUG-2000)
   25:14-15(2000).
  (Numan).
  Yang R., Nirama
   N
A
  sequencing ;
  Roetto A., Cali
brano N., Totaro
  mutated
  rsis of two regions in human chromosome 7q22:
kb of genomic sequence around the EPO and CU
  (ISOFORM GAMMA).
  'n
  Schattevoy
   project.";
EMBL/GenBank/DDBJ
  Τ.,
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   transferrin
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  Vuong
  Piga A., Longo
., Camaschella
  type
  De Gobbi M., Garozzo G.,
Gasparini P.;
type of haemochromatosis mapping
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  A.P., Weber J.
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RESULT 10
PPOX_HUMAN
  Query Match
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Matches 6
  PPOX_HUMAN
P50336;
01-OCT-1996
01-OCT-1996
15-DEC-1998
   CONFLICT
  CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
VARIANT
  SITE
DISULFID
DISULFID
CARBOHYD
CARBOHYD
  EMBL; AF067864; AAD45561.1;
EMBL; AF053356; AAC78796.1;
EMBL; AK022002; BAB13951.1;
EMBL; AK000421; BAA91153.1;
  use by non-profit Institutions as iong as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.lsb-sib.or send an email to license@isb-sib.ch).
  This
   PPOX
   DOMALN
NCBI_TaxID=9606;
                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutherla;
   Pfam; PF02225; PA; Transmembrane; Gly
  TRANSMEM
   XIX:
   Protoporphyrinogen
  Aiternative
   between
   interPro;
   EROPS; M28.973;
   262
  1 RGIRPVGR
  total body lron, which results in midlite in clinical complications including cirrhosis, cardiopathy, diabetes, endocrine dysfunctions, arthropathy, and susceptibility to cancer. Since the disease complications can be effectively prevented by regular phlebotomies, early diagnosis is most important to provide a normal life expectancy to the affect
   European Bioinformatics Institute.
  SIMILARITY: BELONGS TO
  MISCELLANEOUS:
   the beta isoform thus
   604250:
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   RGVDPVGR
  Similarity
6; Conser
   50; -.
; IPR003137; P;
PA; 1.
  (Rel.
  8D1 AA;
   Conservative
  splicing;
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23
108
111
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240
339
540
754
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  Glycoprotein;
   STANDARD;
   34, Creat
34, Last
37, Last
an oxidase
   The variant
  712
88755
   801
108
1111
1111
240
240
339
540
754
171
171
                             Chordata,
Primates;
   69.48;
75.08;
   PA.
  Disease
   Created)
   III affects the putative ini
s preventing its translation.
   sequence
annotations
(EC 1.3.3
  X
  PEPTIDASE FAMILY M28B
  N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
MISSING (IN ISOFORM BETMISSING (IN ISOFORM GAMM -> K (IN HFE3).
  Score 34; DB
Pred. No. 31;
1; Mismatches
  ;
   /FTId=VAR_012738.
R -> RIPLSAQV (IN REF. 2)
; D3D3D82BA835413A CRC64;
   Receptor;
  ENDOCYTOSIS SIGNAL (POTENTIAL).
INTERCHAIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
  CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
   (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                           Craniata; Ve
Catarrhini;
  mutation
   lys-172 found
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  Signai-anchor;
  Vertebrata; Euteleostomi;
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  Length 801;
   hereditary
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   Frank J., Poh-Fitzpatrick M.B., King L.E. Jr., Christiano A.M.; "The genetic basis of 'Scarsdale Gourmet Diet' variegate porphy missense mutation in the protoporphyrinogen oxidase gene."; Arch. Dermatol. Res. 290:441-445(1998).

-I- FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION OF PROTOPORPNY
   Protein
[3]
  MEDLINE-95229621; pubMed-7713909;
MIShimura K., Taketani S., Inokuchi H.;
"Cioning of a human cDNA for protoporphyrinogen oxidase complementation in vivo of a hemg mutant of Escherichia J. Bloi. Chem. 270:8076-8080(1995).
   MeIssner P.N., Dailey T.A., Hift R.J., Ziman M., Corrigall A. Roberts A.G., Melssner D.M., Kirsch R.E., Dailey H.A.; "A R59W mutation in human protoporphyrinogen oxidase results decreased enzyme activity and is prevaient in South Africans variegate porphyria.";
   "Mutations in the protoporphyrinogen variegate porphyria."; Hum. Moi. Genet. 5:407-410(1996).
   MEDLINE=96367087; PubMed=8771201;
Dailey T.A., Dalley H.A.;
"Numan protoporphyrinogen oxidase: expression, characterization of the cloned enzyme.";
   VARIANT VP CYS-152.
MEDLINE-98434271; E
   VARIANT VP ARG-232, AND VARIANT NIS-304
MEDLINE-97005368; PubMed-8852667:
  variegate porphyria.
  VARIANT VP
  Deybach
   SEQUENCE FROM N.A.
  flavoprotein;
  MEDLINE-96241580;
   WITH ITS ACTIVE SITE FACING THE MITOCHONDRIAL INNER MEMBRANE WITN ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.

DISEASE: DEFECTS IN PPOX ARE THE CAUSE OF PORPHYRIA VARIEGATA (VP), A DISEASE CHARACTERIZED BY SKIN HYPERFIGHENTATION AND NAIR HYPERFRICHOSIS, ASSOCIATED WITH ACUTE ATTACKS, LIKE THOSE OF ACTIVITIENT PORPHYRIA.
   COFACTOR: CONTAINS ONE FAD P
PATHWAY: PENULTIMATE STEP IN
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: BOUHD
  1X TO FORM PROTOPORPHYRIN IX.

CATALYTIC ACTIVITY: Protoporphyrinogen-IX + O(2) = IX + O(2)O(2).
   SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY
  D38537;
  U26446;
  J.-C., Puy
   blosynthesis;
  TRP-59, AND VARIANT CYS-168 241580; PubMed-8673113;
   13:95-97(1996).
   5:98-105(1996).
   BAA07538.1;
AAA67690.1;
  N.A.
  FAD;
   CONTAINS ONE FAD PER NOMODIMER
   Nordmann
   PubMed-9763307;
   Mitochondrion;
   N., Robreau A.-M., Lamoril J.,
  Heme
  .
  . .
   agreement (See http://www.isb-sib.ch/announce/
   biosynthesis; OxIdoreductase;
Tion; DIsease mutation; POTENTIAL).
R -> W (IN VP).
   IN HEME AND
  oxidase
   mutation;
   PORPHYRIN BIOSYNTHESIS.
   gene
   purification,
  in patients with
   da Silva
  egate porphyria:
   gene.";
  Polymorphism
  PROTÓPORPNYRINOGEN
   protoporphyrin-
  by co11.";
   a collaboration
   A. V.,
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   its
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RESULT 11
PPOX_MOUSE
  Matches
  Query Match
Best Locai
   PPOX_MOUSE
P51175; P973
01-OCT-1996
  Taketani S., Yoshinaga T., Furukawa T., Kohno H., Tol
Mishimura K., Inokuchi H.;
"Induction of terminal enzymes for heme biosynthesis
differentiation of mouse erythroleukemIa cells.";
Eur. J. Blochem. 230:760-765(1995).
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   TISSUE=Erythroleukem1a;
MEDLINE=95331315; PubMed=7607249;
  Dailey T.A.,
   MEDLINE-96132666; Pu
Dailey T.A., Dailey
  SEQUENCE FROM N.A.
   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
  PPOX
  01-OCT-1996 (Rel. 34, 15-DEC-1998 (Rel. 37,
  SEQUENCE
  VARLANT
  VARIANT
   VARIANT
  VARIANT
   SUBCELLULAR LOCATION.
  SEQUENCE FROM N.A.
  Mus musculus
  Protoporphyrinogen
  59
                                      COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMILARITY).

PATHWAY: PENULTIMATE STEP IN HEME AND PORPHYRIN BIOSYNTHESIS.

SUBURIT: NOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: BOUND TO THE MITOCNONDRIAL INNER MEMBRA

WITN ITS ACTIVE SITE FACING THE CYTOSOLIC SIDE.

INDUCTION: DURING ERYTHROID DIFFERENTIATION.

SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY.
   RGIRPVG
   RGIRPAG
   Biochem.
   Similarity
  A., Dailey N.A., Meissner sequence, and expression
   477
  Conservative
   891
  (Mouse).
   53
   7
   ð,
  Blophys.
  STANDARD;
   PubMed=8554330;
   oxidase
   304
   232
   168
   152
   50765
   67.3%;
85.7%;
   Last
  Created)
Last sequence update)
  324:379-384(1995).
  Ę
  annotation update) (EC 1.3.3.4) (PPO)
   0
  Score 33;
Pred. No.
   /FTId-VAR_003688.
G -> R (IN VP).
  R -> C (IN VP).
/FTId=VAR_003687
R -> C.
   /FTId=VAR_003690.
2444DEAC2E6C33EE CRC64;
  Craniata; Vertebrata; Euteieostomi;
Sciurognathi; Muridae; Murinae; Mus
  /FTId-VAR_003689
  PRT
  MIsmatches
  of mouse
  477
   29;
  Prasad
  ₹
  ۲,
  ad A.R.;
protoporphyrinogen
   ::
  Length 477;
   Tokunaga
   Indels
  PROTOPORPHYRINOGEN
   during
  protoporphyrIn-
  MEMBRANE
  0
  Gaps
  0
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RESULT 12
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  SO FEET WAR DRAW CCC
  Query Match
Best Local Similarity
Matches 6; Conserv
  SYE_BACHD STAN
Q9KGF6;
16-OCT-2001 (Rei. 4
16-OCT-2001 (Rei. 4
16-OCT-2001 (Rei. 4
   NP_BIND
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
  This SWI
between
  "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

-I CATALYTIC ACTIVITY: ATP + L-glutamete + tRNA(Giu) = AMP + diphosphate + L-glutamyl-tRNA(Giu).

-I SUBUNIT: MDNOMER (BY SIMILARITY).

-I SUBCELLULAR LOCATION: CyCoplasmic.

-I SUMCLARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
   STRAIN=C-125 / JCM 9153;
MEDLINE=20512562; PubMed=11058132;
Takami H., Nakasone K., Takaki Y.,
   GLTX DR BH0109.
Bacillus haiodurans.
Bacteria; Pirmicutes;
  EMBL; U25114; AAA96003.1; -.
EMBL; D45185; BAA08126.1; -.
MGD; MGI:104968; Ppox.
  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       EMBL; AP001507; BAB03828.1; ...
InterPro; IPR000924; tRNA-synt_ic.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PP00749; tRNA-synt_ic; 1.
PRINTS; PR00987; TRNASYNTHGLU.
PRDSITE; PS00178; AA_TRNA_LIGASE_I;
   modified and this statement is not removed. Usage by and for commercial contities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A.
   the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
   Fuji F., Hirama C., Nakamura Y.,
  Bacillus/Staphylococcus
NCBI_TaxID=86665;
  Glutamy1-tRNA
  Worlkoshi K.;
  Flavoprotein;
  Porphyrin biosynthesis: Neme
          Aminoacyi-tRNA synthetase;
   GiuRS)
   9
   Н
  SWISS-PRDT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
   RGIRPAG 65
  RGIRPVG 7
  64
66
108
427
477
   (Re1. 40,
(Re1. 40,
(Re1. 40,
  Conservative
   FAD;
   synthetase
   Ä
  STANDARD;
   Chesis; Neme biosynthesis; O

Chicker

Mitochondrion.

14 FAD (PDTENTIAL)

64 A -> T (IN REF.

66 A -> P (IN REF.

66 L -> S (IN REF.

427 W -> C (IN REF.

427 W -> C (IN REF.

427 W -> C (IN REF.

427 W -> C (IN REF.
   67.3%;
85.7%;
   Last sequence update)
Last annotation update)
Last annotation update)
Lase (EC 6.1.1.17) (Giutamate--tRNA ligase)
  Bacilius/Clostridium group
   Created)
  group;
          Protein blosynthesis; Ligase; ATP-blnding;
  0
   Score 33;
Pred. No.
  FAD (PDTENTIAL).
   A -> T (IN REF. 2).
A -> P (IN REF. 2).
L -> S (IN REF. 2).
W -> C (IN REF. 2).
8CFB48120728DE6F CRC64;
  PRT:
  Bacillus.
  Mismatches
   ., Maeno G., Si
Ogasawara N.,
  485
   29.
  5
  1,
  Oxidoreductase;
  Sasaki R.,
., Kuhara S
  Length 477;
  Indeis
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  Masui N.
  gh a coilaboration -
  ior
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RESULT 13
ULA7_HCMVA
ID ULA7_HCMVA
AC P16828;
   RESULT 14
   DO GE DO DO AC
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  Query Match
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Matches 6
  Query Match
Best Local Similarity
Matches 6; Conserv
                     Y361_SYNY3
Q55578;
15-DEC-1998 (
15-DEC-1998 (
16-OCT-2001 (
Hypothetical
SLR0361.
  01-AUG-1990
01-AUG-1990
01-FEB-1991
  SITE
SITE
BINDING
SEQUENCE
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  MEDLINE-90269039; PubMed-2161319; Chee M.S., Bankler A.T., Back S., Bohni R., Brown C.M., Cerny R., Chee M.S., Bankler A.T., Back S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barreli B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain abli90."; Curr. Top. Microbiol. Immunol. 154:125-169(1990).
   PIR; S09872; S09872.
Hypothetical protein.
CARBOHYD 144 14
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
   SEQUENCE
  EMBL; X17403; CAA35343.1;
   Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID-10360;
   SEQUENCE FROM N.A.
  Human cytomegalovirus (straln AD169).
Viruses; dsDNA viruses, no RNA stage;
  Viruses; dsDNA viruses,
  Hypothetical protein UL107.
  149 KGIKPVVRF
  57
   1 RGIRPVGRE
   1 RGIRPVGRF
  RGQRPTGHF
   6
   Similarity
  144
150 AA;
   11
252
255
465
                                  (Rel.
(Rel.
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1 28.2
   (Rel. 15, Created)
(Rel. 15, Last sequence up
(Rel. 17, Last annotation
   Conservative
  Conservative
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  65
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   STANDARD;
   STANDARD;
  37. Created)37. Last sequence update)40. Last annotation update)
                                     kDa
  21
256
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54785
   17373 MW;
   65.3%;
  67.3%;
66.7%;
                                   protein sir0361.
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   0
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   Score 33;
Pred. No.
   Score 32;
Pred. No.
  "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
; 7D34A862918F57B6 CRC64;
  N-LINKED (GLCNAC. . .) (P
; 042707546C7EB878 CRC64;
   PRT:
   PRT:
   M1smatches
  Mismatches
   150 AA
   249 AA
  Nerpesviridae,
   30;
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   Length 150
  Length 485
   .) (POTENTIAL).
   Indels
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   collaboration -
  Gaps
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RESULT 15
AR72_HUMAH
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  몽
  Query
Best L
   Matches
  AR72_HUMAN STANDARD;
AR72_HUMAN STANDARD;
04348B: O75749:
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aflatoxin B1 aidehyde reductase 1 (EC 1.-.-) (AFB1-AR 1)
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   MEDLINE=98244807; PubMed=9576847; Ircland L.S., Harrison D.J., Heal G.E., Hayes J.D.; Ircland L.S., Harrison D.J., Heal G.E., Hayes J.D.; Molecular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin Bi-aldehyde reductase.";
  ÁKR7A2 OR AFAR OR AKŘ7.
HOmo sapiens (Human).
Eukaryota, Metazoa; Chordata, Cranlata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  PROSITE; PS01149; PSI_RSU; 1.
Hypothetical protein: Complete proteome.
SEQUEHCE 249 AA; 28228 MW; 315F208030180326 CRC64;
  EMBL; D63999; BAA10082.1;
Interpro; IPR000613; PseudoU_synth.
Interpro; IPR000748; Psl_RSU.
InterPro; IPR002942; S4.
   Sugiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium Synochocystis sp. strain PCC5803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DHA Res. 2:153-166(1995).
Pram1 C., Savelyeva L., Perri P., Schwab M.; "Cioning of the human aflatoxin Bl-aidehyde reductase gene at 1p35-1p35.1 in a region frequently aitered in human tumor cells."; Cancer Res. 58:5014-5018(1998).
  MEDLINE-99040634; PubMed*9823300;
  TISSUE-Brain;
  Blochem.
  Pfam; PF00849; PseudoU_synth_2; Pfam; PF01479; S4; 1. SMART; SM00363; S4; 1.
  MEDLIHE-96127529; PubMed-8590279;
Kaneko T., Tanaka A., Sato S., Kotani H.,
  SEQUENCE FROM N.A.
   HCBI_TaxID-1148;
  SEQUENCE FROM N.A.
  HCBI_Tax1D=9606;
   SEQUENCE FROM N.A.
   100 KGLHPVGR 107
  Local Similarity
  1 RGIRPVGR 8
   SIMILARITY: BELONGS TO FAMILY 1 OF PSEUDOURIDINE SYNTHASES.
  332:21-34(1998).
   Conservative
  65.3%;
62.5%;
   N
  Score 32; DB
Pred. No. 24;
   Mismatches
  Sazuka T., Miyajima
  ij
  1;
  Length 249
  0:
  Gaps
  0
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Search completed: September 13, Job time: 1138 sec
   몽
  Ş
   Query Match
Best Local
   Matches
   Oxidoreductase.
ACT_SITE 112
CONFLICT 113
SEQUENCE 330 AA;
  [3]
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  Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDIHG

-INTERPOLICE BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE

INTOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC

EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
  EMBL; AF026947; AAC52104.1; -.
EMBL; Y16675; CAA75347.1; -.
EMBL; AL035413; CAB72321.1; -.
MIM; 603418; -.
   InterPro; IPR001395; Aldo_ket_red
Pfam; PF00248; aldo_ket_red; 1.
   215 GKQPVGRF 222
   N
  REDUCTASE:
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELOHGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
   GIRPVGRF
   Similarity
6; Conserv
  FROM H.A.
   Conservative
   9
  112 HYDROGEN-BOND DONOR (PROBABLE).
113 A -> T (IN REF. 1).
36618 MW; 3BBFB7ED0CAF4D54 CRC64;
  .0%
              2002, 09:30:48
  Score 32;
Pred. No.
   Mismatches
  32;
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   U
   Length 330
   Indels
   0
   Gaps
   0
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1)

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Title:
Perfect score:
Sequence:
   Result
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 e
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  Minimum
   Scoring table:
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   Total number of hits satisfying chosen parameters:
  protein -
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6544311987654321
   Pred. No.
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   No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
      protein search, using sw model
  length: 0 length: 20000000000
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   BLOSUM62
Gapop 10.0 ,
   SPTREMBL_19:*
   562222 segs, 172994929 residues
  US-09-446-543A-73_COPY_12_21
  September 13, 2002, 09:29:24;
  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
   sp_archea:*
sp_bacteria:*
sp_fun9i:*
   RGIRPVGRFX 10
   sp_rodent:*
sp_virus:*
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   sp_organelle:*
sp_phage:*
  sp_mhc:*
  sp_human:*
  sp_invertebrate:*
   sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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  3 Q9W624
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Q9RJR7
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09w624 carassius a 093127 streptomyce 097950 thermoplasm 050431 mycobacteri 042924 schizosacch 0981v3 rhizobacteri 042927 mycobacteri 0981v3 rhizobacteri 09x597 mycobacteri 09x597 mycobacteri 09x59 vubrio choi 09v40 drosophila 09v40 drosophila 09v40 drosophila 09v40 drosophila 09v17 straptomyce 09cim8 pleurotus 5075230 homo sapien 075422 homo sapien
  Description
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| 45          | 44          | 43          | 42           | 41          | 40          | 39          | 38          | 37          | 36          | 3           | 34          | 33          | 32          | 31          | 30          | 29          | 28          | 27          | 26          | 25          | 24          | 23           | 22          | 21          | 20          | 19          | 16         | 17          |
|-------------|-------------|-------------|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|--------------|-------------|-------------|-------------|-------------|------------|-------------|
| 32          | 32          | 32          | 32           | 32          | 32          | 32          | 32          | 32          | 32          | 33          | 33          | 33          | 33          | 33          | 33          | 33          | 33          | 33          | 33          | ω<br>ω      | 33          | 33           | 33          | 33          | ü           | 33          | 33         | 34          |
|             |             |             |              |             |             | 65.3        |             |             |             |             |             | 67.3        |             | 67.3        |             |             |             |             | 67.3        |             | 67.3        |              |             | 67.3        |             |             |            | 69.4        |
| 309         | 299         | 292         | 285          | 278         | 266         | 183         | 163         | 154         | 97          | 2104        | 2104        | 1940        | <b>106</b>  | 883         | 589         | 511         | 477         | 445         | 366         | 353         | 335         | 319          | 313         | 253         | 205         | 153         | 139        | 108         |
| N           | 16          | 16          | N            | 16          | 80          | 17          | 16          | 2           | 8           | u           | ហ           | 16          | 16          | 10          | 16          | ω           | 11          | N           | 16          | 16          | 16          | N            | 16          | N           | 4           | 9           | ហ          | 4           |
| _           |             | 092VM1      | _            |             | _           |             |             | _           | Q985K5      |             |             |             |             |             |             |             |             |             |             |             |             | a            |             | שי          |             | _           |            | Q9UP52      |
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| streptomyce | mycobacteri | rhizobium m | pseudomonas  | rhizobium m | dictyosteil | thermoplasm | rhizobium m | streptomyce | balanus gla | cacnorhabdi | caenorhabdi | deinococcus | streptococc | Lycopersico | caulobacter | schizosacch | mus muscuiu | streptomyce | aquifex aeo | mycobacter1 | mycobacter1 | streptomyco  | rhizobium m | streptomyce | homo sapien | bacteriopha | leishmania | sapien      |

## ALIGNMENTS

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SO SEE SEES
 RESULT
Q93LZ7
ID Q9
AC Q9
DT Q9
DT Q9
  Query Match
Best Local Similarity
Watches 7; Conserve
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   O9W624 PRELIMINARY;
O9W624;
O1-NOV-1999 (TrEMBLrel. 12, C
O1-NOV-1999 (TrEMBLrel. 12, L
O1-DEC-2001 (TrEMBLrel. 19, L
 Q93LZ7;
Q93LZ7;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
  C-RP AMIDE.
Carassius auratus (Goldfish).
Chordata; Cranlata;
Ebkaryota; Metazoa; Chordata; Cranlata;
Actinopterygil; Neopterygil; Teleostel;
Cypriniformes; Cyprinidae; Carassius.
  Satake H., Minakata H., Fujimoto M.;
"Carassius Reamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 MW; D50C4CB22038C2B0 CRC64;
   SEQUENCE FROM N.A.
TISSUE-BRAIN;
   NCBI_TaxID=7957;
   67
  1 RGIRPVGRF 9
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RGVRPIGRF
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  Score 46; DB 13
Pred. No. 0.11;
2; Mismatches
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  PRT;
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  DB 13:
  Euteleostel; Ostarlophys1;
  Vertebrata; Euteleostomi;
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C STRAIN-GSS1 / DSM 4299 / JCM 9571;

C STRAIN-GSS1 / DSM 4299 / JCM 9571;

X MEDLINE-20570466; PubMed-11121031:

X MEDLINE-20570466; PubMed-11121031:

X MEDLINE-20570466; PubMed-11121031:

X MEDLINE-20570466; PubMed-1121031:

X MARCHARA I AMARIN N., KOIKE H., Makino S.-I., Higuchi S.,

X Mawashima-Ohya Y., Watchabe K., Yamazaki M., Kamehori K., Kawamca Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

"Archacal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.";

T "Archacal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.";

T sequence of Thermoplasma volcanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

R EMDL; AP000995; BAB60232.1; -.

R InterPro; IPR002035; WFFA.

R InterPro; IPR002035; WFFA.

R FAMR; SMO0327; WAA; 1.
   Duery Ma
Best Loc
Matches
 050431;
D50431;
01-JUN-1998
01-JUN-1998
  TVG1120468 PROTEIN.
   Kormance J., Bistakova J., Novakova R., Homerova D., Rez "Cloning and characterization of a new polyketide gene c Streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY033994; AAK61719.1;
SEDUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
  Streptomyces aureofaciens.
Bacteria; Pirmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Pirmicutes; Actinobacteria; Actinobacteridae;
Streptomyces.
  Complete proteome. SEQUENCE 426 AA;
  Q979S0;
01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
  SEDUENCE FROM N.A.
STRAIN-CCM3239;
   Actinomycetales; Streptomycineae, NCBI_TaxID=1894; [1]
  Thermoplasma voicanium.
Archaea; Euryarchaeota;
   D979S0
   Thermoplasma
   AUR2B
   304 GIRPAGKF 311
  y Match
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   GIRPVGRF
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   GIRPVGRF
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   73.5%;
nilarity 75.0%;
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   Thermoplasmales; Thermoplasmaceae;
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   Score 36; DB
Pred. No. 46;
1; Mismatches
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Last annotation update)
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Pred. No. 1.7
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sequence update)
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  426
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  17; Length 426;
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  MEDLINE-98295987; PubMed-9534230;

A Cole S.T., Brosch R., Parkhill J., Garnler T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Badcock K., Basham D., Brown D., Chililingworth T., Connor R., RA Davies R., Deviin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., RA Davies R., Deviin K., Kroph A., Rclean J., Moule S., Murphy L., AND C., College R., Skelton S., Squares S., Squares R., Raylor K., Whitchead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).

PR HILL ALOIQUAG: CANISTALIIN.

BMBL; ALOIQUAG: CANISTALIIN.

BR Tuberculist, Rv1175c;

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Pfam; PF00774; Oxidored_FMN.

Pfam; PF00774; Oxidored_FMN.

Pfam; PF00775; CRYSTALLIN_BETAGAMAA, UNKNOWN_1.
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STRAIN-97
   042924 PRELIMINARY; PRT; 272 AA.
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01-JAN-1999 (TrEMBLrel. 09, Created)
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 30.9 KDA PROTEIN C16A3.19 IN CHRDMOSOME
SPBC16A3.19.
   Wood V., Rajandream M.A., Uarrell B.G., Beck A., Reinhardt R.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AL021748; CAA16870.1; ... InterPro; IPR001005; Myb_DNA_bind. PROSITE; PS00037; MYB_1; UNKNOWN_1. Hypothetical protein. SEDUENCE 272 AA; 30901 MW; 8FE0EB29217107A8 CRC64;
   01-DEC-2001 (TremBLrel. 19, La 2,4-DIENOYL-COA REDUCTASE. FADH OR RV1175C OR MTV005 11C.
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674 AA;
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l; Mismatches
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  . 75,
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45;
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  Length 272;
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RESULT
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O1-JUN-1998 (TrEMBLrel. 06, Last
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PUTATIVE TWO-COMPONENT SENSOR.
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Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E., III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterlum tuberculosis from the complete genome sequence.";
  Q981V3,
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STRAIN-H37RV;
MEDLINE-98295987;
   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S.;
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   Mesorhlzobium lotl.";
DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54606.1; -.
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   Complete genome structure of the nitrogen-fixing symblotic bacterium
   179
  47
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371 AA; 42385 M
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Last annotation updat
  Created)
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InterPro: IPR003564; H1s_KinA.
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InterPro: IPR004359; HIS_KIN_s1g.
InterPro: IPR004359; HS_KIN_s1g.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
PUTATIVE TWO-COMPONENT SYSTEM SENSOR KINASE,
   Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N. Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
  Q9Z5G7
   SEQUENCE FROM N.A. Harris D., Taylor K.; Submitted (FEB-1999)
   Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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NCBI_TaxlD=1769;
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01-0CT-2000
01-DEC-2001
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STRAIN-EL TOR N19961 / SEROTYPE 01;

MEDLINE-20406833 PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.

McDonald L., Utterback T., Fleischmann R.D., Nlerman W.C., White O.,

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Frascr C.M.;
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Created) Last sequence update)

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RA Geosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
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RA Geosa V.F., Logens M.A., Varioria M.A.,
RA Salveira W.F., Silva M.A., Varioria M.A.,
RA Salveira M.A., Ra M., 
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D9VU79;
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01-DEC-2001
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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  N
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Pred. No. 1.9e
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  RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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01-MAY-2000 (TrEMBLIEL. 1
01-MAY-2000 (TrEMBLIEL. 1
01-DEC-2001 (TrEMBLIEL. 1
PUTATIVE ZINC-BINDING OXII
SCF51.18.
  FlyBase, FB9n0036388; CG10738.

InterPro; IPR001828; ANF_receptor.
InterPro; IPR001719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
InterPro; IPR001054; Guanylt_cyclase.
Pfam; PP01094; ANF_receptor; 2.
Pfam; PP01094; ANF_receptor; 2.
Pfam; PP00011; 9uanylate_cyc; 1.
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PROSITE; PS00152; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
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Last sequence up
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   MEDLINE-97000551; PubMed-8843436;

Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cui
Rinashi H., Hopwood D.A.;

P. A. set of ordered cosmids and a detailed genetic and phy
the 8 mb Streptomyces coelicolor A3(2) chromosome.";
MOL. Microbiol. 21:77-96(1996).

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   Jeong M.-J., Park S.-C.;
"Cloning of the catalase gene from Pleurotus sajor-caju.";
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  N 3
   529
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1.5e+02;
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  Length 329;
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Job time: 1069 sec
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Maximum Match 1008

Listing first 45 summaries
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  747574 seqs, 111073796 residues
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Peptide PrRP0 frag
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19P2 ligand peptid
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19P2 ligand peptid
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Human type G protein
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Bovine pituitary-d
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| 97.7               |          | •                  | ٠         | 97.7     | 97.7               | 97.7       | 97.7     | 97.7               | 97.7               | 97.7     | 97.7     | 97.7     | 97.7     | ٠                  | ٠        | 97.7     | 97.7     | 97.7     | 97.7               | ٠                  | 97.7     | 97.7      | 97.7     | 97.7     | 97.7               |           | 97.7       |            | 97.7     | •          | ٠        | •             | 97.7               |  |
| 22                 | ر<br>د د | 21                 | 21        | 21       | 21                 | 21         | 21       | 21                 | 21                 | 21       | 21       | 21       | 21       | 21                 | 20       | 20       | 20       | 20       | 20                 | 20                 | 20       | 20        | 20       | 20       | 20                 | 20        | 20         | 20         | 20       | 20         | 20       | 20            | 20                 |  |
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| Rat type G protein | 1        | Human CRH releasin | releasing |          | Human oxytocin sec | ytočin sec |          | Bovine pituitary-d | Mammalian 19P2 lig | igand po | н        | g<br>O   | ด<br>ค   | Synthetic G protei | ч        |          |          |          | CRH releasing prot | Human CRH releasin |          | ine ČRH r | ligand   | 11gand   | 19P2 ligand peptid | in secret | an oxytoci | ytocln sec |          | pituitary- | e pitu   | an type ligan | Rat type llgand po |  |

# ALIGNMENTS

AAB46955 RESULT

AAB46955 standard; Protein;

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04-MAY-2001 (first entry)

AAB46955;

Peptide PrRP8 fragment.

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GPR10; UHR-1; PrRP receptor; prolactin-releasing peptide; pain; central nervous system disorder; autonomic regulation; analgesic; hypotensive; blood pressure.
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Modified-site
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   Location/Qualiflers
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  cc nervous system, including those associated with pain or autonomic concerning the control of cont
  Query Mstch
Best Local S
Mstches
   Pituitary-derived ligand polypeptide; G-protein coupled orphsn receptor; GPR10; UHR-1; modulator; pituitsry; central nervous system; pancress; tissue; screen; therspeutic; binding; senlie dementia; ligand; murine;
  C-terminal fragments of prolactin-releasing peptide useful for regulating autonomic functions and in the msnufacture of a medicament for regulating blood pressure -
  Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeid-Jakob disease; poisoning; schlzophrenis; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vssopres
  AAW95178 standard; Protein; i0
  prolactin-releasing peptide (PrRP), referred to as PrRP20 and sequence (S1). The invention also describes (1) a therapeutic (C1) comprising (I) or a C-terminal fragment of PrRP referred
  gene therapy;
  Murine pituitsry-derived ligand polypeptide antigenic epitope.
   10-MAR-1999
   and comprising a sequence (S2); (2) a diagnostic method based on ant against PrRP20 for identification of disorders involving the central
   Claim
                    (TAKE ) TAKEDA CHEM IND LTD
  28-APR-1997;
   27-APR-1998;
  05-NOV-1998.
   Sequence
   This invention describes a novel C-terminal fragment (I)
  Ν
   GIRPVGRF 0
   girpvgrf 8
  Similarity
8; Conserv
   Page 10; 40pp; English
  Φ
   97.7%;
Liarity 100.0%;
Conservative
  ζ
  (first entry)
   transgenic animai; epitope.
  97JP-0109974
   98WO-JP01923
  0:
   Score 43;
Pred. No.
  Mlsmatches
  DB 22;
6.4e+05;
  Length 8;
  Indels
   of an isolated
  0
   vssopressor;
  having a composition
   ដូ
  Gaps
  antisera
   as PrRP8
  0,
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S

WO9724436-A2 Synthetic

18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996;

96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805.

26-DEC-1996;

96WO-JP03821

```
RESULT
AAW31400
  cc which is a ligand for the 6-protein coupled orphan receptor designated coupled that ligand polypeptide encoding DNA are used to produce a recombinant ct ligand polypeptide. The ligand polypeptide, and its fragments, modulate cf function of the pituitary, central nervous system, pancreas and other ct issues and can be used to screen for sgents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a csample and to raise antibodies. They may also be used therspeutically, cc. e.g. to treat senile dementia; Alzhelmer's, Parkinson's or Huntington's cd diseases; creutafeld-Jakob disease; poisoning by heavy metals or drugs; cd diseases; creutafeld-Jakob disease; poisoning by heavy metals or drugs; coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes, as models of cd isease, for drug screening and as source of cell lines. The ligand coplypeptide bNA is used as source of probes and primers; to identify created sequences; in receptor-binding assays; for production of Ab and creative parking the ligand sequences AAM95174 to AAW95178 represent antigenic antigenic antigenic animals. Sequences AAM95174 to AAW95178 represent antigenic senting.
   Query Match
Best Local :
therapeutic agent.
  G protein-coupled receptor;
  06-APR-1998
   AAW31400 stsndard; Peptide; 15
   Sequence
   Disclosure; Page 26; 206pp; English.
  New polypeptide iigand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
  Fukusumi S,
   Synthetic ligand i9P2-L31 peptide II.
   AAW31400;
  Local Similarity
les θ; Conserv
   |||||||||
| girpvgrf 10
  i GIRPVGRF
   u
  invention relates to a murine pituitary-derived ligand polypeptide ch is a ligand for the G-protein coupled orphan receptor designated
   10
  97.7%; Score 43: DB llarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
   (first entry)
  0
   ζ
  central nervous system; psncress; prophylactic;
  ligsnd binding; phsrmaceutical;
   DB 20,
0 029;
  Length 10;
  Indels
  ..
   GSpS
   used
  0
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RESULT
AAW97230
  Ş
  밁
   This peptide contains the partial C-terminal sequence of the synthetic CC ligand polypeptide 1992-131 which is capable of binding to a G CC propare rabbit anti-bovine 1992-131 antibodies which are used in binding CC propare rabbit anti-bovine 1992-131 antibodies which are used in binding CC assays. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific CC applications as a prophylactic or therapeutic agent for dementia, CC depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, CC hyper and polyphagia, hyperilpidaemia, hypercholesterolaemia, the prophylactinaemia, diabetes, cancer, pancreatitis, CC hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, CC sphal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, CC sphal injury, transient brain ischaemia, epilepsy, amylotrophic lateral CC degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis cand/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand CC affecting activation of the G protein-coupled receptor protein.
  Query Match
Best Local S
Matches 8
  G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; piacental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia; prolactin secretion.
   AAW97230 standard;
  Example 43; Page 151; 258pp; English.
23-JUH-1997;
                                  22-JUN-1998;
   30-DEC-1998
   WQ9858962-AJ
   C-terminal ligand polypeptide derived antigen.
   06-MAY-1999
  Ligand peptide for G protein-coupled receptor - function in the central nervous system, pancreas
   WPI; 1997-363672/33
   Kawamata
  Local Similarity
hes 8; Conserv
  8
  1 GIRPVGRP
   4
  girpvgrf 15
   Fukusumi S.
  15
   Conservative
   (first entry)
                                  98WO-JP02765
   central nervous system, pancreas and
   Peptide;
   ü
   97.7%;
   Habata
  0,
   Score 43;
Pred. Ho.
   Ķ
   Mismatches
  Hinuma
   DB 18; Length 15; 0.045;
  s
  Hosoya
  0
  Inde1s
  by modulating pituitary gland
  0,
  Gaps
  0
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8
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   AAY49293
  RESULT
   Matches
   Query Match
Best Local
   brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or
   AAW97229-31 represent a ligand polypeptide derived fragments used to produce antibodies. The specification describes an agent for modulating prolactin secretion which compressor a ligand polypeptide or a sait, for a 6 protein coupied receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting projectin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmne disease, prolactions.
   Use of G protein-coupled receptor ligands - for modulating presecretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
  WO9960112-A1
   AAY49293 standard; peptide;
   Sequence
   (TAKE ) TAKEDA CHEM IND LTD
            (TAKE ) TAKEDA CHEM IND LTD
   21-MAY-1998;
  Monoclonai antibody; 19P2 ilgand; diagnosis; proiactin secretion;
pitultary; regulatory mechanism; central nervous system; pancreat
   19P2 ligand
  AAY49293;
   Example 43;
   20-MAY-1999;
   25-NOV-1999
   Modified-gite
  Homo sapiens
   22-FEB-2000
  8
   1 GIRPVGRF 8
  (s)
  1999-105614/09
   girpvgrf
   h 97.7%; Score 43;
Similarity 100.0%; Pred. No.
8; Conservative 0; Mismatc
   Hinuma S,
   15
   peptide
  Page 123; 241pp; English.
   (first
  15
   ξ
   98JP-0140293
  99WO-JP02650
  Location/Oualifiers
   /note= "C-terminal amide"
   fragment.
   entry)
  Kawamata Y,
  15
  ξ
  Mismatches
  Matsumoto
   DB 20;
0.045;
  Ξ
   for modulating prolactin
  0
  Length 15;
   0
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RESULT
AAY49295
ID 4AY49295
ID AAY4
XX AAY4
XX AAY4
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  Query Match
Best Local :
  Matches
  The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism (e.g. manupoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAV49290-302 represent peptide fragments of the 1992 ligand.
                    Disclosure;
   New monoclonal antibodies, using the studying diseases related to
   WPI; 2000-039381/03
  21-MAY-1998;
  20-MAY-1999;
  25-NOV-1999
   W09960112-A1
  Modified-site
  Modified-site
  pitultary;
   Monoclonal
  19P2 ligand
   22-FEB-2000
  AAY49295;
   AAY49295 standard;
  Sequence
  New monoclonal antibodies,
  Matsumoto
  (TAKE ) TAKEDA CHEM IND
  Local Similarity hes 8; Conserv
   8
  1 GIRPVGRF 8
  6
   |||||||||
|girpvgrf 15
   diseases related
   Ξ,
  regulatory mechanism; central
   antibody;
  15
                    Page
  peptide fragment.
  Conservative
  Page
   (first entry)
   5
   Kitada
  Kitada
  98JP-0140293
  99WO-JP02650
  /note-
15
   Location/Qualifiers
                    26;
   /note-
   /note-
   peptide; 15
   Ó
  97.7%;
   Ó
   19P2 ligand;
   73pp; Japanese.
   "acetylated Tyr"
   "C-terminal amide"
  "N-terminal acetylation"
  LID
   Hinuma
   Hinuma
   ៥
  useful in diagnosis,
o ligand abnormality
   useful in diagnosis,
o ligand abnormality
  0
  Score 43;
Pred. No.
   ۶
  Ś
  Mismatches
   diagnosis; prolactin secretion,
  DB 21;
0.045;
  nervous system; pancreatic
  21;
  ç,
  Length 15
  98
   as drugs
  Indels
   drugs
   and
  and
   0
   j
  'n
   Gaps
   0
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RESULT
AAY49296
   888888888<del>8</del>&
  몽
  Ş
   Query match
Best Local S
Matches 8
   The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pitultary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 1992 ligand.
                        regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 19P2 ligand
   The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 192 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function
 Sequence
   New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
   Matsumoto
  (TAKE ) TAKEDA
   21-MAY-1998;
   25-NOV-1999.
   W09960112-A1
   Modified-site
  HOMO
  pituitary; regulatory mechanism; central nervous system; pancreatic.
   Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
   19P2 ligand
  22-FEB-2000
  AAY49296;
   AAY49296 standard; peptide; 15 AA.
   Sequence
   20-MAY-1999;
   8
   1 GIRPYGRF 8
   7
  sapiens
  2000-039381/03
   Similarity
8; Conserv
  Ŧ,
15
   15 AA;
   Page
  Conservative
   (first entry)
  Kitada C,
  CHEM IND
   98JP-0140293
   99WO-JP02650
   Location/Qualifiers
   27;
  /note=
  97.7%;
   73pp; Japanese.
   "C-terminal amide"
  LTD.
  Hinuma
  0.
  Score 43;
Pred. No.
  (C)
  Mismatches
  DB 21;
0.045;
  0
   Length
   9
  Inde1s
  drugs
  15
  its derivative
  and
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   Gaps
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100.0%;

Pred. No.

0.06:

0

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RESULT
AAW31394
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                       CC ligand polypeptide corresponding to amino acid residues 34 to 53 of the caquence represented in AAW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pluitary function CC modulator. This ligand could have specific applications as a CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC trauma, growth hormone secretory disease, hyper-and polyphagia, CC trauma, growth hormone secretory disease, hyper-glyceridaemia, hypergroplactinaemia, diabetes, cancer, pancreatitis, renal disease, hyper-prolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC transient brain ischaemia, appliepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoprosis and/or coligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting content of the G protein-coupled receptor protein.
  Query Match
Best Local S
Matches 8
  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
   Fujli R,
Kawamata
   Clalm
   WPI; 1997-363672/33.
  G protein-coupled receptor: ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
   AAW31394;
   N-PSDB: AAV02431.
   W09724436-A2
   AAW31394 standard: Peptlde:
 Sequence
  Ligand poptide for G protein-coupled receptor - acts function in the central nervous system, pancreas and
  12-AUG-1996;
   10-JUL-1997
  Homo sapiens
   therapeutic agent.
   Human type G
   06-APR-1998
  (TAKE ) TAKEDA CHEM IND
  œ
  سر
   æ
   sequence represents a peptide fragment from a novel human
   GIRPVGRF 8
   girpvgrf 15
  Similarity
8; Conser
  Page 185; 258pp; English.
   Fukusuml S, Y, Kitada C:
 20
  Conservative
  protein-coupled
   (first entry)
   96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
   96WO-JP03821.
  97.7%;
  Habata
  LTD.
   20
  0
  Score 43;
Pred. No.
  receptor ligand fragment
  κ,
   ζ
  Mismatches
   Hinuma S,
  DB 21; Length 15; 0.045;
   Нозоуа М;
  0;
  Indels
  by modulating pituitary gland
   0
   type
53 of the
   Gaps
   0
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Query Match

97

.78;

Score 43;

18;

Length 20

Query Match Best Local Similarity

97.7%:

Score '

. 43: No.

DB 18;

Length

```
RESULT
AAW31387
                                   This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 33 to 52 of the Sequence represented in ANW31383 and Is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pitultary function CC modulator. This ligand could have specific applications as a comply actic or therapeutic agent for dementia, depression, hyperkinetic CC syndrome, disturbance of consclousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholesterolaemia, hyperglyceridaemia, byperpolactinaemia, diabetes, cancer, pancreatitis, renal disease. CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, CC transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, CC acute myocardial infarction, infertility, spinocerebeliar degeneration, CC bone fracture, trauma, atopic dermatitis, osteoporosis and/or CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
   Best Local Similarity
Matches 8; Conserv
   18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
   G protein-coupled receptor: llgand binding: pharmaceutical;
modulator; pituitary; central nervous system; pancreas: prophylactic;
  AAW31387 standard; Peptide;
Sequence
  Claim 2; Page 180; 258pp; English.
   Fujil R,
   W09724436-A2
   Rat sp
  Rat type G
   06-APR-1998
   AAW31387:
  Ligand peptide for G
  (TAKE ) TAKEDA CHEM IND
  26-DEC-1996;
   10-JUL-1997
  function
   12-AUG-1996;
  13 girpvgrf
   1 GIRPVGRF
  v
   AAV02424
  5
   Fukusumi
  protein-coupled
  20
   lde for G protein-coupled receptor - acts
the central nervous system, pancreas and
   Conservative
   (first entry)
   Kitada
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   96JP-0246573.
95JP-0343371.
96JP-0059419.
  96JP-0211805
  96WO-JP03821
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   Habata
   LTD.
  receptor ligand fragment 4.
   20
   0,
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   Mismatches
   Hinumo
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  Hosoya
   0;
   Indels
   by modulating pitultary gland
   ..
   Gaps
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  CC This sequence represents a peptide fragment of a novel bovine pituitary CC derived ligand corresponding to amino acid residues 34 to 53 of the Sequence in AAW31368 and is used in an assay to monitor ligand binding CC to the G protein-coupled receptor protein. Pharmaceutical compositions CC containing this ligand may be used as a pituitary function modulator. a CC central nervous system modulator or a pancreatic function modulator. CC This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, CC disturbance secretory disease, hyper- and polyphagia, CC hypercholesteroiaemia, hyperglyceridaemia, hyperlipidaemia, hyperglyceridaemia, hyperlipidaemia, for hyperprolactineemia, diabetes, cancer, pancreatitis, renal disease, hyper-solucion protein, acute CC transient brain ischaemia, amylotrophic lateral scierosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, CC transient brain ischaemia, amylotrophic lateral scierosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, CC transient brain ischaemia, and los be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
  RESULT 10
   Query Match
Best Local S
Matches 8
   Matches
  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
   Sequence
   Claim 2; Page 161; 258pp; English
   Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
   N-PSDB; AAV02397
   WPI; 1997-363672/33.
  Kawamata Y,
   (TAKE ) TAKEDA CHEM IND
  26-DEC-1996;
  10-JUL-1997
   909724436-A2
  therapeutic
   modulator;
  Bovine G
  06-APR-1998
  AAW31374 standard; Peptide;
   1 GIRPVGRF 8
|||||||
13 girpvgrf 20
  protein-coupled receptor; iigand binding; pharmaceutical;
dulator; pituitary; central nervous system; pancreas; prophylactic.
   8; Conserv
   8
   protein-coupled receptor ligand peptide fragment 4.
  Fukusumi S,
Kitada C;
   20
97.7%; Score 43; DB 18; Length 20; Llarity 100.0%; Pred. No. 0.06; Conservative 0; Mismatches 0; Indels
  (first entry)
   Conservative
   96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
   96WO-JP03821.
  Habata
   LTD.
  20
   0
  ×
   Mismatches
  Hinuma
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  Новоуа м;
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   Indels
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   0
   Gaps
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RESULT 1
AAW97232
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                                   CC The present sequence represents a bovine pituitary-derived ligand CC fragment. It is used in the course of the invention. The specification CC describes an agent for modulating prolactin secretion which comprises a CC idend polypeptide or a salt, for a 6 protein-coupled receptor (GPCR) CC protein. The agents for promoting prolactin secretion can be used for CC treating or preventing hypoovarianism, gonecyst cacogenesis, menopausal CC syndrome, euthyroid or hypometabolism. They can by used for promoting CC inhibiting prolactin secretion can be used for treating or preventing CC inhibiting prolactin secretion can be used for treating or preventing CC inhibiting prolactin secretion can be used for treating or preventing CC prolactinoma, infertiity, impotence, amenorathea, galactorrhea, CC acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, CC Grobes-Albright syndrome, impotence, amenorathea, galactorrhea, CC Forbes-Albright syndrome, impotence, acontraceptives. The agents for CC modulating placental function can be used for treating or preventing CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, contraction of the
  menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; sheehan syndrome; dyszoospermia; contraceptive; piacental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia.
   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
  G protein-coupled receptor;
   AAW97232 standard; peptide;
  Claim 3; Page 136; 24lpp; English.
   WPI; 1999-105614/09
   Fujii R, Hinuma S,
   22-JUN-1998;
  30-DEC-1998.
   Bos sp
  Bovine
   Bovine pituitary-derived ligand polypeptide fragment.
  06-MAY-1999
  AAW97232;
   (TAKE ) TAKEDA CHEM IND LTD.
   23-JUN-1997;
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  pituitary-derived ligand; modulation;
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  97JP-0165437
   98WO-JP02765
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  ζ
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Query Match Best Local Similarity Matches 8; Conserv

Conservative

97.7%; Su 100.0%; Pr

Score 43; DB 20; Pred. No. 0.06;

Length 20; Indels

Mismatches

0

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Gaps

0

Sequence

20

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12

1 GIRPVGRF ( |||||||| 13 girpvgrf :

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Query Match
Best Local Similarity
Matches 8; Conserv
   printitary adenomatosis, press. competed, amenorrhea, galactorrhea, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Fronmei syndrome, Argonz dei Castilo syndrome, Porbos-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choricosrcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,
  The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocrarianism, genecyst cacegenesis, menopausal syndrome, euthyroid or hypocrarianism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiae. The agents for inhibiting prolactin secretion can be used for treating or preventing pitulitary adenomates being tumour, emmenlopathy, autoimmune disease, are treating to the secretion can be used for treating or preventing pitulitary adenomates, brain tumour, emmenlopathy, autoimmune disease,
   menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; inpotence; amenorrhea; galactorrhea; prolactinoma; infertility; inpotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommei syndrome; Argonz-dei Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; chorlocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
  Use of G protein-coupled receptor ligands - for modulating projectin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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  06-MAY-1999
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   Sequence
   WPI; 1999-105614/09
  (TAKE ) TAKEDA CHEM IND LTD.
  22-JUN-1998;
   30-DEC-1998
  abnormai lipidmetabolism; oxytocia.
   Rat type ligand; modulation; projectin secretion;
   Rat type ligand
  AAW97234;
  protein-coupled
   æ
   Ψ
   gp
   Page 154; 241pp;
   Hinuma S,
   20
97.7%; Score 43; DB itarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
   (first entry)
  97JP-0165437.
  98WO-JP02765
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  receptor;
   Kawamata
   Engiish.
   GPCR; hypoovarianism; gonecyst cacogenesis;
   fragment.
   ¥,
  $
   Matsumoto
                   DB 20
  20;
                                    Length 20;
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0

Indels

0

Gaps

0

Query Match Best Local S Matches 8

n 97.7%; Score 43; Similarity 100.0%; Pred. No. 8; Conservative 0; Mismatc

Mismatches

0

ô

Gaps

0

DB 20;

Length 20;

fetus, for

Sequence

20

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RESULT 1
용
   9
                            treating or preventing hypocovarianism, gonecyst cacogenesis, menopausai syndrome, euthyroid or hypometabbiism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pitulitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhee, galactorrhee, acromegaly, Chiari-Frommei syndrome, Argonz-dei Castilo syndrome, Porbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriccarcinoma, hydatid mole, irruption mole, abortion, unthrifty feture abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
  The present sequence represents a human type iigand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a 6 protein coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for
  Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
   pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chlari-Frommei syndrome; Argonz-dei Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
   G protein-coupled receptor; GPCR; hypoovarianism; gonecyst menopausai syndrome; euthyroid; hypometabolism; lactation;
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   Ciaim 3;
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   23-JUN-1997;
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  30-DEC-1998.
  WO9858962-A1
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   97JP-0165437
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  Matsumoto
   Ξ,
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Pred. No.

0.06;

0;

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AAW95191
  밁
   S
  The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Celis transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the CC polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzhelmer's, Parkinson's or Huntington's CC diseases; Creutzield-Jakob discase; polsoning by heavy metals or drugs; CC disbetes; schizophrenia; discorders of growth hormone secretion; cancer; CC mounatoid arthritis, eplicpsy and many others, also to improve post-CC diseases; for idea to study the function of the polypeptide ecoding DNA or its mutein are used to carrying the ligand polypeptide ecoding DNA or its mutein are used to catudy the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC enthals. The present sequences for growth broads and primers; to identify contained to the polypeptide expressing genes. The ligand CC enthals. The present sequences for growth seasons and primers; to identify contained to the properties of probes and primers; to identify contained to the properties of probes and primers. The ligand contained to the properties of probes and primers to identify contained to the properties of probes and primers.
                              antisera; in drug development; ror yene cherry and animals. The present sequence represents a bowine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.
  Example 19; Page 151; 206pp; Engiish.
   New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and
  WP1; 1999-009423/01.
   28-APR-1997;
   27-APR-1998;
  05-NOV-1998
   W09849295-A1
  Creutzfeid-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rhoumatoid arthritis; epilepsy; vasopr
   tissue; screen; therapeutic; binding; senile dementia; iigand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
  GPR10;
  Pituitary-derived ligand polypoptide; G-protein coupled orphan receptor
   Bovine pituitary-derived ligand polypeptide fragment
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  14
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  UHR-1; modulator; pitu
  Hinuma
   for drug screening
  transgenic animal; bovine.
   97JP-0109974
   98WO-JP01923
   rhcumatoid arthritis; epilepsy; vasopressor
   itary; central nervous system;
  pancreas
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Query Match

97.78;

Score 43;

20;

Length 20

Sequence

20

ş

Sequence

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RESULT 1
AAW95175
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   밁
  Best Local Similarity
Matches 8; Conserv
  GRRIO (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; polsoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumacoid arthritis, epliepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutch are used to
  study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. Sequences AAW95174 to AAW95178 represent antigenic
   The invention relates to a murine pituitary-derived ilgand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector contain!
  GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopress;
  New polypeptide iigand for orphan G protein coupled receptors -
for treating disorders of central nervous system, pituitary and
pancreas, and for drug screening
   Snw
  Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
   AAW95175 standard; Protein; 20 AA.
  Disciosure; Page 26; 206pp; English.
  WPI; 1999-009423/01.
  Fukusumi S, Hinuma
   28-APR-1997;
  05-NOV-1998
  gene therapy; transgenic animal; epitope.
   Murine pituitary-derived ligand polypeptide antigenic epitope
  10-MAR-1999
   AAW95175
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1 GIRPYGREX 9
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| Sequence 8, Appl: | Sequence 7, Appl: | Sequence 97, Appl | Sequence 61, App. | Sequence 47, Appl | Sequence 5, Appl: | Sequence 4, Appl: | Sequence 43, App. | Sequence 37, App. | Sequence 31, App. | -    | Sequence 8, Appl: | Sequence 7, Appl: | •                | Sequence 42, App. | Sequence 36, App. | `<br>>           | Sequence 66, App. |

ALIGNMENTS

#### RESULT 1 US-08-776-971-93 Sequence 93, Application U Patent No. 6228984 GENERAL INFORMATION: APPLICANT: Hinuma, TELEPHONE: 617-523-3400 TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 93: APPLICATION NUMBER: US/08/776,971B FILING DATE: 06-Feb-1997 CLASSIFICATION: <UNKNOWN> PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996 APPLICATION NUMBER: JP 7/343371 FILING DATE: 28-DEC-1995 APPLICATION NUMBER: JP 8/2419 FILING DATE: 15-MAR-1996 APPLICATION NUMBER: JP 8/211805 FILING DATE: 12-RUG-1996 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 APPLICATION NUMBER: JP 8/246573 Habata, Tugo Kawamata, Yuji Hosoya, Masaki Pujii, Ryo Fukusuni, Shoji Kitada, Chieko TITLE OF INVENTION: POLYPROTEINS; TI ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette NAME: CON11n, DAVIG G. REGISTRATION NUMBER: 27,0: REFERENCE/DOCKET NUMBER: . TELECOMMUNICATION INFORMATION: SOFTWARE: FastSEQ fo CORRESPONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, SECUENCE CHARACTERISTICS: CITY: Boston STATE: MA COUNTRY: USA OPERATING SYSTEM: DOS COMPUTER: IBM compatible STREET: 130 Water Street Application US/08776971B Shuji for Windows Version ROBERTS & CUSHMAN, LLP THEIR PRODUCTION AND USE

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FRACMENT TYPE: Internal
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   NAME: CONIIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
  APPLICANT: Moriya, Takeo
APPLICANT: Taneka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
  APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: UP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
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APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
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STATE: MA
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                 CITY: Boston
   COUNTRY:
 COUNTRY:
   1 GIRPYGRF 8
  ADDRESSEE:
   02109
  amino acid
                 ¥
   Application US/09105678A
  130 Water Street
   USA
USA
  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLF
   METHOD OF PRODUCING A 19P2 LIGAND
   97.7%; Score 43; DB 3; Length 20; 100.0%; Pred. No. 0.017; Live 0; Mismatches 0; Indels
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   A 19P2 LIGAND
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Query Match
Best Local Similarity
Best Formula B; Conserve
   US-08-776-97I-8
Sequence 8. Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
   : MOLECULE TYPE: peptide us-09-105-678A-46
  REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105.678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
   SEQUENCE CHARACTERISTICS:
LENGTN: 20 amino acids
   APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY, TAGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
  ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776.971B
FILING DATE: 05-Feb-197
CLASSIFICATION: <Unknown>
  13 GIRPVGRF 20
   TOPOLOGY:
   STRANDEDNESS:
   MEDIUM TYPE:
   I GIRPVGRF 8
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
   Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
   CORRESPONDENCE ADDRESS:
  APPLICANT: Hinuma,
   READABLE FORM:
   amino acid
   COUNTRY:
   STATE: MA
   STREET: I30 Water Street CITY: Boston
   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  Congervative
   linear
   нарата, Yugo
Kawamata, Yuji
  Hosoya, Masaki
  Fukusum1.
   Floppy disk
  USA
  97.7%; 5--
100.0%; Prr
  Ryo
1 Shoji
   Shuji
   48466-342
  Score 43;
Pred. No.
  Mismatches
  Version #1.30
  DB 3;
0.017;
  ..
   2.0
  Length 20;
  Indels
   0;
   Gaps
   ..
   밁
  ŝ
   RESULT 6
US-08-776-97I-50
   US-08-776-971-8
  Sequence 50, Application Patent No. 6228984
GENERAL INFORMATION:
  Query Match
Best Local :
  Matches
   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 8:
   y Match 97.7%; Score 43; DB 4; Length 20;
Local Similarity I00.0%; Pred. No. 0.017;
hes 8; Conservative 0; Mismatches 0; Indels
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|13 GIRPVGRF 20
  I GIRPYGRF 8
   CLASSIFICATION CORRESPONDED APPLICATION OF STATE
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
   FUKUSUMI, Shoji
Kitada, Chieko
Kitada, Chieko
ROMENTION: POLYPROTEINS,
NUMBER OF SEQUENCES: 140
  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
  ATTORNEY/AGENT INFORMATION:
   PRIOR APPLICATION DATA:
  APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
  SEQUENCE DESCRIPTION: SEQ ID NO:
  FRAGMENT TYPE:
  SEQUENCE CHARACTERISTICS:
                     APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
   CITY: Boston
STATE: MA
   TYPE: amino acid
STRANDEDNESS: single
   COUNTRY: USA
   REGISTRATION NUMBER:
  NAME: Conlin, David G.
  APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
   APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
   STREET: I30 Water Street
   ToPoLOGY: linear
   LENGTH: 20 amino acids
  REFERENCE/DOCKET NUMBER:
FILING DATE:
   Application US/08776971B
   Fujii, Ryo
   Kawamata, Yuji
Hosoya, Masaki
  protein
  27,026
   8
   THEIR PRODUCTION AND USE
  0:
   Gaps
```

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```
8
  S
   ; SEQUENCE DESCRIPTION: SEQ ID NO: 50: US-08-776-971-50
   Sequence 64, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
   Query Match
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  TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 50:
   Local Similarity
nes 8; Conserv
  13 GIRPVGRF 20
  I GIRPVGRF 8
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
  ZIP: 02109
COMPUTER READABLE FORM:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  FURUSUMI, Shoji

Kitada, Chieko

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
   APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
   MOLECULE TYPE: protein FRAGMENT TYPE: internal
  SEQUENCE CHARACTERISTICS:
  TELECOMMUNICATION INFORMATION:
   ATTORNEY/AGENT INFORMATION
  ATTORNEY/AGENT
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 11-AUG-1996
APPLICATION NUMBER: JP 98/246573
APPLICATION NUMBER: JP 9/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 9/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 9/246573
FILING DATE: 18-SEP-1996
   COMPUTER: IBM compatible
QPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
  TYPE: amino acid
STRANDEDNESS: single
  NAME: Conlin, David C
REGISTRATION NUMBER:
  STATE: MA
  STREET: 130 Water Street
   FILING
   APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
  MEDIUM TYPE: Diskette
  COUNTRY: USA
   TOPOLOGY: linear
  LENGTH: 20 amino acids
   Conservative
  Boston
   Hosoya, Masaki
   , Ryo
-1 shoji
   97.7%; Score 43; DB 4; 100.0%; Pred. No. 0.017;
  0
   Mismatches
   0
   Length 20;
   Indels
   0
   Gaps
   0
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   ş
   US-08-776-971-98
   US-08-776-971-64
   Sequence 98, Applicati
Patent No. 6228984
GENERAL INFORMATION:
  Matches
  Best Local Similarity
Matches 8; Conserv
   Query Match
   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CMARACTERISTICS:
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNknown>
PRIOR APPLICATION NUMBER: PCT/JP96/03821
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY, AGENT INFORMATION:
   1 GIRPYGRF 8
|||||||
13 GIRPYGRF 20
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
   COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  FUKUSUM1, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
   APPLICANT: Hinuma, Shuji
  OPERATING SYSTEM: DOS
   STRANDEDNESS: single TOPOLOGY: linear
  TYPE: amino acid
  CITY: Boston
   STATE: MA
   STREET:
   REGISTRATION NUMBER: 27,026
   Application US/08776971B
  Conservative
   Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
  Fujii, Ryo
   130 Water Street
  97.78;
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  Score 43;
Pred. No.
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  DB 4;
. 0.017;
  0; Indels
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  Gaps
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
   Patent No.
  Sequence 34, Application US/09421208 Patent No. 625856I
   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
  TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 98:
  FILING DATE:
PRIOR APPLICATION UNMBER: US 09/105,678
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP I72118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
   NAME: CONIIN, David G
REGISTATION NUMBER: 27,026
REFERENCATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  APPLICANT: Suenaga, Masato
APPLICANT: MOTiya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
  SEQUENCE CHARACTERISTICS
   13 GIRPYGRF 20
   COUNTRY: U
   STRANDEDNESS:
TOPOLOGY: II
   CITY: Boston
  STREET:
  LENGTH:
   I GIRPVGRF 8
   SEQUENCE CHARACTERISTICS:
   GIRPVGRF 8
   EQUENCE DESCRIPTION: SEQ ID NO:
  INFORMATION:
   amino acid
  $
  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
  ENGTH: 20 amino acids
  20 amino acids
  130 Water Street
  USA
   617-523-6440
   Conservative
                                       Conservative
                                 97.7%; Score 43: DB 4: Length 20; 100.0%; Pred. No. 0.017; Live 0; Mismatches 0; Indels
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  DB 4; Length 20: 0.017;
   0; Indels
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   Gaps
                                     Gaps
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; STRANDEDNESS:
; TOPOLOGY: Iin
; MOLECULE TYPE:
US-09-42I-208-40
  RESULT 11
US-09-421-208-46
  밁
  RESULT IO
US-09-421-208-40
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  Sequence 46, Application US/09421208 Patent No. 6258561
   Patent No.
   Matches
   Query Match
Best Local :
   Sequence 40,
   FILING DATE:
PRIOR APPLICATION UNMER: DS 09/105,678
APPLICATION NUMBER: DS 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
              GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Morlya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Hishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
   GENERAL INFORMATION:
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-5400
TELEPAX: 617-523-6400
INFORMATION FOR SEQ ID NO: 40:
   APPLICANT: Suenaya, ....
APPLICANT: MOY1ya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODDCING A 19P2 LIGAND
TITLE OF SECUENCES: 52
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #I.0, Version #1.30
CURRENT APPLICATION DATA:
   SEQUENCE CHARACTERISTICS:
   NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
STREET: 130 Water Street
CORRESPONDENCE ADDRESS
  1 GIRPVGRE 8
|||||||
| 13 GIRPVGRE 20
   STATE: MA
COUNTRY: US
ZIP: 02109
  ||||||||
|13 GIRPVGRF
   Local Similarity 100 nes 8; Conservative
  NAME: Conlin, David G.
REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
   STREET: 130 |
CITY: Boston
  TYPE: amino acid
  APPLICATION NUMBER:
   LENGTH:
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   20 amino acids
  USA
   Iinear
  20
   20
   peptide
  97.7%; 50.
100.0%; Pred. No.
100.0%; Mismatches
  US/09/42I, 208
  27,026
   Score 43; DB 4;
Pred. No. 0.017;
   48466-342
   ROBERTS & CUSHMAN, LLP
   Length 20;
   Indels
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   Gaps
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밁
   Ś
  , MOLECULE TYPE: peptide US-09-421-208-46
   US-09-105-678A-28
   Sequence 28, Application US/09105678A Patent No. 6103882
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   Matches
  COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #I.0, Ve
CURRENT APPLICATION DATA:
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
APPLICATION NUMBER: JP 172118/1997
ETILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, DAVID G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
   APPLICANT: Suenag
   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #I.30
CURRENT APPLICATION DATA:
  APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                 FILING DATE: 26-JUN-
PRIOR APPLICATION DATA:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, HRONSTEIN, ROBERTS & CUSHMAN, LLP
  SEQUENCE CNARACTERISTICS
   Local Similarity
hes 8; Conserv
  CITY: Boston
   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
CITY: Boston
 APPLICATION NUMBER:
   APPLICATION NUMBER:
   STREET:
   13 GIRPVGRF 20
  STRANDEDNESS
TOPOLOGY: 1:
  TYPE: amino acid
   FILING DATE:
  APPLICATION NUMBER:
  COUNTRY: U:
ZIP: 02I09
  1 GIRPVGRF 8
   ¥
   I30 Water Street
   20 amino acids
   Suenaga, Masato
  617-523-6440
   Conservative
  linear
                                   26-JUN-1998
  97.7%;
   US/09/105,678A
JP 172118/1997
  US/09/421,208
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  Score 43;
Pred. No.
  Version #1.30
  OB 4;
0.017;
   Length 20
   Indels
   0
   Gaps
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RESULT 13
US-09-I05-678A-35
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APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:

APPLICATION UNUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNET/AGENT INFORMATION:
NAME: CON110, DAV10 6.
   Sequence 35, Application US/09105678A Patent No. 6103882
  Best Local Similarity Matches 0; Conserv
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   Patent No.
   GENERAL INFORMATION:
  TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CNARACTERISTICS:
   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  APPLICANT:
   OTHER INFORMATION: /product- "Ala or Thr" FEATURE:
   TELEPHONE: 617-523-3400
   FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
  FEATURE:
TELECOMMUNICATION INFORMATION
  NUMBER OF SEQUENCES:
   APPLICANT: Nishlmura, Osamu
   1 GIRPVGRF B
|||||||
| I3 GIRPVGRF 20
   FEATURE:
   MOLECULE TYPE: peptide
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
            REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
  CITY: Boston
STATE: MA
   NAME/KEY: modified-site
LOCATION: 21
OTNER INFORMATION: /product= "Gly-OH or Gly-Arg"
   STREET:
  COUNTRY:
  OTNER INFORMATION:
  NAME/KEY: Modified-site
   STRANDEDNESS:
  TYPE: amino acid
  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
  LOCATION:
  NAME/KEY: Mod1fied-site
  TOPOLOGY:
   TELEPHONE:
  LENGTH: 21 amino acids
   INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
   130 Water Street
   Morlya, Takec
Tanaka, Yoko
   617-523-6440
   USA
  Suenaga, Masato
  Conservative
   Iinear
  Takeo
  97.7%;
  /product-
  48466-342
  0
  Score 43; DB 3; Length 21; Pred. No. 0.017;
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  Mismatches
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  Version #1.30
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  0
  Gaps
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TELEPHONE:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version $1.30
CURRENT APPLICATION NUMBER: US/09/105,678A
FILING DATE: 25-JUN-1998
PRIOR APPLICATION NUMBER: JD 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G
                 ş
  밁
   9
   ; TOPOLOGY: iinear
; MOLECULE TYPE: peptide
US-09-I05-678A-35
   US-09-105-678A-41
  RESULT 14
US-09-I05-678A-41
  Query Match
Best Local Similarity 100
Matches 8; Conservative
  Ouery Match
Best Local Similarity
Matches 8; Conserv
  Sequence 41, Application US/09105678A Patent No. 6103882
  TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
  GENERAL INFORMATION:
  TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
   APPLICANT: Suenzga, Massito
APPLICANT: MOTiya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
   STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
  SEQUENCE CHARACTERISTICS:
  CORRESPONDENCE ADDRESS
  LENGIN: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
   TYPE: amino acid
  ZIP: 02109
   COUNTRY:
  CITY: Boston
   STREET:
  13 GIRPVGRF 20
  LENGTH:
   ADDRESSEE:
  1 GIRPVGRF 8
1 GIRPVGRF 8
  MA
  21 amino acids
  E: DIKE, BRONSTEIN,
130 Water Street
   USA
  97.7%; Score 43; DB ilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
  : 617-523-3400
617-523-6440
  97.7%; Score 43; DB 3; Length 21; 100.0%; Pred. No. 0.017; tive 0; Mismatches 0; Indels
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  4 I :
  48466-342
   ROBERTS & CUSHMAN, LLP
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   DB 3; Length 21;
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US-09-105-678A-47
  COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/105,678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN. DAVId G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELECOMMUNICATION: INFORMATION:

TELEPHONE: 617-523-3400

INFORMATION FOR SEG ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids

TYPE: milo acids
  밁
Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
  Ş
   US-09-I05-678A-47
  В
   Sequence 47,
Patent No. 6
   Query Match 97.7
Best Local Similarity 100
Matches 8; Conservative
  GENERAL INFORMATION:
  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
   APPLICANT: NIShimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
  CITY: Boston
STATE: MA
  |||||||||
13 GIRPVGRF 20
  TYPE: amino acid
   COUNTRY: USA
ZIP: 02109
  STREET:
  13 GIRPVGRF 20
   STRANDEDNESS:
  I GIRPVGRF 8
   ADDRESSEE:
  7, Application US/09105678A
6103882
  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
  peptide
   97.7%; Score 43; DB 3; Length 21; 100.0%; Pred. No. 0.017;
   0
   Mismatches
   Indels
   ç,
   Gaps
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Run
   Database
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Scoring table:
   OM protein -
  Max1mum
   Minimum
  Total number of hits satisfying chosen parsmeters:
   Sequence:
   Perfect score:
   DB
BG
  seq length:
seq length:
   protein search, using sw model
    ≗ ພ ∾ ∺
  PIR_71:*
   BLOSUM62
   US-09-446-543A-73_COPY_13_21
44
1 GIRPVGREX 9
  283138 seqs, 96089334 residues
  Gapop 10.0 , Gapext 0.5
  September 13,
plr1: *
pir2: *
pir3: *
pir4: *
   2000000000
  2002, 09:24:03
   ; Search time 172.41 Seconds (without alignments) 5.016 Million cell updates/sec
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

#### SUMMARIES

фD

| 226522221176544422                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Result<br>No.                  |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Score                          |
| 77777777777777777777777777777777777777                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | - 1 유격                         |
| 1056<br>353<br>353<br>353<br>366<br>367<br>409<br>309<br>1059<br>209<br>209<br>209<br>209<br>209<br>209<br>209<br>209<br>209<br>20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                |
| , , , , , , , , , , , , , , , , , , ,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 2                              |
| 870875<br>870821<br>145447<br>145447<br>882557<br>882557<br>C705057<br>C70365<br>C70365<br>C95926<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883<br>1400883 | ID<br>JC7607                   |
| probable oxidoredu hypothetical prote probable two-compo hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable saccharid hypothetical prote short-chain dehydr probable saccharid hypothetical prote conserved hypothet hypothetical prote transporter BMEII5 hypothetical prote transporter BMEII5 hypothetical prote probable isocitrat probable jocitrat probable jocitrat probable jocitrat probable jocitrat probable dihydrone hypothetical prote                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Description prolactin-releasin |

| 45                 | 44                 | 43                 | 42                 | 41                 | 40                 | 39                 | 38                 | 37                | 36     | 35                 | 34                 | u                 | 32                 | 31                 | 30                 |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31                | 31     | 31                 | 31                 | 31                | 31                 | 31                 | . 31               |
| 70.5               | 70.5               | 70.5               | 70.5               | 70.5               | 70.5               | 70.5               | 70.5               | 70.5              | 70.5   | 70.5               | 70.5               | 70.5              | 70.5               | 70.5               | 70.5               |
| 643                | 612                | 612                | 612                | 545                | 485                | 413                | 413                | 413               | 409    | 403                | 368                | 319               | 308                | 308                | 286                |
| -                  | N                  | _                  | _                  | N                  | N                  | Ŋ                  | N                  | Ŋ                 | Ŋ      | Ŋ                  | 2                  | N                 | N                  | 7                  | N                  |
| T07064             | T36210             | B39019             | A39019             | A67448             | E83663             | B86094             | D83310             | D72260            | E91246 | C82228             | 887402             | T36845            | AG1751             | AF1382             | A70667             |
| seed blotin-contai | conserved hypothet | glucose dchydrogen | glucose dehydrogen | conserved hypothet | glutamyi-tRNA synt | probable L-sorbose | conserved hypothet | sminotransferase, |        | probabie trypsin v | conserved hypothet | probable membrane | dipeptidsses homol | dipeptidases homol | hypothetical prote |

### ALIGNMENTS

A;Cross-references: DDBJ:AB040612; DDBJ:AB040613 C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pitultary. 밁 S A; Molecule type: DNA A; Residues: 1-83 < YAM> R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashlda, T.; Ishizuka, T.; Hosoya, Blochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Accession: JC7607 prolattin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001 C;Accession: JC7607 A; Introns: 33/1 A;Gene: PrRP C; Genetlcs: Query Match
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probable oxidoreductase (EC 1.5.99.-) - Mycobacterium tuberculosis (strain H37RV) C:Species: Mycobacterium tuberculosis C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000 C:Accession: G70875

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gor; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holro Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeiton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Reference number: A70500; MUID:98295987

A;Reference number: A70500; MUID:98295987

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Holroyd,

geno

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GLRPVGR

194

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  A; Note: MLCB373.27
C; Superfamily: env2 protein; sensor histidine kinase homology
  A; Molecule type: DNA
A; Residues: 1-519 <JAM>
A; Cross-references: EMBL: AL035500;
A; Experimental source: cosmid L373
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  A;Cross-references: GB:AL021999; GB:AL123456; NID:g3261538; PIDN:CAA17581.1; PID:g29169
A;Experimental source: strain H37Rv
   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-504 <CDL>
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  Ş
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  В
  A; Accession: B70821
  Query Match
Best Local
  Best
  Query Match
  Genetics:
  Query Match
Best Local :
  Matches
  Ma tches
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  188 GLRPVGR 194
  Local Similarity 85.
   Local Similarity
   1 GIRPVGR 7
   1 GIRPVGR 7
   1 GIRPVGR 7
   Rv0982
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85.7%;
  79.5%;
  81.8%;
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  2,
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                               9
  0
  0,
  Length 674;
   Length 519
  Length 504
   #status predicted
  dehydrogenase
                               0
  0
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   D.; Gordon,
.; Holroyd,
  0
                               0
  0
   genome
  ល
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  밁
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.B.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

J.D.; Junqueira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Maxino, C.L.; Marques, M.V.; Martins A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Dliveira, M.A.; de Oliveira, M.C.; Jelliveira, R.C.; Palmieri, Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Siiva Jr., W.A.; da Silva, M.A.; de Silva, M.A.; da Silva, M.A.; da Silva, M.A.; da Silva, M.A.; da Silva, M.A.; da Silva, M.A.; Vertoveki-Almeida, S.; Vettore, A.L.
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A;Note: for a complete list of authors see reference number A59328 below
  R; anonymous, The Xyle Nature 406, 151-157,
  C;Species: Xylella fastidiosa
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   C; Accession:
  hypothetical
  protein XF2445 [imported] - Xylella fastidiosa (strain 9a5c)
  Xylella fastidiosa
  Consortium of the Organization for Nucleotide
Ņ
Length 1056
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Matches
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Best Local :
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         1 GIRPVGR 7
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6; Conserv
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617

A;Accession: A65057
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75.0%;
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Pred. No.
   ٤,
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not

shown

1 GIRPVGRF Conservative 0 ñ Indels

Gaps

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C;Decies: Mycobacterium tuberculosis
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Rajandream, M.A.; Rogers, J: Rutter, S: Seeger, K.; Skelton, S:, Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squres, R: Sulston, J.E.: Taylor, K.; Whitehead, S.: Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500: MUID:98295987
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A;Accession: C70502
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   R; Deckert, G.; Warren, P.V.; Gaasterland,
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  Query Match
Best Local S
Matches 6
  Query Match
Best Local S
Matches 6
  Superfamily:
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  87
  25
   p11T
  1 GIRPVGRF
  1 GIRPVGRF 8
  Rv1692
  æ
  GVRGVGRF
   GLRPVRRF 114
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  75.0%:
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   000
  Streptomyces
  Score 33; DB
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l: Mismatches
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 Barrell,
   H
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  4 pg
  coelicolor
   NID: 93261839,
   Young. W.G.; Lenox, A.L.; Graham,
   PIDN:AAC06903.1; PID:g2983313; GB:AE0006
   2:
  2:
 B.G.:
  shown;
  :
  ::
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  Length 353
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  Indels
 Rajandresm,
  Indels
  translation
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   PIDN:CAB10949.1;
  Aguifex aeolicus.
  ö
  0:
  not shown
   not shown
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   Holroyd,
   D.E.;
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T40334
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A:Accession: E82221
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   밁
   ş
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  A: Molecule type: DNA
A: Residues: 1-511 <LYN>
   밁
  A:Status: prellminary
  A:Cross-references: EMBL:AL022244: PIDN:CAA18295.1; A:Experlmental source: strsin 972h-; cosmid c3B8
   A: Status: preliminary: translated from GB/EMBL/DDB:
  A:Status: prellminary: translated
  Query Match
Best Local Similarity
Matches 6; Conserv
   Query Match
Best Local :
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  248 RPVGRF
  Local Similarity 100.0%; hes 6; Conservative
   98
   3 RPVGRF 8
   10
   3 RPVGRF 8
  SCQEDB:SC9B10.24c
   RPVGRF
   253
  Conservative
   EMBL:AL009204;
ce: strain A3(2)
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   75
   .08:
  GB:AE003852; NID:g9655740; Ol; strain N16961; biotype
   Score 33;
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ored. No. 68;
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   GSPDB:GN00070; SCDEDB:SC9Bl0.24c
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  GSPDB:GN00067:
  Length 445
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El Tor
  Gwinn, M.L.; Dodson, R.
H.: Dragoi, I.; Sellers
  ..
  ..
  SPDB: SPBC3B8
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  Gaps
   GSPDB:GN
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  2
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DNA

topoisomerase

(ATP-hydrolyzing) chain

**≯** 

phage T4

DNA

topoisomeras

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A; Attens, preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-149 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75354.1; PID:g17132788; GSPDB:GN00179
A; Cross-references: GB:BA000019; PIDN:BAB75354.1; PID:g17132788; GSPDB:GN00179
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Best Local Similarity
"---hes 5; Conserv
  R:Martin, V.J.; Mohn, W.W.
J. Bacterlol. 181, 2675-2682, 1999
A;Title: A novel aromatic-ring-hydroxylating dioxygenase
A;Reference number: Z35281; MUID:99235742
A;Accession: T50932
  short-chain dehydrogenase/reductase DitI [imported] - Pseudomonas abietaniphila C:Species: Pseudomonas abietaniphila C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000 C:Accession: T50932
  Nakazaki, N.; Shimpo, S.; Suglmoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, ; DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH2262
   C;Accession: AH2262
C;Accession: AH2262
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguci R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguci R;Kaneko, T.; Shimpo, S.; Suglmoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Nakazaki, N.; Shimpo, S.; Suglmoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Nakazaki, N.; Shimpo, S.;
  먕
  A;Cross-references: EMBL:AF119621; PIDN:AAD21071.1
A;Experimental source: strain BKME-9; ATCC700689
   A; Molecule type: DNA
A; Residues: 1-285 < MAR>
  문
   C;Genetics:
A;Gene: alr3655
   A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
C;Accession: AH2262
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   Query Match
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Tatches 5; Conserve
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  A; Status: preliminary; translated from GB/EMBL/DDBJ
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    RESULT
   hypothetical protein air3655 [imported] - Anabaena sp.
  Query Match
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  Superfamily: rlbitol dehydrogenase; short-chaln alcohol dehydrogenase
   Genetics:
   |:||:||
734 GYRPMGR 740
  228 GLRPLGR 234
    14
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  Local Similarity
les 5; Conserv
  12
   1 GIRPVGR 7
  1 GIRPVGR 7
  6 LRPVGRY 12
   2 IRPYGRF 8
  Conservative
  Conservative
   Conservative
  72.78;
71.48;
   72.78;
  Score 32; DB
Pred. No. 31;
2; Mismatches
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  Score 32; DB
Pred. No. 60;
  Score 33; DB 2;
Pred. No. 1.2e+02;
  M1smatches
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   Length 149;
  Length 894;
   Length 285;
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A; Molecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-292 < KUR>
A; Cross-references: GB: AL591985; PIDN: CAC49079.1; PID: 915140564; GSPDB: GN00167
A; Cross-references: GB: AL591985; PIDN: CAC49079.1; PID: 915140564; GSPDB: GN00167
A; Experimental source: strain 1021, megaplasmid psymB
A; Experimental source: strain 1021, megaplasmid psymB
A; Calibert, F: Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barid
Pela, D.: Chain, P.: Cowle, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Atthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C., Atthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Weigh, C., A; Title: The composite genome of the legume symblont Sinorhizobium meliioti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
   probable saccharide deacetylase, slightly similar to NodB protein (EC 3.5.1.-) [Impor C; Species: Sinorhizoblum mellicti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C; Accession: G95926
R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing e A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Accession: G95926
A; Status; preliminary
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6; Conserv
   Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, Nature 393, 537-544, 1998
A;Authors: Sqares, F.; Sulston, J.E.; Taylor, K.; Whitehead, S. A;Title: Deciphering the biology of Mycobacterium tuberculosis A; Reference number: A70500; MUID:98295987
A;Accession: C70643
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C;Genetics:
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  A; Molecule type: DNA
A; Residues: 1-299 <COL>
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   A; Gene: SMb21100
  C; Genetics:
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  A; Contents: annotation
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Best Local Similarity
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  1 GIRPVG 6
  1 GIRPYGRF 8
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GTSPVGRF
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  72.7%;
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   Score 32; DB
Pred. No. 63;
  Mismatches
  Mismatches
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  #text_change 22-Oct-1999
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   Length 299
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  Komp, C.; Lelau
Wong, K.; Yeh,
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N.: Holroyd,
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completed: September 13,

2002,

09:24:03

Job time: 778 sec

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OM protein - protein search, using sw modei
  Run on:
September 13, 2002, 09:30:48 : Search time 80.21 Seconds (without alignments) 4.345 Million ceil updates/sec
  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Titie: Perfect score: Sequence: US-09-446-543A-73\_COPY\_13\_21 44 1 GIRPVGRFX 9

Scoring table:

Scarched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databasc : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| 3<br>3<br>2              | 31         | 30         | 29         | 28         | 27                 | 26         | 25         | 24         | 23         | 22                 | 21         | 20         | 19        | 16         | 17         | 16         | 15         | 14         | 13        | 12        | 11         | 10         | 9          | 80         | 7          | σ            | <sub>G</sub> | 4          | نيا        | 2          | _        | No.         | Result |    |
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| 30<br>30                 | 30         | 30         | 30         | 30         | 30                 | 30         | 30         | 30         | 30         | 30                 | 30         | 30         | 31        | 31         | 31         | 31         | 31         | 31         | 31        | 31        | 31         | 31         | 31         | 31         | 32         | 32           | ¥            | 34.        | 43         | 43         | 43       | Score       |        |    |
| 68.2<br>68.2             | 68.2       |            |            |            |                    | •          | •          | •          | •          | •                  | •          | •          | •         | 70.5       | •          | 70.5       | •          |            | •         | 70.5      | 70.5       | •          | 70.5       | 70.5       | 72.7       | 72.7         | 75.0         |            | 97.7       | 97.7       | 97.7     | •           | Query  | مو |
| 1164<br>4499             | 924        | 916        | 912        | 882        | 480                | 393        | 391        | 376        | 372        | 364                | 292        | 249        | 1565      | 1561       | 719        | 676        | 625        | 625        | 485       | 413       | 250        | 233        | 230        | 207        | 331        | 330          | 922          | 224        | 96         | 87         | 83       | Length I    |        |    |
|                          | _          | <b>–</b> 1 | ا د        | <b>-</b>   | ا د                | <b>-</b>   | ₽.         | ۳.         | _          | <u>_</u>           | <b>-</b>   | ۳          | Н         | ۳.         | ۳.         | _          | ۳          | _          | _         | ۳         | ۳          | _          | _          | ۳          | _          | μ            | _            | ۲          | _          | <u>_</u>   | щ        | ᇤ           |        |    |
| KELi_YEAST<br>DYHA_CHLRE | ICA5_HUMAN | GYRA_NEIGO | ICAS RABIT | KEL2 YEAST | GLG1 RHIME         | RPA2_THECE | THIL_ZOORA | MPK5_ARATH | MK11_HUMAN | MK11_MOUSE         | CNT8_HUMAN | Y361_SYNY3 | PAC_STRMU | SPAP_STRMU | NRP1_YEAST | EXL1_HUMAN | DHGL_DROPS | DHGL_DROME | SYE_BACHD | CSD_THEMA | LINC_PSEPA | PYRF_PASMU | PYRF_HAEIN | YDQ5_SCHPO | AR73_HUMAN | AR72_HUMAN   | GYRA_AERSA   | YGCI_ECOLI | PRRP_BOVIN | PRRP_HUMAN | PRRP_RAT | B           |        | 1  |
|                          | homo sapie |            | _          |            | P58393 Thizobium m |            |            | arab       | homo       | Q9wuil mus musculu |            |            |           |            | _          |            |            |            |           | _         | -          |            |            |            |            | 8 homo sapie | Ψ            | æ          | -          | 7 homo sa  | ttus no  | Description |        |    |

| 45          | 4           | 43          | 42          | 41          | 40          | 39          | 38         | 37          | 36          | ω<br>G     | 34          |  |
|-------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|-------------|------------|-------------|--|
| 29          | 29          | 29          | 29          | 29          | 29          | 29          | 29         | 29          | 29          | 29         | 29          |  |
| 65.9        | 65.9        | 65.9        | 65.9        | 65.9        | 65.9        | 65.9        | 65.9       | 65.9        | 65.9        | 65.9       | 65.9        |  |
| 334         | 328         | 306         | 292         | 292         | 289         | 268         | 235        | 229         | 149         | 130        | 106         |  |
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| YI11_HALN1  | RS1A_SYNY3  | RS1_SYNP6   | CITG_ECOLI  | CITG_ECO57  | THTR_CHICK  | TIPA_ARATH  | PYRF_BARBA | TDX1_BRUMA  | ENRN_BPT7   | RL3_PIG    | BOLA_VIBCH  |  |
| P23464      | P73530      | P46228      |             |             | _           | -           | 044843     | ••          |             | 029293     | Q9kps0      |  |
| halobacteri | synechocyst | synechococc | escherichia | escherichia | gallus gall | arabidopsis | bartonelia | brugia mala | bacteriopha | sus scrofa | vibrio chol |  |
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ALIGNMENTS

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  Query Match
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  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP31).
   SIGHAL
   EMBL; AB015419; BAA29027.1;
MIM; 602663; -.
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   Hinuma S., Habata Y., Fujii R., Kawamata Y., Nosoya M., Fu
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Hature 393:272-276(1998).
   Regul. Pept. 83:1-10(1999).
  TISSUE-Brain;
MEDLIHE-98268781;
  Hormone;
   -1- FUNCTION: Stimulates prolactin (PRL) release and regulates the
expression of prolactin through its receptor GPR10. May stimulate
iactotrophs directly to secrete PRL.
iactotrophs directly: MEDULLA OBLONGATA AND NYPOTHALAMUS.
  Sumino Y., Fujino M.;
  Fujii R., Fukusumi S., Ho
Sekiguchi M., Kitada C.,
   TISSUE SPECIFICITY.
   SEQUENCE FROM N.A.
  Eukaryota; Metazoa;
Mammalia; Eutheria;
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  SEQUENCE
  "Tissue distribution of projectin-releasing
  PubMed-10498338;
   NCBI_TaxID-9606;
   Homo sapiens (Human)
   PRRP_NUMAH
P81277;
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   GIRPVGRF 52
  GIRPVGRF
  Similarity 100.0%;
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  Conservative
  53421
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  STANDARD;
   PubMed-9607765;
Y., Fujii R., K
  9639
   Signal.
22
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   Chordata;
Primates;
   97.78
   Hosoya M.,
., Kurokawa
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  0
   Score 43; DB 1;
Pred. No. 0.023;
0; Mismatches
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Pred. No.
   BY SIMILARITY.

PROLACTIH-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
  Craniata; Vertebrata; l
Catarrhini; Hominidae;
  Mismatches
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  DB 1;
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  Habata Y.,
  Length 87
  Length 83;
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01-MAR-2002 (Rei. 4
  YGCI_ECOLI
Q45898;
16-OCT-2001
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SIGNAL
PEPTIDE
PEPTIDE
  MEDIINE-98266781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fuk Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda N., Fujino M.;
"A prolactin-releasing peptide in the brain.";
"A prolactin-releasing peptide in the brain.";
Hature 393:272-276(1998).
-I-FUHCTION: Stimulates prolactin (PRL) release and regula expression of prolactin through its receptor GPRIO. May lactotrophs directly to secrete PRL.
-I-TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
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SEQUENCE FROM
STRAIN-K12 / M
  Hypotheticai protein ygcI
YGCI OR B2757.
Escherichia coll.
Bacteria; Proteobacteria;
  16-OCT-2001
16-OCT-2001
   EMBL; AB015417; BAA29025.1;
   Eukaryota; Metazoa;
Mammaiia; Eutheria;
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01-MAR-2002 (Rei. 41, Last annotation update)
Prolactin-releasing peptide precursor (PPRP) (Pr
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   46
   1 GIRPVGRF
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   Similarity
8; Conser
  Amidation;
  Bovinae;
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  AND
   Chordata; Craniata; Vertebrata; Eute
Cetartiodactyla; Ruminantia; Pecora;
  ygcI precursor
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  PROLACTIN-RELEASING PEPTIDE PI
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   (PRL) release and regulates hits receptor GPRLO. May sti
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01-FEB-1996
01-NOV-1997
  GYRA_AERSA
P48369;
  κοοGene; EG13116; ygc1,
Nypothetical protein; Signal;
SignaL
  MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Coliado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick N.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
*The complete genome sequence of Escherichia coli K-12.*; Science 277:1453-1474(1997).
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  Oppegaard H., Sorum H.;

"gyrA mutations in quinolone-resistant isolates of the fish pathogen

"gyrA mutations in quinolone-resistant isolates of the fish pathogen

Aeromonas salmonicida.";

Antimicrob. Agents Chemother. 38:2460-2464(1994).

-1- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-

STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES INE

INTERCONVERSION OF OTHER TOPOLOGICAL ISOBERS OF DOUBLE-STRANDED
   SEQUENCE FROM N.A. STRAIN-2148/89;
   SEQUENCE
   SEQUENCE OF 33-179 FROM STRAIN-ATCC 14174;
   Oppegaard
   Bacteria;
  Aeromonas
  EMBL; U29579; AAA69267.1; ALT_INIT.
  NCBI_TaxID=645;
  %EDLINE=95142596; PubMed=7840589;
   23
   DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS. CATALYTIC ACTIVITY: ATP-dependent breakage, passes of double-stranded DNA.
SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS REBREAKAGE AND REJOINING: THE B CHAIN CATALYZES ATP ENZYME FORMS AN A2B2 TETRAMER.
  gyrase
  GIRPVGRF
   GTRPTGRF
  AE000359; AAC75799.1; ALT_INIT.
   Similarity
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  salmonicida.
Proteobacteria;
   (OCT-1995)
  subunit
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  224 AA;
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   043488; 075749;
15-JUL-1999 (Rel. 38, Created)
15-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aflatoxin BI aldehyde reductase 1 (EC 1.-.-.)
(Aldoketoreductase 7).
AKR7A2 OR AFAR OR AKR7.
  modified
  Prami C., Savelyeva L., Perri P., Schwab M.; "Cioning of the human aflatoxin Bl-aldehyde reductase gene 1p36.1 in a region frequently altered in human tumor cells. Cancer Res. 58:5014-5018(1998).
  "Molecular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductate perfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin BI-aldehyde reductase.";

Blochem. J. 332:21-34(1998).
   EMBL; 147978; AAB41037.1; -.
EMBL; L42453; AAA877239.1; -.
HSSP; P09097; 1AB4.
InterPro; 1PR002205; DNA_topoisoIV.
Pfam; PF00521; DNA_topoisoIV; 1.
SMART; SM00434; TOP4C; 1.
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  Isomerase; Topoisomerase; DNA-binding.
ACT_SITE 122 122 DNA CLEAVAGE (BY SIMILARITY).
SEQUENCE 922 AA; 101333 MW; 8894965DC4217077 CRC64;
  MEDLINE-99040634; PubMed-9823300;
   SEQUENCE FROM N.A.
T1SSUE=Liver;
  Eukaryota; Metazoa;
Mammalia; Eutheria;
   HUMAN
   SEQUENCE
   SEQUENCE FROM N.A.
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   MEDLINE-98244807; PubMed-9576847;
   NCBI_TaxID=9606;
  Homo sapiens (Numan).
  AR72_HUMAN
   759 GVRPMGR
   Local Similarity
   1 GIRPVGR
  SUBCELLULAR LOCATION: OSIMILARITY: BELONGS TO
   non-profit institutions as iong d and this statement is not removed s requires a license agreement (See an email to license@isb-sib.ch).
  L.S., Harrison D.J., Neal
  FROM N.A.
   Conservative
   765
  STANDARD;
  Chordata;
Primates;
  49
  Cytoplasmic.
O THE ALDO/KETO REDUCTASE
   <u>ب</u>
   Score
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   Craniata; Vertebrata; Euteieostomi; Catarrhini; Nominidae; Homo.
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   Migmatches
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  Hayes J.D.;
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InterPro;
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   EMBL;
EMBL;
   Knight L.P., Primiano T., "cDNA cioning, expression B1-metabolizing member of AKR7A3.",
   Oxidoreductase.
ACT_SITE 113
  EMBL; AF040639; AAD02195.1; -.
EMBL; AL033413; CAB72322.1; -.
InterPro; IPR001395; Aldo_ket_red.
Pfam; PF00248; Aldo_ket_red; 1.
  entities requires a license agreement (S or send an email to license@isb-sib.ch).
   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-I. FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINGENIC EFFECTS OF AFLATOXIN B1.

-I. SUBCELLULAR LOCATION: Cytoplasmic.
-I. SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
  Oxidoreductase.
ACT_SITE 112
CONFLICT 113
   TISSUE-Liver;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
   PRINTS;
   Carcinogenesis 20:1215-1223(1999)
   MEDLINE-99315412; PubMed-10383892;
  Homo sapiens (Human).
   AKR7A3.
   SEQUENCE
   Pfam;
   SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
  SEQUENCE FROM N.A., AND CHARACTERIZATION
  1 GIRPVGRF 8
  603418;
   Pro; IPR001395; Aldo_ket_red
PF00248; aldo_ket_red; 1.
   AF026947; AAC52104.1; -.
Y16675; CAA76347.1; -.
AL035413; CAB72321.1; -.
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   d and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
   PR00069; ALDKETRDTASE
   330 AA;
   Conservative
  STANDARO;
  112
113
   36618 MW;
  72.78;
75.08;
  Last sequence update)
Last annotation update)
reductase 2 (EC l.-.-.-)
  Created)
  f., Groopman J.O., Kensler T.W., Sutter T.R.;
ion and activity of a second human aflatoxin
of the aldo-keto reductase superfamily,
  A -> T (IN REF. 1).
  Score 32; DB
Pred. No. 20;
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   3BBFB7ED0CAF4D54 CRC64;
   Mismatches
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AC 943812:
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DT 01-NOV-1995 (Rel. 32, Las.
DT 01-MAR-2002 (Rel. 41, Las.
DE Orotidine 5'-phosphate de.
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OS Haemophilus influenzae.
OC Haemophilus.
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  YDQ5_SC
014198;
   EMBL: Z98056; CAB10853.2;
Hypothetical protein.
SEQUENCE 207 AA; 24027
  Skelton J., Churcher C.M., Wood V., Barrell B.G., Rajandream Submitted (OCT-1999) to the EMBL/GenBank/DD8J databases.
  STRAIN-972;
  Schizosaccharomyces.
   Schizosaccharomyces pombe (Fission
   SCHPO
  SEQUENCE FROM N.A.
   NCBI_TaxID-4896;
   Eukaryota; Fungi; Ascomycota;
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  Lyase; De
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Q9CMM1;
   InterPro; IPRO01754; OMPdecase. Pfam; PF00215: OMPdecase; 1. PROSITE; PS00156; OMPDECASE; 1.
  EMBL; U32802; AAC22877.1; -. TIGR; HI1224; -.
  MEDLINE-95350630; PubMed-7542800; Fielschmann R.D., Adams M.D., White
   MEDLINE-21145866;
  SEDUENCE
  Bacteria; Proteobacteria;
   Pasteurclla
  PYRF DR PM0797
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  Science 269:496-512(1995).
  "Whole-genome random sequencing and
lnfluenzae Rd.";
   NCBI_TaxID-727;
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Matches 5
  LINC_PSEPA STAND....

LINC_PSEPA STAND....

p50197;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation dehydrogenase
   Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;

"Cloning and sequencing of a 2,5-dichioro-2,5-cyclohexadlene-1,4-dioi
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohexane in Pseudomonas paucimobilis.";

J. Bacteriol. 176:3117-3125(1994).

-I- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
(2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCH)

-I- PATHWAY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.
Aromatic
NP_BIND
  use by non-profit institutions as iong a modified and this statement is not removed. entitles requires a license agreement (See ) or send an email to license@isb-sib.ch).
  Lyase; Decarboxylase; Pyrimidlne biosynthesis; Complete proteome. ACT_SITE 61 61 PROTON DONOR (BY SIMILARITY). SEQUENCE 233 AA; 25501 MW; 6CD84E5931A60628 CRC64;
  the
   This
   PROSITE; PS00156; OMPDECASE; 1.
  EMBL; AE006118; AAK02881.1; -.
InterPro; IPR001754; OMPdecase.
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  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                         Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
  EMBL; D14595; BAA03444.1;
HSSP; P19992; 1HOC.
  This
   SEQUENCE FROM N.A.
  Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria; Proteobacteria; alpha subdlvision; Sphingom
   InterPro; IPROL
Pfam; PF00215;
  between
  MEDLINE-94252977; PubMed-7515041;
  InterPro;
  NCBI_TaxID-13689;
  178 GIRPIG
   1 GIRPVG
  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Bioinformatics Institute. There are no restr
   European Bioinformatics Institute.
  SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
  SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
   (SDR)
   SWISS-PROT entry is copyright. It is produced through a collaboration -
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   the Swiss Institute of Biolnformatics
   IPR002198; ADH_short.
   FAMILY.
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  Conservative
  OMPdecase;
  70
83
 catabollsm;
   : Score 31; DB
: Pred. No. 23;
1; Mismatches
   YB)
               Oxidoreductase;
  (See http://www.isb-sib
   (See http://www.lsb-slb.ch/announce/
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  Matches
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SEQUENCE
  Probable cysteine desulfurase (EC 4.4.1.-). CSD OR TM1371.
  InterPro; IPR000192; AmInotransf_class_V.
Pfam; PF00266; aminotran_5; 1.
PROSITE: PS00595; AA_TRANSFER_CLASS_5; FALSE_NEG.
  EMBL; AE001791; AAD
HSSP; P77444; LCON.
TIGR; TM1371; -.
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  Nelson K.E., Clayton R.A., Gill S.R., Gwlnn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linber K.D., Garrett M.H., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from the state of the
  SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
  16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
   or send an email to license@lsb-slb.ch).
  entities requires a license agreement (See http://www.lsb-slb.ch/announce/
  Thermotoga maritima.
Bacteria; Thermotogales;
  Q9X191;
  CSD_THEMA
142 IRPSGRF 148
  209 IHPIGRE 215
   2 IRPVGRF 8
                                       2 IRPVGRF 8
   Pyrldoxal phosphate; Complete proteome.

G 223 223 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

CE 413 AA; 46748 MW; 092866323FF984F0 CRC64;
   1 Similarity
6; Conserv
   154
250
  (Rel. 40, Grenceu, (Rel. 40, Last sequence update) (Rel. 40, Last annotation updat (Rel. 40, Last annotation "FC 4.4.1.").
  Conservative
  Conservative
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  STANDARD;
   AAD36460.1; -.
   154 E
25644 MW;
   70.5%;
   70.5%;
71.4%;
  Thermotoga.
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   Score 31; DB
Pred. No. 42;
   Score 31; DB
Pred. No. 25;
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   / SIMILARITY.
FFC1CAEB47DF789D CRC64;
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  Mismatches
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  Length 413;
   Length 250
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RESULT 13
   OCCUPATION 
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   Query Match
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   Matches
   SYE_BACHD STANDAKU;

SYE_BACHD STANDAKU;

O9KGF6;

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)
   DHGL_DROME STANDARD; PRT; 625 AA. P18173; G9V187; 01-NOV-1990 (Rel. 16, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) Glucose dehydrogenase [acceptor] precursor (EC Glucose dehydrogenase [acceptor] short protein] GLD OR CG1152.
  DROME
   BINDING
SEQUENCE
  SITE
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  Drosophlia
Eukaryota;
  EMBL; AP001507; BAB03828.1; ...
InterPro; IPR000924; tRNA-synt_1c.
InterPro; IPR001412; tRNA-synt_1.
Pfam; PF00749; tRNA-synt_1c; 1.
  halodurans and genomic sequence comparison with Bacillus sul
Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: ATP + L-9litamate + tRNA(Glu) - AMP
  MEDLINE-20512582; PubMed-11058132; Takami H., Nakasone K., Takaki Y., Maeno Fuji F., Hirama C., Nakamura Y., Ogasawar Horikoshi K.;
  PRINTS; PR00987; TRNASYNTHGLU.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
   *Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtili-
  Bac111us/Staphylococcus
NCBI_TaxID-86665;
  GLTX OR BH0109.
   Complete
   SEQUENCE FROM N.A.
   Bacilius halodurans.
  Amlnoacyl-tRNA synthetase;
   Bacterla; Flrmicutes;
  150 GIKPVVRF 157
   1 GIRPVGRF 8
  dlphosphate + L-glutamyl-tRNĀ(Glu).
dlphosphate + L-glutamyl-tRNĀ(Glu).
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmlc.
SINILARITY: BELONGS TO GLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
  Similarity
6; Conserv
   proteome.
melanogaster (Frult fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
   Conservative
  ξ.
   JCM 9153;
   256
255
A
54785 MW;
  21
   70.5%;
75.0%;
  Bacillus/Clostrldlum us group; Bacillus.
   Score 31; DB; Pred. No. 49; 1; Mlsmatches
   Protein blosynthesis; Ligase;
  "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
W; 7D34A862918F57B6 C
   ., Maeno G., Sa
Ogasawara N.,
   1.
  Sasaki R., Masul
., Kuhara S.,
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  Length 485
  CRC64;
   Indels
   99.10) [Contains:
   ATP-blndlng;
   subtllls.";
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RA Adams M.D. (Caniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. (Caniker S.E., Holt R.A., Shburner M., Henderson S.N., RA Amanatides P.G., Scherer S.E., H. P.M., Hoskins R.A., Galle R.F., RA Galler R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandeli M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandeli M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandeli M.D., Zhang Q., Change M., Pfeiffer B.D., RA George R.A., Levis R.G., Helt G., Nelson C.R., Miltos G.L.G., RA Abril J.F., Agbaynal A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boltshakov S., Ra Ballew R.M., Bouck J., Broksteln P., Brottler P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Burtis K.C., Busam D.A., Butler N., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dukov B.C., Dunn P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., J. Dutkov B.C., Dunn P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., J. Dutkov B.C., Dunn P., RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Anderson D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Anderson D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Anderson D., Louston K.A., Howland T.J., Hernandez J.R., Nelson D.L., Ratfit C., Kraft C., Krantis J., Moshrefi A., Noult S.M., Naltei B., McIntosh T.C., McLeod M.P., Moshrefi A., Nelson D.R., Nelson D.R., Nelson D.L., Naft C., Kraft C., Kraft C., Krantis J., Moshrefi A., Nunth S.M., Naltei B., McIntosh T.C., McLeod M.P., Many D.M., Nelson D.L., Ratfit D., Kraft C., Krantis J., Moshrefi A., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Rang D.C., Scheeler F., Spradling A.C., Stapleton M., Strong R., Sun E., Rang C., Zhao Q., Zheng L., Wang S., Yao Q.A., Yeng S.M., Woodage T., Worley K.C., Wu. Shao Q., Zheng L., Then S., Zhu S., Zhu S., 
   Whetten R., Organ E., Krasney P., Cox-Fo
"Molecular structure and transformation
gene in Drosophila melanogaster.";
Genetics 120:475-484(1988).
                      "Incorporation of selenocysteine at a UGA codon of Gld.";
(In) Annu. Dros. Res. Conf. 39:414C(1998).
-I- FUNCTION: ESSENTIAL FOR CUTICULAR NODIFICATION DURING DEVELOPMENT
  Cavener D.R., Krasney P.
  SIMILARITY TO YEAST ALCOHOL MEDLINE-91163320; PubMed-200
  SEQUENCE OF 1-96 FROM N.A. MEDLINE-89065357; PubMed-3
   MEDLINE-90205602; PubMed-2108306;
Krasncy P.A., Carr C.M., Cavener D.R.;
"Evolution of the glucose dehydrogenase
   SEQUENCE FROM N.A.
   "Drosophila glucose dehydrogenase and yeast alcohol homologous and share N-terminal homology with other Mol. Biol. Evol. 8:144-150(1991).
   MEDLINE-20196006;
  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
  Perlaky S.,
   SELENOCYSTEINE
FUNCTION: ESSENTIAL CATALYTIC ACTIVITY:
  Evol. 7:155-177(1990).
  65357; PubMed=3143620;
Organ E., Krasney P.,
  Merritt
  PubMed=2002763;
   PubNed=10731132;
  ~
   D-glucose +
  Cavener D.;
  Cox-Foster D., Cavener D.R.; mation of the glucose dehydrogenase
acceptor
  gene
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  'n
D-glucono-1,5-lactone
   Drosophila.";
  oxidase are
flavoenzymes.";
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RESULT 15
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   Query Match
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   Matches
   EMBL; AE003672; AAF54038.1; AIT_SEQ.
EMBL; X13582; CAA31918.1; -
PIR; A39019; A39019
PIR; S06628; S06628
FlyBase; FB90000112; Gld.
InterPro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
  Eukaryota; Metazo
Pterygota; Neopte
Ephydroidea; Dros
NCBI_TaxID=7237;
   DHGL_DROPS
P18172;
01-NOV-1990
   NP_BIND
ACT_SITE
SE_CYS
CONFLICT
SEQUENCE
           (In) Annu
   01-NOV-1990 (Rel. 16, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Glucose dehydrogenase [acceptor] precursor (E)
Glucose dehydrogenase [acceptor] short protei
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  entities requires a license agreement (S or send an email to license@lsb-sib.ch).
  Krasney P.A., Carr C.M., Cavener D.R.; "Evolution of the glucose dehydrogenase Moi. Bioi. Evol. 7:155-177(1990).
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                                 Perlaky S., Merritt
Incorporation of se
  SELENOCYSTEINE
   SEQUENCE FRON N.A. MEDLINE-90205602; PubMed-2108306;
  Drosophila
  SIGNAL
  PRQSITE;
   PROSITE;
   207
          corporation of selenocysteine at a UGA Annu. Dros. Res. Conf. 39:414C(1998) CATALYTIC ACTIVITY: D-glucose + accep
  SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES CAUTION: REF.5 BELIEVES RESIDUE 613 IS A SELEN
   TRANSFERRED SIMILARITY:
  COFACTOR: FAD.
SUBCELLULAR LC
   GLLPVGKF
   GIRPVGRF 8
   M29298; AAA28571.1; ALT_SEQ
  5; Conserv
   PS00623; GMC_OXRED_1; 1.
PS00624; GMC_OXRED_2; 1.
uctase; Flavoprotein; FAD;
  Neoptera; Endopta; Drosophilidae;
  Metazoa; Arthropoda,
  pseudoobscura (Fruit fly)
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  STANDARD;
  TO FEMALES.
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  LOCATION:
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   Endopterygota;
   [acceptor] precursor (EC 1.1.99.10) (Contains: [acceptor] short protein].
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  -> R (IN REF. 1).
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   Tracheata; Hexapoda:
  Signal; Selenium;
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   Diptera;
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           D-glucono-1,5-lactone
   Drosophila.";
  SEMINAL FLUID
   FAMILY
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   [ACCEPTOR]
  Selenocysteine.
   Insecta:
   Muscomorpha;
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   collaboration
  outstation
   Gaps
  commercial
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Search completed: September 13,
Job time: 1139 sec
  -!- COFACTOR: FAD.
-!- SUBCELLULAR LOCATION: SECRETED AS PART OF THE SEMINAL FLUID TRANSFERRED TO FEMALES.
-!- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
-!- CAUTION: REF. 2 BELIEVES RESIDUE 613 IS A SELENOCYSTEINE.
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   1 GIRPVGRF 8
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|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------|-----------|--------|----------|--------------------|--------|--------------------|--------|--------------------|--------|--------|------------|--------------------|--------------------|--------------------|-----------|--------|-------------------------|--------------------|
| ŭ                  | 1                  | 4      | 31                 | 1      | 31                 | 31                 | 31     | 31     | 31     | 1      | 3<br>2    | 32     | LJ<br>SJ | ب<br>ده            | L)     | ب<br>2             | 3<br>2 | ب<br>2             | 32     | 3<br>2 | 3<br>2     | 32                 | 32                 | 32                 | <u></u> 2 | ب<br>د | 32                      | 32                 |
| 70.5               | 70.5               | 70.5   | 70.5               | 70.5   | 70.5               | 70.5               | 70.5   | 70.5   | 70.5   | 70.5   | 72.7      | 72.7   | 72.7     | 72.7               | 72.7   | 72.7               | 72.7   | 72.7               | 72.7   | 72.7   | 72.7       | 72.7               | 72.7               | 72.7               | 72.7      | 72.7   | 72.7                    | 72.7               |
| 352                | 319                | 308    | 286                | 258    | 233                | 172                | 163    | 148    | 129    | 125    | 1059      | 1057   | 869      | 704                | 492    | 439                | 439    | 435                | 409    | 374    | 366        | 356                | n<br>n             | 315                | 309       | 299    | 292                     | 285                |
| N                  | N                  | 16     | 16                 | N      | 16                 | w                  | N      | 12     | 16     | 16     | IJ        | 13     | 16       | 10                 | 16     | 10                 | 10     | 17                 | 2      | 16     | 11         | 16                 | N                  | H                  | N         | 16     | 16                      | 2                  |
| Q9EW95             | 088067             | Q928H6 | P95150             | 005664 | Q9CMM1             | Q96VF9             | Q45285 | Q9DWG5 | Q9KUJ6 | Q9A6F2 | 019370    | P79999 | Q98BZ1   | Q9FF49             | 010884 | Q940M3             | Q9FKJ4 | CHEALED            | Q9KK77 | 053319 | Q9p157     | Q986C9             | Q9RJI0             | Q9DCM1             | 086546    | P95060 | Q92VM1                  | 09X4W7             |
| Q9ew95 atreptomyce | 088067 atreptomyce | Φ      | P95150 mycobacteri | -      | Q9cmml paateurella | Q96vf9 schizosacch | baci   |        |        |        | caenorhab | •      |          | Q9ff49 arabidopsis |        | Q940m3 arabidopsia |        | Q9ye81 aeropyrum p | м      |        | mus muscul | Q986c9 rhizobium 1 | Q9rjiO streptomyce | Q9dcm1 mus muaculu | CO .      |        | $\overline{\mathbf{L}}$ | Q9x4w7 pseudomonas |

## ALIGNMENTS

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Q9W624;
Q9W624;
01-NOV-1999
01-NOV-1999
   SEQUENCE FROM N.A.

STRAIN-CCM3239;

KOrmanec J., Biattakova J., Novakova R., Homerova D., Rezuchova Cloning and characterization of a new polyketide gene cluster streptomyces aureofaciens CCM3239.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databascs.

EMBL; AV033994; AAK61719.1;

SEQUENCE 420 AA; 43011 MW; 3C27E22BE88CZDEA CRC64;
   093LZ7 PRELIMINARY; PRT; 420 AA. 093LZ7; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) CHAIN LENGTN FACTOR-LIKE PROTEIN.
  Streptomyces aureofaciens.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
  NCBI_TaxID=1894;
  48 GIRPVGRF
  1 GIRPVGRF 8
  l Similarity
8; Conserv
  97.7%; So ilarity 100.0%; I Conservative 0;
(TrEMBLrel. 12, (TrEMBLrel. 12,
   PRELIMINARY;
  55
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D50431;
  STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDINE-20570466; PubMed-11121031;

Kawashima T., Amano N., Kolke H., Nakino S.-I., Higuchi S.,

Kawashima-Ohya Y., Watenabe K., Yamazaki M., Kanehori K., Kan

Nunoshiba T., Yamamoto Y., Aramaki N., Nakino K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by genor

sequence of Thermoplasma voicanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

EMBL; AP00995; DAD6023.1;

InterPro; IPR002881; DUF58.

InterPro; IPR002035; VNFA.
  Satake H., Minakata H., Fujimoto M.;

"Carassius Reamide (C-RF amide).";

Submitted (NOY-1998) to the EMBL/GenBank/DDBJ databases

EMBL; AB020024; BAA76652.1;

SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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01-DEC-2001 (TrEMBLre1.
   Carasslus auratus (Goldfish).
Eukaryota; Mecazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
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     01-JUN-1998
01-JUN-1998
  Thermoplasma volcanlum.
Archaea: Euryarchaeota;
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C-RF AMIDE.
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  NCBI_TaxID-7957;
  NCBI_TaxID-50339;
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304 GIRPAGKF 311
  В
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  GVRPIGRF 75
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   Similarity 75.
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   49092
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sequence update)
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Euteleostei; Ostariophysi;
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RX MEDLINE-98295987; PubNed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Narris D.
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Narris D.
RA Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Tekala F.,
RA Gordon S.V., Basham D., Brown D., Chillingworth T., Connor R.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Namilin N., Nolroyd S.,
RA Davies R., Devlin K., Krogh A., McLean J., Moule S., Murphy L.,
RA Nornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
ROIlver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Nornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Decliphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
RI Complete genome sequence.";
RI Nature 393:537-544(1998).

CC -1- SIMILARITY: TO PROKARYOTE SENSDRY TRANSDUCTION PROTEINS.
  D53895
D53895;
O1-JUN-1998
O1-JUN-1998
O1-DEC-2001
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COLE S.T., Brosch R., Parkhill J., Garnler T., Churcher C., Narris
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
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Dliver S., Daborne J., Quall M.A., Rajandream N.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
"Deciphering the blology of Nycobacterlum tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
   NYU964 vm martine tuberculosis.
Nycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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  EMBL; ALO10186; CAA15852.1; -.
Tuberculist; Rv1175c; -.
InterPro; IPR001064; Crysttallin.
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InterPro; IPR001327; NAD_binding.
InterPro; IPR00125; Dx1dored_FMN.
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PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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  <u>,,</u>
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01-MAX-1999 (TREMBLIFEL 11, Las
01-DEC-2001 (TREMBLIFEL 19, Las
PUTATIVE TWO-COMPOHEMT SYSTEM S)
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Cole S.T., Elglmeler K., Parkhill J., James K.D., Thomson H.R.,
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Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
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Squares S., Stevens K., Tayior K., Whitehead S., Woodward J.R.,
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Bacteria; Firmicutos; Actinobacteria; Actinobacteridae;
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Harris D., Taylor K.
Submitted (FEB-1999)
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Barrell B.G.;
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  InterPro;
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); IPRO04359; HIS_KIH_919.
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   RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Ra Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Ra Barros M.H., Bonaccorai E.D., Bordin S., Bove J.M., Briones M.R.S.,
Ra Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Ra Colauto H.B., Colombo C., Coata F.F., Costa M.C.R., Coate-Meto C.M.,
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Ra Facincani A.P., Ferreira A.J.S., Ferrelra V.C.A., Ferro J.A.,
Ra Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Ra Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Ra Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Ra Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Ra Machado M.A., Madelra A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
Ra Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Ra Manda A. Jr., Hobrega F.G., Miyaki C.Y., Monteiro-Vitoreilo C.B.,
Ra Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
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Ra da Silva A.C.R., Meldania J., Setubal J.C.;
Rat Mallada H., Van Sulys M.A., Verjovaki-Almeida S., Vettore A.L.,
Ra Agoqua A.P., Terenzi M.F., Truffi D., Taai S.M., Tsuhako M.H.,
Ra de Souza A.P., Terenzi M.F., Truffi D., Taai S.M., Tsuhako M.H.,
Ra Marter 406:151-159(2000).
DR Embl., AEOMOD3; Alvestri M.E., Comblete proteome.

EMBL., AEOMOD3; Alvestri M.S., Comblete proteome.
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Matches 6
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Q1-OCT-2000
Q1-DEC-2001
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SMART; SM00387; HATPase_C; 1.
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Complete proteome; Kinase; Phosphorylation; Sensory transduction;
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Bacteria, Proteobacteria,
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7 GLRPVGR 1053
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  13,
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   Drosophila
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  Insecta;
  Muscomorpha,
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"Cloning of the cataiase ger
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EMBL; AF286097; AAKIS159.1;
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   Jeong
   Pleurotus sajor-caju (Dyster mushroom).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pleurotaceae; Pleurotus.
  Myler P.J.;
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   Loca1
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   2 IRPVGRF
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  1 G1RPVGRF 8
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RA Rutter S., Seeger K., Skelton S., Squares R.,
Suiston J.E., Taylor K., Whitehead S., Barrell B.G.;
R Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.*:
RI Lattre 393:537-544(1998).
REMBL; 298268; CAB10949.1; -.
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REMBL; PF00702; Hydrolase.
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MEDLINE-98196666; PubMed-9537320; Deckert G., Warren P.V., Gaasterland T., Young W.G., Graham D.E., Overbeek R., Snoad M.A., Keller M., Aujs Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
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GLRPVRRF
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6; Conserv
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353 AA; 37
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  "The complete ge
aeoIicus.";
Nature 392:353-3
EMBL; AE000705;
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Mol. Microbiol. 21:77-96(1996).
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Oliver K., Harris
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Redenbach M., Kieser H.M., Denapaite D.,
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1 (NOV-1997)
  , Harris D.;
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Search completed: September 13, 2002, 09:29:25 Job time: 1070 sec

GenCore veraion 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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26: /SIDS1/gcgdata/hold-geneaeq/geneaeqp-embl/AA1999.DAT:*
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21: /SIDS1/gcgdata/hold-geneaeq/geneaeqp-embl/AA1999.DAT:*
               37
37
37
37
37
  protein search, using sw model
  Query
Match
  is the number of results predicted by chance to have a ster than or equal to the score of the result being printed. Then by analysis of the total score distribution.
               97.4
97.4
97.4
97.4
97.4
97.4
97.4
  US-09-446-543A-73_COPY_14_21
  747574 seqs, 111073796 residues
   BLOSUM62
Gapop 10.0 , Gapext 0.5
  September 13,
   IRPVGRFX 8
  Length
   2000000000
            115
115
115
115
120
20
20
   DB
  2002, 09:18:36;
  Ħ
          AAB46955
AAW91178
AAW97230
AAW97230
AAX49295
AAX49296
AAW31397
AAW31397
AAW31374
AAW31374
  SUMMARIES
  ; Search time 399.68 Seconds
(without alignmenta)
2.223 Million cell updates/sec
Peptide PRRP8 frag
Murine pituitary-d
Synthetic ligand 1
C-terminal ligand
1992 ligand peptid
1992 ligand peptid
1992 ligand peptid
1992 ligand peptid
Human type G protein
Bovine G protein-
Bovine girottin-c
  Description
```

| 45                                       | 43                 | 42                | 4                  | 40                 | 39                 | 38       | 37                 | 36       | 35       | 34                 | υ<br>U   | 32       | 33                 | 30       | 29       | 28       | 27                 | 26                 | 25                 | 24       | 23        | 22        | 21       | 20                 | 19                 | 18                 | 17         | 16         | 15       | 14       | 13            | 12                 |
|------------------------------------------|--------------------|-------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|----------|-----------|-----------|----------|--------------------|--------------------|--------------------|------------|------------|----------|----------|---------------|--------------------|
| 37<br>37                                 | 37                 | 37                | 37                 | 37                 | 37                 | 37       | 37                 | 37       | 37       | 37                 | 37       | 37       | 37                 | 37       | 37       | 37       | 37                 | 37                 | 37                 | 37       | 37        | 37        | 37       | 37                 | 37                 | 37                 | 37         | 37         | 37       | 37       | 37            | 37                 |
| 97.4                                     | 97.4               | 97.4              | 97.4               | 97.4               | 97.4               | 97.4     | 97.4               | 97.4     | 97.4     | 97.4               | 97.4     | 97.4     | 97.4               | 97.4     | 97.4     | 97.4     | 97.4               | 97.4               | 97.4               | 97.4     | 97.4      | 97.4      | 97.4     | 97.4               | 97.4               | 97.4               | 97.4       | 97.4       | 97.4     | 97.4     | 97.4          | 97.4               |
| 22                                       | 21                 | 21                | 21                 | 21                 | 21                 | 21       | 21                 | 21       | 21       | 21                 | 21       | 21       | 21                 | 20       | 20       | 20       | 20                 | 20                 | 20                 | 20       | 20        | 20        | 20       | 20                 | 20                 | 20                 | 20         | 20         | 20       | 20       | 20            | 20                 |
| 18                                       | 22                 | 22                | 22                 | 21                 | 21                 | 2        | 20                 | 20       | 20       | 18                 | 18       | 18       | 18                 | 22       | 22       | 22       | 22                 | 22                 | 22                 | 22       | 22        | 21        | 21       | 21                 | 21                 | 21                 | 21         | 21         | 20       | 20       | 20            | 20                 |
| AAW31396<br>AAW31389                     | AAG 62535          | AAG62528          | AAG62520           | AAB10366           | AAB10359           | AAB10351 | AAW95192           | AAW87616 | AAW97227 | AAW31375           | AAW31388 | AAW31395 | AAW31397           | AAB46954 | AAB90996 | AAB90994 | AAB90992           | AAG62538           | AAG62534           | AAG62527 | AAG 62519 | AAY 49302 | AAY49301 | AAY49294           | AAB10369           | AAB10365           | AAB10358   | AAB10350   | AAW95175 | AAW95191 | AAW97236      | AAW97234           |
| Human type G prote<br>Rat type G protein | Human CRH releasin | Rat CRH releasing | Bovine CRH releasi | Human oxytocin aec | Rat oxytocin aecre |          | Bovine pituitary-d | an 19P2  | _        | Bovine G protein-c | ğ        |          | Synthetic G protei | ч.       |          |          | Prolactin releasin | CRH releasing prot | Human CRH releasin |          | ne CRH z  |           | ligand   | 19P2 llgand peptld | Oxytocin secretion | Human oxytocin sec | ytocin aec | oxytocin s |          | pitu     | an type ligan | Rat type ligand po |

# ALIGNMENTS

```
RESULT
AAB46955
GPR10; UHR-1; PTRP receptor; prolactin-releasing peptide; pain; central nervous system disorder; autonomic regulation; analgesic;
   03-AUG-1999; 99US-0365756.
20-MAR-2000; 2000US-0531567.
   Key
Modified-site
   Unidentified.
   04-MAY-2001 (first entry)
  AAB46955 standard;
             Panula PAJ,
  03-AUG-2000; 2000WO-FI00664
   08-FEB-2001.
   WO200109182-A1.
   hypotensive; blood pressure.
  Peptide PrRP8 fragment.
  AAB46955;
                             (JUVA-) JUVANTIA PHARMA LTD OY
  _
             Pertovaara A,
  Location/Qualifiers
   /note- "C-terminal amlde"
  Protein;
             Kalso E,
  8
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             Korpi
             ņ
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믕
   δ
  AAW95178
   and comprising a sequence ($2); (2) a diagnostic method based on antisera comparison as sequence ($2); (2) a diagnostic method based on antisera against prap20 for identification of disorders involving the central concerns prapagation of autonomic conservations system, including those associated with pain or autonomic regulation, where specific antisera against the N-and/or C-terminal commands of prap is used to identify alterations in prap synthesis or conservations; (3) a rat or human receptor encoded by a 1122 nucleotide sequence ($3), fully defined in the specification; (4) treating a person suffering from a disorder regulated by a receptor (II) encoded by a sequence of 1122 nucleotide sequence, fully defined in the specification, located in the contrain nervous system, by administering an agonist or antegonist to the receptor; and (5) treating blood pressure, by blocking of receptors of the reventue system by administering and hypotensive activity. The products of the invention have analgesic and hypotensive activity. C1) is useful for regulating autonomic functions, such as increasing biood pressure. (1) is useful for treating pain, for manufacturing a medicament for regulating blood pressure, and for treating pain. Agonist and anteropathic pain, for regulating autonomic functions and
   Query Match
Best Local S
Matches 7
  Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UNR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; sentile dementia; ligand; murine; Aizhelmer's disease; Parkinson's disease; Huntington's disease; drug; creutzfeid-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor
  This invention describes a novel C-terminal fragment (I) of an isolated prolactin releasing peptide (PrRP), referred to as PrRP20 and having a sequence (S1). The invention also describes (I) a therapeutic composition (C1) comprising (I) or a C-terminal fragment of PrRP referred to as PrRP8
   C-terminal fragments
regulating autonomic
   28-APR-1997;
  27-APR-1998;
  05-NOV-1998.
   gene therapy:
  Murine pituitary-derived ligand polypeptide antigenic epitope
  10-MAR-1999
   AAW95178
   Sequence
  Claim 2;
  for regulating bicod
           (TAKE ) TAKEDA CHEM IND LTD
   Local Similarity
les 7; Conserv
   N
  1 IRPVGRF 7
   L
   1rpvgrf 8
  neuropathic pain, fo
   standard; Protein; 10
  Page 10; 40pp;
   6
   Conservative
   Ā
  (first entry)
   transgenic animai; epitope
   97JP-0109974
   98WO-JP01923
  97.4%; 500
100.0%; Pr/
0;
   of projectin-releasing peptide useful functions and in the manufacture of a
  pressure
  Engiish.
   Score 37;
Fred. No.
   ≥
   Mismatches
   DB 22;
6.4e+05;
  Length 8;
   Indeis
   for medicament
  0
  vasopressor
   0
```

```
RESULT
AAW31400
   몆
   å
  cc which is a ligand for the G-protein coupled orphan receptor designated Cd GPRLO (human) or UHR-1 (rat). Cells transformed with a vector containing ct the ligand polypeptide encoding DNA are used to produce a recombinant cd (ligand polypeptide. The ligand polypeptide, and its fragments, modulate cf function of the pituitary, central nervous system, pencreas and other ctissues and can be used to screen for agents that modulate binding of ct the polypeptide to the receptor; to quantify the amount of receptor in a csample and to raise antibodies. They may also be used therapeutically, ce. 9. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's cd diseases; Creutzfedd-Jakob diseases; poisoning by heavy metals or drugs; cd diseases; schizophrenia; disorders of growth hormone secretion; cancer; cremmatoid arrhritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding DNA or its mutein are used to carrying the ligand polypeptide encoding DNA or its models of cc study the function of the polypeptide encoding polypens, as models of cc study the function of the polypeptide encoding polypens, as models of cc study the function of the polypeptide encoding polypens, as models of cc study the function of the polypeptide encoding polypeptide. The polypeptide encoding polypept
  Matches
  Query Match
               18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
   G protein-coupled receptor; ligand binding; pharmaceutical;
  The invention relates
   New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
  26-DEC-1996;
  W09724436-A2
   Synthetic
  therapeutic
  Synthetic ligand 19P2-L31 peptide II.
   06-APR-1998
  AAW31400
   AAW31400 standard; Peptide; 15
   Sequence
   Disclosure; Page 26;
  Fukusumi S,
   10-JUL-1997
   nodulator;
   Local Similarity hes 7; Conserv
   4 irpvgrf 10
   1 IRPVGRF 7
   w
  pituitary;
c agent; an
   10
  Conservative
   Hinuma
  (first entry)
   Š
               96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
  96WO-JP03821
  antigen
   97.48;
   206pp; English.
  to a murine pituitary-derived ligand polypeptide the G-protein coupled orphan receptor designated
   central nervous system;
  0
  Score 37;
   Pred. No.
  Mismatches
   DB 20
0.21;
   20:
   pancreas; prophylactic;
  0
  Length 10;
  Indels
  0
   used
```

```
Query Match
Best Local Similarity
Thes 7; Conserv
  SXCCCCCCCCCCCCCCX SXFFX X FFX 
  cc protein coupled receptor protein. This peptide is used as an antigen to cessays. Pharmaceutical compositions containing this ligand may be used cessays. Pharmaceutical compositions containing this ligand may be used cessays. Pharmaceutical compositions containing this ligand may be used cessays. Pharmaceutical compositions containing this ligand may be used cessays. Pharmaceutical containing this ligand could have specific containing the protein modulator. This ligand could have specific containing the protein modulator. This ligand could have specific containing the protein modulator. This ligand could have specific containing the protein modulator of therapeutic agent for dementia. Containing the protein modulator of the protein could have specific contained the protein protein discusses. The protein protein protein protein discusses, cancer and polyphagia, hyperilipidaemia, hyperchoidsterolaemia, phyperilipidaemia, hyperchoidsterolaemia, containing the protein protein protein lateral discusses. Turner's syndrome, neurosis, asthma, rheumatoid arthritis, contained and protein protein, bone fracture, trauma, atopic dermatitis, spinocerebellar contained and protein protein. The protein compounds which are capable of altering the binding activity of the ligand confidence of the G protein coupled receptor protein.
밁
  Š
  AAW97230
  RESULT
   G protein-coupled receptor; GPCR; hyponvarianism; gonecyst cacogenesis; menopausai syndrome; euthyroid; hyponetabolism; lactation; modulation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; proiactinoma; infertility; impotence; amenorrhea; galactorrhea; ecromegaly; Chiari-Frommel syndrome; Argonz-dei Castiio syndrome; Forbes-Albright syndrome; lymphoma; Sheshan syndrome; dyszoospermia; contraceptive; placentai function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal ilpidmetabolism; oxytocia; prolactin secretion.
  C-terminal ligand
   AAW97230 standard; Peptide; 15
23-JUN-1997;
   22-JUN-1998;
   WO9858962-A1
  Synthetic.
  06-MAY-1999
   AAW97230;
  Sequence
  This peptide contains the partial C-terminal sequence of the ligand polypeptide 19P2-L31 which is capable of binding to
   Example 43; Page 151;
  Ligand peptide for G protein-coupled receptor - acts function in the central nervous system, pancreas and
   WPI; 1997-363672/33.
   (TAKE ) TAKEDA CNEM IND LTD
  30-DEC-1998
  H
  9
   4
   IRPVGRF 7
   Fukugumi S, I
  15
  97.4%; Score 37; DB
ilarity 100.0%; Pred. No. 0.
Conservative 0; Mismatches
  (first entry)
  ξ
   98WO-JP02765
  polypeptide derived antigen.
   258pp; English
  Habata
  K
   Hinuma
  DB 18; Length 15; 0.32;
  'n
  нозоуа
  0,
  Indels
  by modulating pituitary giand
  of the
  o,
  synthetic
G
  Gaps
  0
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9
   8
   AAY49293
  RESULT
   AAM97229-31 represent a ligand polypeptide derived fragments used to C produce antibodies. The specification describes an agent for modulating productin secretion which comprises a ligand polypeptide or a salt, for a g protein-coupled receptor (GPCR) protein. The agents for promoting C protactin secretion can be used for treating or preventing protection for a domestic proportion and as an aphrodistac. The agents for inhibiting protectin secretion can be used for promoting lactation in a domestic mammal and as an aphrodistac. The agents for inhibiting protactin secretion can be used for treating or preventing pituitary adenomatosis, c brain tumour, emmenlopathy, autoimmune disease, protactinoma, adenomatosis, c chari-Frommel syndrome, Argonz-dei Castilo syndrome, Forbes-Albright CC Syndroms, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory Cagents can also be used as contraceptives. The agents for modulating piacental function can be used for treating or preventing unthrifty c agents can also be used as contraceptives. The agents for modulating CC choicoarcinoma, hydatid moie, irruption mole, abortion, unthrifty c fetus, abnormal saccharometabolism, abnormal lipidmetabolism or
   Query Match
Best Local S
Matches 7
  Example 43; Page 123; 241pp; Engilsh.
   secretion
  Use of G protein-coupled receptor ligands - for modulating prolectin
   (TAKE ) TAKEDA CHEM IND LTD
   21-MAY-1998;
   Monoclonal antibody; 1992 ligand; diagnosis; proiactin secretion;
pituitary; regulatory mechanism; centrai nervous system; pancreat
  AAY49293 standard;
   Sequence
            (TAKE ) TAKEDA CNEM IND LTD
  20-MAY-1999;
   WO9960112-A1
   Key
Modified-site
   Nomo sapiens.
  19P2 ligand
  22-FEB-2000
  AAY49293
   Local Similarity
wes 7; Conserv
   9
  1 IRPVGRF 7
  UI
  1999-105614/09
   or piacental function, e.g. for treating menopaus tumours, autoimmune disease or abnormal pregnancy
   Hinuma S,
  15
  pept1de
  Conservative
   (first entry)
  ζ
   98JP-0140293
  99WO-JP02650
   Location/Qualifiers
  /note- "C-terminal amide"
   peptide;
   Kawamata Y,
   97.48: Score 37;
100.08; Pred. No.
   15
  0,
   ζ
  Mismatches
   Matsumoto
   for treating menopausai
   DB 20:
   0
   Length 15;
   ô
   Gaps
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RESULT
AAY49295
밁
   S
   SXCCCCCCCX SXPTX SXI
   Matches
   Query Match
Best Locai
  The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. sequences AAV49290-302 represent peptide fragments of the 1992 ligand.
                             New monocional antibodies, u
studying diseases related to
  AAY49295 standard; peptide; 15
   New monoclonal antibodies, u
studying diseases related to
                            studying
   (TAKE ) TAKEDA CHEM IND
  21-MAY-1998;
  20-MAY-1999;
   25-NOV-1999
  W09960112-A1
  Modified-site
   Modified-site
   Modified-site
   Homo sapiena
   pituitary;
   Monoclonal
   19P2 ligand peptide fragment
   22-FEB-2000
  AAY49295
   Seguence
  Disclosure; Page 26; 73pp; Japanese.
  Matsumoto H,
   1 IRPVGRF 7
|||||||
9 irpv9rf 15
  Local Similarity
les 7; Conser
   o,
   2000-039381/03
   Ŧ
   antibody; 19P2 ligand; diagnosis; prolactin secretion;
regulatory mechanism; central nervous system; pancreatic.
   15
       Page
  Conservative
  (firat entry)
   3
   Kitada
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   99WO-JP02650
  98JP-0140293
  /note=
15
   /note-
   Location/Qualifiera
         26:
  /note=
  97.48;
  'n
       73pp; Japanese
  "acetylated
   "N-terminal acetylation"
   "C-terminal amide"
   CTD
  Hinuma
  Hinuma
                            useful in diagnosis,
o iigand abnormality
   useful in diagnosis, o iigand abnormality
  ..
   Score 37;
Pred. No.
  119and
   >
   ç
  ŝ
  Mismatches
  Tyr
  DB 21
0.32;
  21;
  0
  Length
                                9
   as drugs
  Indels
                                       drugs
  and
   and
  0
  5
   'n
   Gaps
  0
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RESULT
AAY49296
   Query Match
Best Local Similarity
7; Conserv
Ş
  888888888888
  닭
   The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19p2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of projectin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAX49290-302 represent peptide fragments of the 19P2 ligand.
                       regulatory mechanism (e.g. promotion of projactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
   The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function
  Key
   Disclosure; Page
   WPI; 2000-039381/03
  Matsumoto H,
   20-MAY-1999;
  WO9960112-A1
   Homo sapiens
  pituitary;
   AAY49296 standard; peptide; 15 AA
   Sequence
   New monoclonai antibodies,
  (TAKE ) TAKEDA CHEM IND LTD.
  21-MAY-1998;
   Modified-aite
  Monoclona1
  19P2 ligand
  22-FEB-2000
  AAY49296;
   1 IRPVGRF 7
|||||||
9 1rpvgrf 15
   clonai antibodies, usefui in diagnosis, diseases related to ligand abnormality
  regulatory
  antibody;
  15 AA;
  pept1de
  Conservative
  (first entry)
  Kitada
  98JP-0140293
   99WO-JP02650
  Location/Qualifiers
  27;
  /note-
   97.4%; 5-
100.0%; Pr
  fragment.
  Ö
   19P2 ligand; diagnosis; prolactin secretion; y mechanism; centrai nervous system; pancreatic.
   73pp; Japanese.
  "C-terminal amide"
  Hinuma
  Score 37;
Pred. No.
  S
   Mismatches
  DB 21;
   0
   Length 15
  89
   Indeis
   drugs
  its derivative
  its derivative
   and
   0
   5
   Gaps
   .
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Sequence

15

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Best Local Similarity Matches 7; Conserv

Conservative

Pred. No. 0.43;

Mismatches

Indeis

0

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片
   Ş
   cc ligand polypeptide corresponding to amino acid residues 34 to 53 of the csequence represented in AAW31390 and is used in an assay to monitor cligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. A central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementla, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, cs. syndrome, growth hormone secretory disease, hyper- and polyphagia, ctrauma, growth hormone secretory disease, hyper- and polyphagia, ctrauma, growth hormone secretory disease, hyper- and polyphagia, ctrauma, growth hormone secretory disease, hyper- and polyphagia, ctrauma growth hormone secretory disease, hyper- and polyphagia, ctrauma growth hormone secretory disease, hyper- and polyphagia, ctrauma growth hormone secretory disease, hyper- and polyphagia, ctrauma growth hormone secretory disease, hyper- and polyphagia, ctrauma growth hormone secretory disease, hyper- and polyphagia, ctrauma growth hormone secretory disease, hyper- and polyphagia, ctrauma, scheme, scheme, hypergiyceridaemia, hypergiyceridaemia, hypergiyceridaemia, cc hyperprolactina schemenia, sepines scheme, compounds spinai injury, cure my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, cc antient my disease, hyper- and polyphagia, hypergiycer- antient my disease, hyper- and polyphagia, hypergiycer- antient hypergiycer- antient my disease, hyper- 
   Matches
  Query Match
Best Local
   18-SEP-1995;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
   Ciaim
   modulator; pituitary;
   06-APR-1998
  AAW31394;
  AAW31394 standard; Peptide;
Sequence
                                      capable of altering activation of the G
  Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
   N-PSDD; AAV02431.
   Fujii R,
  10-JUL-1997
   WD9724436-A2
  Homo sapiens
   therapeutic agent.
   Human type G
  Kawamata
  (TAKE ) TAKEDA CHEM IND
   26-DEC-1996;
  protein-coupled receptor; ligand binding; pharmaceutical;
   ø
   1 IRPVGRF
  8
  sequence represents a peptide fragment from a novei human
  irpvgrf 15
  Similarity
7; Conserv
   Page 185; 258pp; English.
  ζ,
   Fukusumi S,
Y, Kitada C;
20
  Conservative
   7
   protein-coupled receptor 11gand fragment
  (first entry)
   96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
   96WO-JP03821.
   protein-coupled
  97.4%; Score 37;
100.0%; Pred. No.
  central nervous system; pancreas; prophylactic;
   Habata
  ..
   20
   ۲,
   Mismatches
   Hinuma S,
                                    receptor protein.
  DB 21;
0.32;
   Hosoya
  0
   Length 15;
  Indels
   3
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  Gaps
  0
```

Query Match

48

Score

37;

B 18;

Length

20

Query Match Best Local Similarity

97.4%;

Score Pred.

. 37 . NO.

0B 18; 0.43;

Length

20

```
RESULT
AAW31387
                                    CC This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 33 to 52 of the CC sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This ligand could have specific applications as a central nervous system modulator or a pancreatic function CC prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, diabetes, cancer, pancreatitis, renal disease, hyperrolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC Turner's syndrome, neurosis, asthma, rhewmatoid atternal sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, CC bone fracture, trauma, atopic dematitis, osteoporosis and/or coligogalactia, assays can also be developed to screen compounds which are CC capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
  G protein-coupled receptor; ilgand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
  Ligand peptide for G protein-coupled receptor - acts function in the central nervous system, pancreas and
  W09724436-A2
   Rat type G
  06-APR-1998
   AAW31387 standard; Peptide; 20
Sequence
   Ciaim 2; Page 180; 258pp; English.
  Fuj11 R,
   (TAKE ) TAKEDA CHEM IND LTD
  26-DEC-1996;
  10-JUL-1997
  Rat sp
  AAW31387
  1 IRPVGRF 7
|||||||
14 irpvgrf 20
   14
   9
  AAV02424.
  Fukusumi S,
20
   protein-coupied
   (first entry)
  Kitada
ξ
   96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
  96WO-JP03821
  ü
  100.0%; ---
  Habata
  receptor ligand fragment
   ۲,
   ξ
   Hinuma S,
   Hosoya
   0
   by modulating pituitary gland
  0;
   Gaps
```

```
derived ligand corresponding to amino acid residues 34 to 53 of the csequence in AAW31368 and is used in an assay to monitor ligand binding to to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. Compositions 11 sigand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, compositional could have specific applications as a prophylactic or constituibance of consciousness, anxiety syndrome, schizophrenia, trauma, compositional contents and polyphagia. Trauma, compositional contents and polyphagian.

Compositional contents of the concernation, spinal injury, concernation arthritis, spinal injury, concernation arthritis, spinal injury, concernation bain ischaemia, amylotrophic lateral scherosia, acute concernation, atopic dermatitis, osteoporosis, asthma, epilepsy, infartility conformation, spinocerebellar degeneration, bone fracture, concernation, and polyphagian.

Conformation is chaemia, and so be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
  밁
  Ş
   RESULT 10
  Matches
  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
   G protcin-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
   This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 34 to 53 of the
   Ligand peptide for {\tt G} protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
  06-APR-1998 (first entry)
  AAW31374 standard; Peptide;
Sequence
  Claim 2; Page 161; 258pp; English.
   WP1; 1997-363672/33.
   (TAKE ) TAKEDA CHEM IND LTD.
  26-DEC-1996;
  10-JUL-1997
   W09724436-A2
   Bos taurus.
  Bovine G
   AAW31374
   ||||||||
|14 irpvgrf 20
   1 IRPYGRF 7
   AAV02397
  7;
  protein-coupled receptor ligand peptide fragment 4.
   Fukusumi S,
K, Kitada C;
20
  Conservative
   96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
  96WO-JP03821
   Habata
   20
  0:
   ۲,
  Mismatches
   Hinuma
   ß
   Hosoya
  0
  indels
   X
  0
  Gaps
  0
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Query Match Best Local S Matches 7

Similarity 7; Conserv

Conservative

97.4%; >---100.0%; Pr

Score 37; DB 18; Pred. No. 0.43;

Length 20; Indels

Mismatches

0

0

Gaps

0

Query Match
Best Local Similarity
Matches 7; Conserv

97.4%; Score 37; ilarity 100.0%; Pred. No. Conservative 0; Mismatc

Mismatches

0

0

Gaps

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DB 20 20;

Length 20; Indels

Sequence

20

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RESULT 11
AAW97232
  밁
  S
  The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a g protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, genecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisia. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary ademomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorihas, galactorrhes,
   menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Fronmel syndrome; Argonz-del Castillo syndrome; rorbes-Albright syndrome; imphoma; sheehan syndrome; dyszoospermia; contraceptive; piacental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
  prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbea-Albright syndrome, lymphoma, Sheehan syndrome or dyszospermia. The inhibitory agents can also be used as contraceptives. The agents for the inhibitory agents can also be used for treating or preventing modulating placental function can be used for treating or preventing
  Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
  Bos
  Bovine
   06-MAY-1999
   AAW97232 standard; peptide;
   Claim 3; Page 136; 241pp;
   WPI; 1999-105614/09
  Fujii R, Hinuma S,
   (TAKE ) TAKEDA CHEM IND LTD.
   30-DEC-1998.
   Bovine pituitary-derived ligand polypeptide fragment.
  AAW97232;
   23-JUN-1997;
  22-JUN-1998;
   WO9858962-Al
   1 IRPVGRF 7
|||||||
14 irpvgrf 20
  protein-coupled
  pituitary-derived ligand; modulation;
                                       rcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus saccharometabolism, abnormal iipidmetabolism or oxytocia.
   (first entry)
  98WO-JP02765
   97JP-0165437
  receptor;
  Kawamata Y
   English.
   20
  GPCR; hypoovarianism; gonecyst cacogenesis;
oid; hypometabolism; lactation;
  Matsumoto
  prolactin secretion;
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IRPVGRF

7

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14 irpvgrf 20

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RESULT
AAW97234
The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes a period of the invention. The specification describes in agent for modulating prolactin secretion which comprises a comprises a comprise and the protein. The agents for promoting prolactin secretion can be used for treating or preventing hypowarianism, gonecyst cacogenesis, menopausal syndrome, euthyrold or hypometabolism. They can by used for promoting contextion in a domestic mammal and as an aphrodisia. The agents for continiting prolactin secretion can be used for treating or preventing continiting prolactinomal secretion can be used for treating or preventing continiting prolactinoma, infertility, impotence, amenorrhea, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, coromegaly, chlari-grommel syndrome, Argonz-del Castilo syndrome, composition, and the syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing continuating placental function can be used for treating or preventing continuation, hydatid mole, liruption mole, abortion, unthrifty fetus, abortman associations.
   Use of G protein-coupled receptor ilgands - for modulating protactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
  menopausal syndrome; euthyrold; hypometabollsm; lactation; plutitary adenomatosla; brain tumour; emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galatorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid moie; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
   AAW97234 standard; peptide;
   Clalm 3;
  06-MAY-1999
  WPI; 1999-105614/09
   (TAKE ) TAKEDA CHEM IND
  Rattus
  abnormal lipidmetabolism; oxytocia.
   Rat type llgand;
   Rat type
Sequence
  23-JUN-1997;
  22-JUN-1998;
   30-DEC-1998.
   ₩09858962-A1
  protein-coupled receptor;
   12
  ģ
   llgand
   Page 154; 241pp; English.
   Hinuma S,
20
  (first entry)
ζ
  97JP-0165437.
  98WO-JP02765.
   polypeptide
   modulation; projactin secretion;
   Kawamata
   20 AA
  GPCR;
   fragment.
   ×
  hypoovarianism; gonecyst cacogenesis;
   Matgumoto
   Ξ
  unthrifty fetus,
   for
```

Query Match Best Local S Matches 7

Similarity 7; Conser

97.4%; Score 37; DB llarlty 100.0%; pred. No. 0. Conservative 0; Mismatches

DB 20 0.43;

Length 20; Indels

<u>..</u>

0,

Gaps

0

Query Match Best Local S Matches 7

Similarity 7; Conser

97.4%; Score 37; DB. larity 100.0%; Pred. No. 0. Conservative 0; Mismatches

DB 20; 0.43;

Length 20; Indels

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Gaps

0,

Sequence

20

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RESULT
AAW97236
The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a g protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypowerialnism, generyst cacegenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting inhibiting prolactin secretion can be used for treating or preventing pilutitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, coromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, for The inhibitory agents can also be used for treating or preventing choriccarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocla.
   prolactinoma; infertility; Impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphome; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; lruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
  Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
  Fujii R,
  Homo sapiens
  pltuitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
  Rat type ligand; modulation; prolactin secretion;
   Human type ligand polypeptide fragment
   AAW97236 standard; peptide; 20 AA
  Claim
   WPI; 1999-105614/09
  (TAKE
   23-JUN-1997;
  22-JUN-1998;
   30-DEC-1998
  WO9858962-A1
  G protein-coupled receptor; GPCR; hypoovarlanism; gonecyst cacogenesis; menopausal syndrome; euthyrold; hypometabolism; lactation;
   06-MAY-1999
   AAW97236;
   14 irpvgrf 20
  13
  _
  IRPVGRE
   ü
   Page 166; 24lpp; English.
  Hinuma S,
  (first entry)
   CHEM
  97JP-0165437
  98WO-JP02765
   Kawamata
  Ķ
   Matsumoto
   Ξ
   fetus
   for
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Dy

Pred. No.

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RESULT AAW95191
밁
                           The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designsted CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector contsining CC the ligsnd polypeptide encoding DNA sre used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise sntibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzhelmer's, Parkinson's or Huntington's CC disease; Creutrfeld-Jakob disease; poisoning by heavy metals or drugs; CC disbetes; schizophrenia; disorders of growth hormone secretion; cancer; CC creative nutritionsl status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to catudy the function of the polypeptide expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide sequences; in receptor-binding assays; for production of Ab and CC polypeptide fragment which is similar to the murine ligand-polypeptide.

CC animals. The present sequence represents s bovine genome-derived ligand CC polypeptide fragment which is similar to the murine ligand-polypeptide.
  tissue; screen; therapeutic; binding; sential nervous system; pancreds; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Croutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis orilano.
   New polypeptide ligand for orphan G protein coupled receptors - used for tresting disorders of central nervous system, pituitsry and pancreas, and for drug acreening
  AAW95191 standard; peptide; 20 AA
  Example 19; Page 151; 206pp; English.
  WPI; 1999-009423/01
   Fukusumi S,
   (TAKE ) TAKEDA CHEM IND
  20-APR-1997;
  27-APR-1998;
   05-NDV-1998
   WO9849295-AL
   gene therapy;
  Pitultary-derived ligand polypeptide; G-protein coupled orphan receptor,
   Bovine pituitsry-derived ligand polypeptide fragment.
   10-MAR-1999
  AAW95191
   14
   1 IRPVGRF 7
   Hinuma S;
   (first entry)
   transgenic animal; bovine.
  97JP-0109974
  98WD-JP01923
   GI.
  rheumatoid arthritis; epilepsy; vasopressor
```

Query Match

97 .48;

Score 37;

DB 20;

Length

Sequence

Sequence

20

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RESULT 1
AAW95175
CC which is a ligand for the grant coupled orphan receptor designsted CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing Ct the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other Ct issues and can be used to screen for sgents that modulate binding of CC the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Schizophrenia; disorders of growth hormone secretion; csncer; CC rheumatoid arthritis, epilopsy and msny others, also to improve post-coperative nutritional status and ass vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide bNA is used as a source of cell lines. The ligand CC related sequences; in receptor-binding sasays; for production of Ab and CC antisers; in drug development; for gene therspy snd to develop continues which can be used for the preparation of anti-ligand polypeptide entity continues which can be used for the preparation of anti-ligand polypeptide.
   Best Local Similarity 100 Matches 7; Conservative
   GPR10; UHR-1; modulator; pituitary; centrs1 nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; disbetes; cancer; rheumatoid arthritis; epliepsy; vasopress;
  Pituitary-derived ligand polypeptide; G-protein coupled orphsn receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
   New polypeptide ligand for orphan G protein coupled receptors for treating disorders of central nervous system, pituitsry and
  Disclosure; Page 26;
   pancreas, and for drug screening
  WPI; 1999-009423/01.
  Fukusumi S, Hinuma S;
   28-APR-1997;
  27-APR-1998;
  05-NOV-1998.
   W09849295-A1
  gene therspy; transgenic animal; epitope.
   Murine pituitary-derived ligand polypeptide antigenic epitope
  10-MAR-1999 (first entry)
  AAW95175;
  AAW95175 standard; Protein; 20
   (TAKE ) TAKEDA CHEM IND LTD.
   15
  1 IRPVGRF 7
  invention relates to a murine pituitary-derived ligand polypeptide
   97JP-0109974.
  98WO-JP01923
  100.08; --
  206pp; English.
   Mismatches
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   Indels
   0;
   vasopressor
   used
   Gaps
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US-09-105-678A-34
US-09-105-678A-46
US-09-105-678A-971-8
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US-09-105-678A-42
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US-09-105-678A-42
US-08-776-971-52
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   Description
93, Appl
404, Appl
46, Appl
50, Appl
50, Appl
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405, Appl
417, Appl
41
  RESULT 1
US-08-776-971-93
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Result No.

| 45                | 44                | 43                | ړ2                | 1                 | ô                 | 39              | 38                | 37                | 36                | 35                | 4                 | <b>33</b>         | 32               | 31               | 30                | 29               | 28                |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|------------------|-------------------|
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| 31                | 31                | 31                | 31                | 31                | 31                | 31              | 31                | 31                | 31                | 31                | 31                |                   | 22               |                  |                   |                  | 22                |
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| US-09-421-208-8   | US-09-421-208-7   | -776-971          | US-08-776-971-61  | US-08-776-971-47  | US-08-776-971-5   | US-09-172-353-4 | -09               | US-09-105-678A-37 | US-09-105-678A-31 | US-09-105-678A-9  | US-09-105-678A-8  | US-09-105-678A-7  | US-09-421-208-48 | US-09-421-208-42 | US-09-421-208-36  | US-08-776-971-73 | US-08-776-971-66  |
| Sequence 8, Appli | Sequence 7, Appli | Sequence 97, Appl | Sequence 61, Appl | Sequence 47, Appl | Sequence 5, Appli | 4,              | Sequence 43, Appl | •                 |                   | Sequence 9, Appll | Sequence 8, Appll | Sequence 7, Appli | •                | •                | Sequence 36, Appl | 73,              | Sequence 66, Appl |

## ALIGNMENTS

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Sequence 93, Application US/0877
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                 INFORMATION
   APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON111, David G.
REGISTRATION NUMBER: 27,026
  CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
                                     REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
   FURUSINAL Shoji

Kitada, Chieko

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
SEQUENCE
  PRIOR APPLICATION DATA:
   ZIP: 02109
COMPUTER READABLE FORM:
  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
  APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
  COMPUTER:
  C1TY: Boston
STATE: MA
   MEDIUM TYPE: Diskette
  COUNTRY: USA
   Application US/08776971B
FOR SEQ ID NO: 93
  Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
   Fujli, Ryo
  IBM compatible
  .
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Query Match
Best Local Similarity
""" 7; Conserve
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  US-09-105-678A-34
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Matches 7; Conservative
   APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 AFTORNEY/AGENT INFORMATION: NAME: Conlin, David G.
   GENERAL INFORMATION:
  TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
   COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 20 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
  MOLECULE TYPE: peptide
   STREET: 1.
STREET: 1.
STRY: Boston
14 IRPVGRF 20
   TOPOLOGY:
  TYPE: amino acid
  STRANDEDNESS:
   COUNTRY:
   TELEPHONE;
  9 IRPVGRF 15
                               1 IRPVGRF 7
  1 IRPVGRF 7
   MOLECULE TYPE: protein FRAGMENT TYPE: internal
  SEQUENCE DESCRIPTION: SEQ ID NO:
   02109
  LENGTH: 15 amino acids TYPE: amino acid STRANDEDNESS: single
  TOPOLOGY: llnear
   130 Water Street
  USA
   Conservative
  617-523-3400
   97.4%; Sur
100.0%; Pr
  97.4%; Score 37;
100.0%; Pred. No.
tive 0; Mismatc
  Score 37;
Pred. No.
  48466-342
   Mismatches
   DB 4;
   OB 3;
   0; Indels
   Length 15;
   0; Indels
   Length 20;
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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-09-105-678A-40
  밁
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""" heg 7; Conserve
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US-09-105-678A-40
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   RESULT
  Patent No. 6103882
GENERAL INFORMATION:
   sequence 46, Application US/09105678A Patent No. 6103882
  Patent No.
   Sequence 40,
   SOFTWARE: Patentin Release #1.0, Versor Application Data:
APPLICATION DATA:
APPLICATION NUMBER: U$/09/105,678A
PILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Toko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
   GENERAL INFORMATION:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlisk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
  APPLICANT: Suenaga, masat
APPLICANT: MORIYA, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osa
  TELECOMMUNICATION.INFORMATION: TELEPHONE: 617-523-3400
   NUMBER OF SEQUENCES:
  TITLE OF INVENTION:
  14 IRPVGRF 20
  TYPE: amino acid
   COUNTRY: U
ZIP: 02109
   STREET: 130 v
  ADDRESSEE:
  LENGTH:
  TELEPHONE:
   1 IRPVGRF 7
COUNTRY: USA
                                Boston
               Š
   Š
   Application US/09105678A
  130 Water Street
   E: DIKE, BRONSTEIN,
130 Water Street
  20 amino acids
  USA
   Conservative
  linear
   peptlde
  METHOD OF PRODUCING A 19P2 LIGAND
   97.4%; Score 37; OB 3; 100.0%; Pred. No. 0.12; Live 0; Mismatches
   Release #1.0, Version #1.30
  OF PRODUCING A 19P2 LIGAND
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  TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
  NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
  APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
  SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
  STRANDEDNESS:
TOPOLOGY: 11
  14 IRPVGRF 20
   TYPE: amino acid
   MEDIUM TYPE:
   1 IRPVGRF 7
  Habata, Yugo
Kawamata, Yuji
Nosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
  COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
   APPLICANT:
  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
   READABLE FORM:
  CITY: Boston
   STATE: MA
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   Floppy disk
  97.4%; Pr/
100.0%; Pr/
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   48466-342
  Score 37;
Pred. No.
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  Version #1.30
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US-08-776-971-50
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GENERAL INFORMATION:
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TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
  1 IRPVGRF 7
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14 IRPVGRF 20
   Local Similarity es 7; Conserv
  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION MADER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CUNknown>
   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   Fukusum1, Shoj1
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
   MOLECULE TYPE:
FRAGMENT TYPE:
  APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996 ATTORNEY/AGENT INFORMATION:
  PRIOR APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  APPLICANT: Hinuma, Shuji
   SEQUENCE DESCRIPTION: SEQ ID NO: 8:
   LENGTH: 20 amino acids TYPE: Bmino acid STRANDEDNESS: single TOPOLOGY: linear
  CITY: Boston
STATE: MA
   NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
  APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
   APPLICATION NUMBER: JP 9/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 9/211805
FILING DATE: 12-AUG-1996
                              APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
  APPLICATION NDMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
  COUNTRY: USA
  STREET: 130 Water Street
                 APPLICATION NUMBER:
   Application US/08776971B
   Conservative
   Fujii, Ryo
   Hosoya, Masaki
  Habata, Yugo
Kawamata, Yuji
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   97.4%; Score 37; DB
100.0%; Pred. No. 0.
Live 0; Mismatches
NUMBER: JP 8/211805
12-AUG-1996
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TELEPHONE: 617-523-3400
TELEPHAX: 617-523-6440
INFORMATION FOR SEO ID NO: 50:
SEQUENCE CHARACTERISTICS:
                     APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
   14 IRPVGRF 20
  I IRPVGRF 7
  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
  CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
   APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
  FRAGMENT TYPE:
  FILING DATE: 18-SEP-19
ATTORNEY/AGENT INFORMATION:
   SEQUENCE DESCRIPTION: SEQ ID NO: 50:
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Similarity 100.0%; Pred. No. 0.12;
7; Conservative 0; Mismatches
  TYPE: amino acid
   NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
  COUNTRY: USA
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  STATE: MA
   CITY: Boston
   STRANDEDNESS: single
   APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
  APPLICATION NUMBER: PCT/JP96/03821 FILING DATE: 28-DEC-1996
  STREET: 130 Water Street
  TOPOLOGY: linear
  TYPE: protein TYPE: internal
  HOSOJE.
Fujli, Ryo
Fumil. Shoji
   0
   Length 20;
   Indels
   0
   Gaps
   0
  Query Match
Best Local Similarity
Thes 7; Conserve
   片
   Ś
  ; SEQUENCE DESCRIPTION: US-08-776-971-64
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US-08-776-971-98
  Sequence 98, Applicati
Patent No. 6228984
GENERAL INFORMATION:
   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
  APPLICATION NÜMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
APPLICATION NUMBER: JP 8/246573
ATTORNEY/ACENT INFORMATION:
   14 IRPVGRF 20
   1 IRPYGRF 7
  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
   REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47-
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617-523-3400
   ZIP: 02109
COMPUTER READABLE FORM:
  PRIOR APPLICATION DATA:
  CORRESPONDENCE ADDRESS:
   Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
   APPLICANT: Hinuma, Shuji
  MOLECULE TYPE: protein FRAGMENT TYPE: internal
   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
  STATE: MA
   CITY: Boston
   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  MEDIUM TYPE: Diskette
   COUNTRY: USA
  STREET:
   ENGTH: 20 amino acids
  Application US/08776971B
   OF SEQUENCES: 140
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  Fujii, Ryo
Fukusumi, Shoji
  Hosoya, Masaki
   Kawamata, Yuji
  Habata, Yugo
  130 Water Street
  97.4%; 5-100.0%; Pr
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  Score 37;
Pred. No.
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Patent No. 6258561
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   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 98: SEQUENCE CHARACTERISTICS:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICANT: Suenaga, Masato
APPLICANT: Morlya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTIOM: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
  FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
   PRIOR APPLICATION DATA:
  SEQUENCE CNARACTERISTICS:
   TELECOMMUNICATION IMPORMATION:
   NAME: Conlin, Davld G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET MUMBER: 48
  APPLICATIOM NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATIOM NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
   STREET: 130 W
  Local Similarity res 7; Conserv
  STRANDEDNESS:
TOPOLOGY: 11
   FILING DATE:
  ZIP: 02109
   STATE: MA
  14 IRPVGRF 20
   TYPE: amino acid
   APPLICATION NUMBER:
  TELEPHOME:
  ADDRESSEE:
   1 IRPVGRF 7
 I IRPVGRF 7
  LENGIN: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
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   130 Water Street
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                              97.4%; Score 37; DB ilarity 100.0%; Pred. No. 0.: Conservative 0; Mismatches
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  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  617-523-3400
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Query Match
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Patent No. 6
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Patent No. 6
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TELEPHONE: 617-523-5400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 40:
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   GENERAL INFORMATION:
   APPLICANT:
  FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORMEY/AGENT INFORMATIOM:
   COMPUTER READABLE FORM:
MEOIUM TYPE: Floppy of COMPUTER: IBM PC com
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                                TITLE OF INVENTION:
   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
   CORRESPONDENCE ADDRESS:
   APPLICANT: Nishimura, Osamu
TITLE OF INVENTIOM: METNOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
   APPLICANT:
                NUMBER OF SEQUENCES:
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
  NAME: Conlin, David G.
REGISTRATIOM NUMBER: 27,
REFERENCE/DOCKET NUMBER:
   COUNTRY: U
ZIP: 02109
   14 IRPVGRF
  14 IRPVGRF 20
   TOPOLOGY:
  STATE:
  STRANDEDNESS:
  APPLICATION NUMBER:
   1 IRPVGRF 7
   CENGTH:
  ADDRESSEE:
   Boston
   5, Application US/09421208 6258561
  0, Application US/09421208
6258561
  amino acid
  ž
   E: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP 130 Water Street
Nishimura, Osamu
VENTION: METHOD OF PRODUCING A 19P2 LIGAND
SEQUENCES: 52
   20 amino acids
  USA
   Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
  Conservative
  linear
  20
   peptide
   Floppy dlsk
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100.0%; Pr/
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  27,026
   48466-342
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Pred. No.
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  0; Indels
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RESULT 12
US-09-105-678A-28
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  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: MPTHICA
  GENERAL INFORMATION:
  TELEFAX: 617-523-6440
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version
CURRENT APPLICATION DATA:
   NAME: CONIIN, David G.
REGISTARTION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
  TITLE OF INVENTION: METHOD OF PRODUCING A 1972 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
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LENGTH: 20 amino acids
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  1 IRPVGRF 7
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14 IRPVGRF 20
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  CITY: Boston
STATE: MA
  FILING DATE:
   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
APPLICATION NUMBER:
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JP 172I18/I997
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Pred. No.
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Best Local Similarity
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  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
  NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   APPLICANT: Moriya, Takeo APPLICANT: Tanaka, Yoko
  OTHER INFORMATION: /product= "Ala or Thr" FEATURE:
   TELEPHONE: 617-523-3400
  FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
   APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
  APPLICANT:
   TITLE OF INVENTION:
  FEATURE:
   MOLECULE TYPE: peptide
ELECOMMUNICATION INFORMATION:
  STREET: 130 |
CITY: Boston
   14 IRPVGRF 20
            NAME: CONIIN, David G. REGISTRATION NUMBER: 27 REFERENCE/DOCKET NUMBER:
  NAME/KEY: Modified-site
LOCATION: 21
COTHER INFORMATION: /product- "Gly-OH or Gly-Arg"
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   TELEPHONE:
  1 IRPVGRF 7
   NAME/KEY: Modified-site
  ENGTH:
  02109
  M
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  USA
  Conservative
  Suenaga, Masato
  linear
   METHOD OF PRODUCING A 1992 LIGAND
  97.4%; Score 37; DB 3; Length 21; 100.0%; Pred. No. 0.12;
  /product-
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  0;
  48466-342
               48466-342
  Mismatches
  "Gly or Ser"
  0; Indels
  0
  Gaps
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   ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-105-678A-35
   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-4I
  RESULT 14
US-09-105-678A-41
  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
APTONNEY/ACENT INFORMATION:
NAME: CON111, DAY16 G
  Query Match 97.4%; Score 37; DB Best Local Similarity 100.0%; Pred. No. 0. Matches 7; Conservative 0; Mismatches
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
   GENERAL INFORMATION:
   TELEPHONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  NAME: CON11n, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
  CORRESPONDENCE ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Toko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
  TYPE: :
  CITY: Boston
STATE: MA
  ZIP: 02109
  COUNTRY:
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Search completed: September 13, 2002, 09:20:59 Job time: 624 sec
   В
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  APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UUN-1998
PRIOR APPLICATION DATA: APPLICATION UMBER: JP 172118/1997
APPLICATION TIMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: CORLIN, DAVId G.
REGISTRATION NUMBER: 27,026
   GENERAL INFORMATION:
  TELEFAX: 617-523-6440
INFORMATION FOR SEO ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
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OM protein protein search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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September 13,

2002, 09:24:03 ;

; Search time 172.41 Seconds
(without alignments)
4.459 Million cell updates/sec

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Searched:

Total number of hits satisfying chosen parameters: 283138

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

PIR\_71:\*
1: plr1:\*
2: plr2:\*
3: plr3:\*
4: plr4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| 29                 | 28     | 27                 | 26                 | 25                | 24                 | 23                 | 22                 | 21                 | 20     | 19                 | 18     | 17       | 16     | 15                | 14     | 13     | 12     | 11     | 10     | 9      | . 00   | 7                  | 6                  | Ů.     | 4-                 | ·                  | 2                  | 1             | ŏ      | Rosult |  |
|--------------------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|----------|--------|-------------------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|---------------|--------|--------|--|
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| 609                | 601    | 559                | 533                | 522               | 501                | 457                | 435                | 4 06               | 393    | 393                | 376    | 374      | 373    | 313               | 292    | 292    | 274    | 198    | 173    | 154    | 107    | 1551               | 612                | 413    | 149                | 511                | 445                | 83            | Length |        |  |
| Ν                  | ພ      | N                  | N                  | N                 | N                  | N                  | N                  | N                  | N      | N                  | N      | N        | N      | 2                 | 2      | N      | N      | N      | N      | N      | N      | N                  | 2                  | N      | N                  | N                  | N                  | N             | DB     |        |  |
| A99946             | H69274 | G83897             | T20015             | н97509            | S66763             | AG2728             | нв3307             | D84898             | T47803 | \$25565            | S40471 | S52645   | T13024 | в98339            | T52257 | T34529 | D96840 | A96520 | S76779 | T34825 | AC3538 | AH3488             | T36210             | D72260 | AH2262             | T40334             | T35893             | JC7607        | ID     |        |  |
| conserved hypothet | _      | uroconase (urocana | hypothetical prote | probable glycosyl | hypothetical prote | polysaccharide bio | probable porin PA2 | probable mitogen-a |        | DNA-directed RNA p | ₩.     | 1-acyl-g |        | integral membrane | 4      |        |        |        |        |        | prot   | gramicidin s blosy | conserved hypothet | H      | hypothetical prote | hypothetical prote | FAD-dependent oxid | lactin-releas | tton   |        |  |

| 45                 | 4                  | £.3                | 42                 | 41                 | ô                  | 39                 | 38                | 37     | 36     | 35                 | 34                 | 33                 | 32                 | 31                 | 30                 |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 29                 | 29                 | 29                 | 29                 | 29                 | 29                 | 29                 | 29                | 29     | 29     | 29                 | 29                 | 29                 | 29                 | 30                 | 30                 |
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| 2                  | N                  | 2                  | N                  | N                  | N                  | N                  | N                 | μ      | N      | N                  | N                  | N                  | N                  | N                  | 2                  |
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| probable two-compo | probable DNA-direc | DNA-directed RNA p | butyryl-CoA dehydr | proline-rich prote | probable proline-r | hypothetical prote | probable membrane | CO     | pr     | ribonuclease C (EC | hypothetical prote | protein ByJ15 - co | hypothetical prote | hypothet1cal prote | probable oxidoredu |

## ALIGNMENTS

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C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.
   C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishil, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, Biochem. Blophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
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  Nakazaki, N.; Shimpo, S.; Suglmoto, M.; Takazawa, M.; Yamsda, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
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submitted to the EMBL Dats Lil
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A:Accession: T40334
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 aminotrsnsfersse, class V - Thermotoga msritims (strain MSB8)
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C;Date: 11-Jun-1999 fsequence_revision 11-Jun-1999 ftext_chan
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   Ş
   R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
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   Nature 399, 323-329, 1999
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melltens A;Reference number: AD3252; PMID:11756688
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulfar, L.
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Althors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocya
  D96840
  A; Molecule type: DNA
A; Residues: 1-198 <STO>
   RESULT
   A;Croas-references:
  A;Status: preliminary
   Matches
   Query Match
Best Local :
  127 VRPVGR 132
   Local Similarity
nes 5; Conserv
  94 KPVGRE
   12
  11
  1 IRPVGR 6
  2 RPVGRF 7
   Conaervative
  99
   Conservative
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  78.9%;
83.3%;
  78.98;
83.3%;
   <u>;</u>
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  Score 30;
Pred. No.
   Score 30; DB
Pred. No. 49;
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   Mlamatches
  NID:g1653715; PIDN:BAA18691.1; to the EMBL Data Library, June
   2
  2
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1996
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31-Mar-2001

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C;Species: Homo sapiens (man)
C;Opte: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52257
R;Fidler, C.; Wainscoat, J.S.; Boultwood, J.
Genomics 56, 134-136, 1999
A;Attle: The human PoP2 gene: identification, sequencing, and mapping to the critical A;Reference number: 226006; MUID:99156866
A;Accession: T52257
A;Accession: T52257
A;Accession: T52257
A;Residues: preliminary; translated from GB/EMBL/DD8J
A;Residues: 1-292 <FIID)
A;Residues: 1-292 <FIID)
A;Cross-references: EMBL:AF053318; PIDM:AAD02685.1
   R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federsplei, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziaii, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talion, Kor, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A;Accession: D96840
  RESULT 14
T52257
   C; Geneti
A; Note:
  hypothetical protein DKFZp434M1515.1 - human C;Speccies: Homo sapiens (man) C;Speccies: Homo sapiens (man) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34529 R;Bioecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, October 1999
  용
  S
   A; Moiecule type: mRNA
A; Residues: 1-292 <BLO>
A; Cross-references: EMBL: AL122045
   A;Reference number: Z21539
A;Accession: T34529
  문
  S
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A; Rcsidues: 1-274 <STO>
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   A;Status: preliminary
  A; Map position: 1
  A; Experimental source: adult testis; clone DKFZp434M1515
   A; Status: preliminary
   Query Match
Best Local Similarity
  Genetics:
  Best Local Similarity
Matches 5; Conserv
  Query Match
Best Locai
  Gene: F23A5.13
   Matches
  48 VRPVCTF 54
  48 VRPIGEF 54
   1 IRPVGRF 7
  DKFZp434M1515.1
  IRPVGRF 7
   Conservative
  Conservative
   GB:AE005173; NID:g6503290; PIDN:AAF14666.1; GSPDB:GN00141
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71.4%;
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Pred. No. 82;
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  DB
77;
   B2,
   2
  <u>ب</u>
  ŗ
   ŗ
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   Gaps
  Gaps
   0
  0
```

```
C;Genetics:
A;Gene: POP2
A;Map position:
   몽
  Ş
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   R;Goodner, B.; Hinkle, G.; Gattung, S.; Mllier, N.; Blanchard, M.; Qurollo, B.; Goldra, A.; Llu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194

A;Accession: B98339
  integrai membrane protein (D85027) [imported] - Agrobacterium tumefaciens (strain
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: B98339
   밁
   Ş
Search completed: Job time: 779 sec
  A; Molecuie type: DMA
A; Residues: 1-313 <KUR>
  A;Gene: AGR_L_3320
   C; Genetics:
  A;Cross-references: GB:AE007870; PIDM:AAK90236.1: PID:915160251; GSPDB:GN00170
  A: Status: preliminary
  Query Match
Best Local Similarity
Matches 5; Conserv
   Query Match
Best Local :
  Matches
   17 IRPIGR 22
   48 VRPIGEF 54
   15
  i IRPVGR 6
   1 IRPVGRF 7
  Similarity
4; Conserv
  Conservative
   Conservative
                September 13,
  78.9%;
   78.9%;
57.1%;
              2002, 09:24:04
   1; Mismatches
  Score 30; DB
Pred. Mo. 82;
2; Mismatches
  Score 30;
Pred. No.
  88;
   2
   <u>ب</u>
  0:
   Length 313;
   Length 292,
  Indela
  0
  <u>.</u>
  Gaps
  Gaps
   B.; Goldm; Markelz,
  0
  0
```

```
OM protein -
protein search, using sw modei
  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

Run on:

September 13, 2002, 09:30:49; Search time 80.21 Seconds (without alignments) 3.862 Million cell updates/sec

Title: Perfect score: Sequence: US-09-446-543A-73\_COPY\_14\_21 38 1 IRPVGREX 8

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Searched:

Total number of hits satisfylng chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| 33 22 28                                                                             | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Result           |
|--------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------|
| 222222                                                                               | 22222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Score            |
| 73.7<br>73.7<br>73.7<br>73.7<br>73.7                                                 | //////////////////////////////////////                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Ouery<br>Match 1 |
| 313<br>376<br>378<br>380<br>382                                                      | 1691<br>1691<br>1691<br>1691<br>1691<br>1691<br>1691<br>1691                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Length DB        |
| 1 METKU<br>1 METKU<br>1 METKU<br>1 METKU<br>1 METKU<br>1 METKU                       | PRRE PRRE PRRE PRRE PRRE PRRE PRRE PRRE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | B ID             |
| YHCI_BACEU YHCI_BACEU WHK4_ARATH METK_BUCAI METK_RICPR METK_RICTY METK_ECOLI         | PRRP_ RAT<br>PRRP_ BOVIN<br>LINC_PSEPA<br>CSD_THEMA<br>CNTE HUMAN<br>MPK5_ARATH<br>MPK5_ARATH<br>MPK5_ARATH<br>MPK5_ARATH<br>MPK5_ARATH<br>MPK5_ARATH<br>MPK5_ARATH<br>MPK5_ARATH<br>MPK5_CHICK<br>AR72_HUMAN<br>AR73_HUMAN<br>AR73_HUMAN<br>AR73_HUMAN<br>AR73_PYRHO<br>CATA_ORYSA<br>CATZ_OUCPE<br>CATA_ORYSA<br>CATZ_CUCPE<br>HEX3_YEAST<br>POLN_HEVBU<br>MAUF_METFL<br>PSTA_RHICO<br>MAUF_METME<br>YAAD_RHISN<br>MURB_LEDLA<br>WROB_LEDLA<br>WROB_LEDLA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                  |
|                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                  |
| י פי ס פי פי ס פי                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ы                |
| = 0 00 01 × 00 0                                                                     | 10000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Description      |
| bacillos su<br>arabidopsis<br>buchnera ap<br>rickettsia<br>rickettsia<br>escherichia | 4662622224486667726666444746274                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | tion             |
| Sia<br>Sia<br>Sia<br>Chia                                                            | is norv sapien domonas domonas sapien ococcu bium m sapien scrofa richia richia sapien sccus sapien sccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien sapien cccus sapien sapien cccus sapien cccus sapien cccus sapien sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien cccus sapien c |                  |

| 45          | 44          | 43          | 42          | 41          | 40          | 39          | 38          | 37          | 36          | 35          | 34          |
|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| 28          | 28          | 28          | 28          | 28          | 28          | 28          | 28          | 28          | 28          | 28          | 28          |
| 73.7        | 73.7        | 73.7        | 73.7        | 73.7        | 73.7        | 73.7        | 73.7        | 73.7        | 73.7        | 73.7        | 73.7        |
| 1057        | 847         | 526         | 512         | 433         | 400         | 399         | 399         | 397         | 396         | 384         | 384         |
| -           | _           | _           | _           | _           | <b>,</b>    | _           | H           | _           | _           | _           | -           |
| ANPA_MOUSE  | MDOH_ECOLI  | CATA_BRARE  | ATPA_RHOBL  | ZUO1_YEAST  | METK_BACSU  | METK_LACLA  | METK_BACHD  | METK_STAAU  | METK_TREPA  | METK_PASKU  | METK_HAEIN  |
| -           | P33137      | •           | _           | _           | _           | _           | 09k7q9      | _           | 083772      | P57897      | P43762      |
| mus musculu | escherichia | brachydanio | rhodopseudo | saccharomyc | bacillus su | lactococcus | bacillus ha | staphylococ | treponema p | pasteurelia | haemophllus |

# AL1GNMENTS

| SQ FITTERS                                                                                                                                                                                                                                                                                                                         | 88888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 4888888                                                                                                                                                                                                                                                                                                      | RRA A A A A                                                                                                                                                                                                                                                                       | RA RA RA RA RA RA RA RA RA RA RA RA RA R                                                                                                                                                                                                                                                                                                                                  | PRRP. AC DT DT DT DT DT DT DT DT DT DT DT DT DT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RESULT |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------|
| HORMORE; AB015418; BAA29026.1; HORMORE; Amidation; Signal; Cleavage on pair of basic residues. SIGNAL 1 21 BY SIMILARITY. PEPTIDE 22 52 PROLACTIN-RELEASING PEPTIDE PRRP31. PEPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20. MOD_RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUP). SEQUENCE 83 AA; 9215 MW; DOC75A264EEE4F29 CRC64; | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch). | Regul. Pept. 83:1-10(1999).  -:- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.  -:- TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus. | PINSUE SPECIFICITY.  PubMed-10498338;  Fujli R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,  Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,  Sumino Y., Fujino M.;  "Tissue distribution of prolactin-releasing peptide (PrRP) and its  receptor.": | SEQUENCE FROM N.A.  TISSUE-Brain; TISSUE-Brain; MEDLINE-9268781: PubMed-9607765; MEDLINE-9268781: PubMed-9607765; Kitada C., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998). | P_RAT STANDARD; PRT; 83 AA.  PR1278;  30-MAY-2000 (Rel. 39, Created)  30-MAY-2000 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  71-MAR-2002 (Rel. 39, Last sequence update)  72-MAR-2002 (Rel. 39, Last sequence update)  73-MAR-2002 (Rel. 39, Last sequence update)  74-MAR-2002 (Rel. 39, Last sequence update)  75-MAR-2002 (Rel. 39, Last sequence update)  76-MAR-2002 (Rel. 39, Last sequence update)  77-MAR-2002 (Rel. 39, Last sequence update)  77-MAR-2002 (Rel. 39, Last sequence update)  78-MAR-2002 (Rel. 39, Last sequence updat | OLT 1  |

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RESULT 2
PRRP_HUMAN
  밁
                                   S
  밁
  Š
  Query Match
Best Local S
Matches 7
   Matches
  Query Match
Best Local
  PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
   PRRP_HUMAN STANDARD; PRT; 87 AA.
P81277;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing peptide PrRP31; Prolactin-releasing Prolac
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  MEDLINE-98268781; PubMed-9607765; Ninuma S., Nabata Y., Fujii R., Kawamata Y., Ri Kitada C., Masuo Y., Asano T., Mathaumoto N., Si Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin-releasing peptide in the brain."; Nature 393;272-276(1998).
   Oleman).
Nomo sapiens (Numan).
Nomo sapiens (Numan).
Nomo sapiens (Numan).
Norta; Metazoa; Chordata;
   EMBL;
   Fujii R., Fukuaumi S.
Sekiguchi M., Kitada
  SIGNAL
   Hormone;
   receptor.
   Sumino Y., Fujino M.; Tissue distribution of prolactin-releasing
   PubMed=10498338;
  TISSUE SPECIFICITY.
   MEDLINE-98268781;
  TISSUE-Brain;
   SEQUENCE FROM N.A.
   releasing peptide PTRP20].
  47
  46
                                   1 IRPVGRF 7
  1 IRPVGRF
  ; AB015419; BAA29027.1; 602663; -
IRPVGRF 53
   IRPVGRF
   Similarity
7; Conserv
  Similarity 100 7; Conservative
   Amidation;
   Fukuaumi S., Nosoya M., M., Kitada C., Kurokawa
   Conservative
   52
  7
   534
231
  ξ
  9639
   Signai.
22
53
53
   97.4%;
  100.0%;
  ž
  Score 37; DB; Pred. No. 0.2 0; Mismatches
  0
   0
  Score 37;
Pred. No.
  PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
AMIDATION (G-54 PROVIDE AMIDE GROUP
229A2F3F50CF981B CRC64;
  BY SIMILARITY.
   Craniata; Vertebrata; Euteieostomi; Catarrhini; Hominidae; Homo.
   Mismatches
   Kawamata Y., I
T., Niahimura
  0.08
   DB 1;
0.21;
   ۳.
  peptide
   Nosoya M., Fu
Sekiguchi M.,
  0
   0
   Habata Y.,
   Length 87
  Length 83;
   Indels
  Indels
  (PrRP)
  Fukusumi
  Prolactin-
   .
:
  Hiouma
   0
  0
   Gapa
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  S
   0
  0
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HARRED BOOKS F
   밁
   5
   Query Match
Best Local S
Matches 7
   LINC_PSEPA STANDARD
P50197;
01-0CT_1996 (Rel. 34, C
01-0CT_1996 (Rel. 34, L
01-0CT_1996 (Rel. 34, L
2,5-dichloro-2,5-cycloh
   _PSEPA
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  Hinuma S., Nabata Y., Fujii R., Kawamata Y., N
Kitada C., Masuo Y., Asano T., Mataumoto H.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
wature 393:272-276(1998).
  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prhormone) [Contains: Prolactin-releasing peptide
  EMBL; AB015417; BAA29025.1; -.

NORMONE; Amidation; Signal; Cleavage on SIGNAL 1 2
PEPTIDE 23 53 PROLACTIN-R PEPTIDE 33 53 PROLACTIN-R PAGENCIAN STORM
   Mammaiia; Eutheria;
Bovidae; Bovinae; Bo
   Pseudomonas paucimobilis Bacteria; Proteobacteria;
   MEDL1NE-98268781;
  TISSUE-Brain;
  SEQUENCE FROM N.A.,
  NCBI_TaxID=9913
  Bos taurus (Bovine)
Eukaryota; Metazoa;
   releasing peptide
SEQUENCE FROM N.A
   47
   5-DDQL
   1 IRPVGRF
  FUNCTION: Stimulates prolactin (PRL) release and regulates expression of prolactin through its receptor GPR10. May stillactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: MEDULLA OBLONGATA AND NYPOTNALAMUS.
   IRPVGRF
   Similarity 7; Conserv
   dehydrogenase)
  86
   Conservative
  Š
   el. 34, Last sequence update)
el. 34, Last annotation updat
,5-cyclohexadiene-1,4-diol de
   STANDARD;
  Bos.
   PubMed-9607765;
  PrRP20]
  97.4%; 50.
100.0%; Pr
  10544
   Chordata; Craniata; Vertebrata; Cetartiodactyla; Ruminantia; Pec
  Chordata;
   AND SEQUENCE
  Created)
  (Sphingomonas paucimobilis).
; alpha subdivision; Sphingomonadaceae;
  ¥
   Score 37;
Pred. No.
   PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35A13B0FA908 CRC64;
  PRT;
  PRT:
   Miamatches
   ဓ္
   23-52.
   update)
  98
   DB 1;
0.24;
   pair of basic
   dehydrogenase
   Sekiguchi M.,
  Nosoya
  (Prolactin-releasing
   ç
  Length
   Pecora;
  X
  Euteleostomi;
   residues
  8
  Fukusumi
   Bovoidea;
  PRRP20
   stimulate
   0
   the
  Gaps
  0
```

```
RESULT 5
     밁
   S
  Haft D. H.; Hickey E.K.; Peterson J.D., Nelson W.C., Ketchum K.A.;
A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
A Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
A Heldelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Tevidence for lateral gene transfer between Archaea and Bacteria from
Tevidence sequence of Thermotoga marilima.";
A Nature 399:323-329(1999)
C. INATURE TO PRODUCE THE REMOVAL OF ELEMENTAL SULFUR AND SELENIUM
C. ATOMS FROM L-CYSTEINE, L-CYSTINE, L-SELENOCYSTEINE, AND L-
SILENOCYSTINE TO PRODUCE L-ALANINE (BY SIMILARITY).
C. SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
C. AMINOTRANSFERASES. CSD SUBFAMILY.
  Query Match
Best Local S
Matches S
  This SWI
   STRAIN-MSD8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
MELSON K.E., Clayton R.A., Gill S.R., Gwinn M.L.,
   Probable cysteine CSD OR TM1371.
   PRINTS; PRO0080; SDRFAMILY.
PROSTIE; PS00061; ADH_SHORT: 1.
AROMATIC hydrocarbons catabollsm; Oxidoreductase:
NP_BIND 9 34 NAD (BY SIMILARITY).
ACT_SITE 154 154 BY SIMILARITY.
SEQUENCE 250 AA; 25644 MW; FFC1CAEB47DF789D CE
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  Thermotoga maritima.
Bacteria; Thermotogales;
  CSD_THEMA
   EMBL: D14595; BAA03444.1; -.
HSSP; P19992; 1HCC:
InterPro, IPR002198; ADH_short.
Pfam; PP00106: adh_short; 1.
   STRAIN=UT26;
MEDLINE=94252977; PubMed=7515041;
   16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
   09XI91;
  SEQUENCE
  NCBI_TaxID=2336;
  209
   н
  Ç
  IRPVGRF
  (SDR) FAMILY.
  5; Conserv
   FROM N.A
   81.6%;
milarity 71.4%;
Conservative
  ٦,
  STANDARD;
   40. Last sequence update)
40. Last annotation update)
desulfurase (EC 4.4.1.-).
   666
  Created)
   Thermotoga.
  Score 31; DB Pred. No. 13: 1; Mismatches
  413
   13:
80
  ₹
  1;
  Length 250;
  CRC64
   Dodson
  NAD.
  Indels
  Bacteria from
  R.J.,
  0
   collaboration
  Caps
  0
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RESULT 6
   S
   SEE DE DE DE COCOCOCO
  밁
   Query Match
Best Local S
Matches 6
  Homo sapiens (Human).
Eukaryota; Metazoa: Cl
Mammalia; Eutheria: Pr
NCBI_TaxID=9606;
   the European Bloinformatics Institute of Biolnformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Towards a catalog of human genes and proteins: analysis of 500 novel complete protein coding human genes. 11:422-435(2001).
-I- FUNCTION: UBIQUITOUS TRANSCRIPTION FACTOR RESET OF PROCESSES. IT IS A COMPONENT OF THE CIN THE CONTROL OF GENE EXPRESSION.
   CNT9_HUMAN STANDARD: PRT; 292 AA.

Q9UFF9: 095709;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
CCR4-NOT transcription complex, subunit 8 (CAF1-ilke
  Lyase: Pyridoxal phosphate; Complete proteome.
BINDING 223 223 PYRIDOXAL PHOSPHATE (BY S
SEQUENCE 413 AA; 46748 MW; 092866323FF984F0 CRC64;
  MEDLINE-21154917; PubMed-11230166;
Wlemann S. Well B., Wellenreuther R., Gassenhuber J., Gl
Mlemann S., Well B., Wellenreuther R., Bauersachs S., Blum
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heu
Wambutt R., Korn B., Klein M., Poustka A.;
  "The
  SEQUENCE FROM N.A.
MEDLINE-99156866: PubMed-10036195;
Fidler C., Wainscoat J.S., Boultwood J.;
  Pfam; PF00266; aminotran_5; 1.
PF00595; AA_TRANSFER_CLASS_5; FALSE_NEG
  EMBL; AE001791; AAD36460.1:
HSSP: P77444; ICON.
TIGR; TM1371; -
  Thls
  Nucleic Acids
   SEQUENCE FROM N.A. MEDLINE=20105461: PubMed=10637334;
  CNOTS OR CALIF OR POP2.
   SEQUENCE FROM
  Timmers H.T.M.;
  Albert T.K.,
   InterPro;
   'Isolation and characterization of human orthologs
  (CALIFP)
  142 IRPSGRF
   Local Similarity
nes 6; Conserv
  1 IRPVGRF
   human POP2 gene: identification, Ical region of the 5g-syndrome."; mics 56:134-136(1999).
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  subunits
  IPR000192; Aminotransf_class_v.
  Conservative
  ~
  Lemaire
  Z.A.
   Res.
   28:809-817(2000)
  Chordata:
Primates:
   <u>*</u>
  8 8
  van
  ..
   Score 31;
Pred. No.
  Berkum
  Craniata; Vertebrata; Euteleostomi; Catarrhinl; Homlnidae; Homo.
  Mismatches
  N.L., Gentz R.,
   sequencing, and mapping to the
   22:
               FACTOR REQUIRED FOR A DIVERSE OF THE CCR4 COMPLEX INVOLVED
   ;
  numan
   ļ,
   Length 413
  sequencing and uman cDNAs.":
  of yeast CCR4-NOT
  Collart M.A.,
   protein)
   SIMILARITY).
   Glassl
   a collaboration -
   0
  ;
;
   Gaps
   0
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THE PROOF OF THE P
  망
  5
   Query Match
Best Local S
Matches 4
  Q39025;
01-NOV-1997
01-NOV-1997
30-MAY-2000
  This SWISS-PROT entry is copyright. It is produced the Ebetween the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest the European Bioinformatics Institutions as long as its content.
   CONFLICT
CONFLICT
SEQUENCE
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   InterPro;
InterPro;
   EMBL;
  use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridipliantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
   ARATH
  *ATMPKS: a gene family of plant MAP kinases in Ar FEBS Lett. 336:440-444(1993).

11- ENZYME REGULATION: ACTIVATED BY TYROSINE AND PHOSEHORYLATION (BY SIMILARITY).

11- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF MAP KINASE SUBFAMILY.
   Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Shinozaki K.;
   Mitogen-activated (AtMPK5).
  HSSP;
  STRAIN-CV. COLUMBIA;
MEDLINE-94109583; PubMed-8282107;
  SEQUENCE FROM N.A
  NCBI_TaxID-3702;
  MPK5_ARATH
   Transcription CONFLICT
  8
  1 IRPVGRF 7
  SUBCELLULAR
SIMILARITY:
  VRPIGEE
  603731;
  AF053318; AAD02685.1; -. AF180476; AAF29830.1; -. AL122045; CAB59181.1; -.
  P27703;
   D21841;
  Similarity
4; Conserv
                    IPR000719; Euk_pkinase.
IPR003527; MAP_kin.
IPR002290; Ser_thr_pkin
  (Rel.
(Rel.
(Rel.
  Conservative
   Ģ.
  1ERK
   BAA04868.1;
   regulation;
   Α
  STANDARD;
  LOCATION: Nuclear.
BELONGS TO THE CAF1 FAMILY.
  32
182
189
33540 »
  35, Created)
35, Last'sequence update)
39, Last annotation update)
protein kinase homolog 5 (EC 2.7.1.-) (MAP kinase
  78.9%;
57.1%;
    Ser_thr_pkinase
se; 1.
   Repressor;
L -> P (
F -> L (
   Ž
  N
  Score
Pred.
   PRT.
   81027A966E51AFDB CRC64;
  Mismatches
  N 30;
   (IN REF.
  376
   26;
   produced through a collaboration
  http://www.isb-sib.ch/announce/
   ۲.
   Usage by
   protein.
  core eudicots; Rosidae;
   ۲
  Arabidopsis thaiiana.";
   Length 292;
   PROTEIN KINASES
   THREONINE
  Indels
  Kamada
  restrictions
   EMBL outstation
   for
  0
  5
   Gaps
   commercial
  8
   5
   0
```

```
RESULT 8
RPA2_THECE
  20
  밁
  Query Match
Best Local s
Matches 5
  Phosphorylation; Phosphorylation; Phosphorylation; 43
NP_BIND 49
BINDING 72
ACT_SITE 169
MOD_RES 201
   01-DEC-1992
01-JUL-1993
16-OCT-2001
EMBL;
   SMART; SM00220; S_TKC; 1.

PROSITE; PS01351; MAPK; 1.

PROSITE; PS00101; PROTEIN_KINASE_ATP;

PROSITE; PS50011; PROTEIN_KINASE_ST;

PROSITE; PS00108; PROTEIN_KINASE_ST;
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   *Rienk H.-P., Schwass V., Ziliig W.;
*Nucleotide sequence of the genes encoding the L3D, Sequency to the server the archaeum Therm Nucleic Acids Res. 19:6047-6047(1991).
-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES
  RPOA2
                                    entities requires a license agreement (See or send an email to license@isb-sib.ch).
   use by non-profit institutions as long modified and this statement is not removed
   STRAIN-OSM 2476;
MEDLINE-92051399; PubMed-1840672;
  celer.":
  "Nucleotide sequence
   RPA2_THECE P29158;
  SEQUENCE OF 195-393
  MEDLINE-93027167; PubMed-1408768;
  STRAIN-OSM 2476;
   SEQUENCE FROM N.A.
  Thermococcus
   DNA-directed
  SEQUENCE
  MOD_RES
  Transferase;
   Nucieic Acids Res. 20:4659-4659(1992).
[2]
  NCBI_TaxID=2264;
  Archaea;
  46 IRPIGR 51
   1 IRPVGR
   the DNA-dependent
   SUBSTRATES.
CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
  SIMILARITY:
  OF ONA INTO RNA USING
   [RNA](N)
 x67313;
x60305;
  Similarity
5; Conserv
   Euryarchaeota;
  s; Serine/threonine-protein k
stion; Multigene family.
43 329 PROTEIN KI
49 57 ATP (BY SI
72 72 72 ATP (BY SI
169 169 BY SIMILAR
201 PHOSPHORYL
  376
   (Rel.
(Rel.
(Rel.
d RNA p
  σ
   Conservative
   celer
 CAA47724.1;
CAA42846.1;
  Š.
  STANDARD;
  BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
   . 24, Created)
. 26, Last sequence update)
. 40, Last annotation update)
polymerase subunit A" (EC 2.7.7.6).
  FROM
  V., Lottspeich F., Zillig W.; of the genes encoding the three largest subunits RNA polymerase from the archaeum Thermococcus
   78.9%;
83.3%;
  43120
   Thermococcales; Thermococcaceae;
   Z.A
  MW;
  THE FOUR RIBONUCLEOSIDE
  ..
   Score 30;
Pred. No.
   PROTEIN KINASE.
AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE KINASE)
(BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE KINASE)
PHOSPHORYLATION (ACTIVATES THE KINASE)
   (BY SIMILARITY)
   PRT;
  0631F9E9654A22EB CRC64;
   Mismatches
   393
  kinase;
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  There are no rest
  B
   3
  http://www.isb-sib.ch/announce/
   1,
   Usage by
  ç
  ATP-binding;
  Length 376
  Thermococcus
  TRIPHOSPHATES
   Indels
   S12 and
   THE TRANSCRIPTION
  Thermococcus
   ö
  0
  celer.";
   1,
  Gaps
  5
  0
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SONDR
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                      9
   RESULT 9
GLG1_RHIME
   밁
  9
  Query Ma
Best Loc
Matches
  Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

A Boistard P., Becker A., Boutry M., Caddeu E., Dreano S., Gloux S.,

A Boistard P., Becker A., Boutry M., Caddeu E., Dreano S., Gloux S.,

A Boistard P., Becker A., Boutry M., Caddeu E., Dreano S., Gloux S.,

A Boistard P., Becker A., Boutry M., Caddeu E., Dreano S., Gallbert P.,

A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

A Renard C., Thebault P., Vandenbol M., Weidner S., Gallbert F.;

"Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

E Sinorhizobium meliloti strain 1021.";

E Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

C -1- RUNCTION: Synthesizes alpha-1.4-glucan chains using ADP-glucose.

C -1- CATALYTIC ACTIVITY: ADP-glucose + {(1,4)-alpha-D-glucosyl}(N) -

C -1- CATALYTIC ACTIVITY: ADP-glucosyl)(N+1).

C -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE

C -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
  Query Ma
Best Loc
Matches
  Glycogon synthase 1 (EC 2.4 synthase 1).
GLGA1 OR R02846 OR SMC03924
Rh1zobium mellioti (Sinozhi Dacterla; Proteobacterla; a
   PIR; S25565; S25565.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF01854; RNA_pol_A2; 1.
Transferase; Transcription; DNA-directed RNA polymerase.
393 AA; 43888 MW; 23BPAD738E10792E CRC64;
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  GLG1_RH:
P58393;
   Complete proteome.
BINDING 15
SEQUENCE 480 AA;
   01-MAR-2002 (Rel.
01-MAR-2002 (Rel.
01-MAR-2002 (Rel.
   EMBL; AL591792; CAC47425.1; -.
Glycogen blosynthesis; Transferase;
  SEQUENCE FROM N.A.
  Rh1zob1aceae;
   MEDLINE-21396507;
   320
ķ
  Local
   Loca 1
  Match
   щ
   Match
                          N
   | IRPVGR 6
KPVGRF
                          RPVGRF 7
   RHIME
   IRPIGR 325
   Similarity
5: Conserv
  Similarity
5; Conserv
60
  Conservative
   Conservative
  Slnorhlzoblum
   STANDARD;
  41, Created)
41, Last sequence update)
41, Last annotation update)
1 (EC 2.4.1.21) (Starch | bacterial
   Pubmed-11481430;
   (Sinorhizobium meliloti).
cterla; alpha subdivision; Rhizobiaceae
  SMC03924.
   15
51408
  83
83
   78.9%;
83.3%;
   Ξ
   ï
   Score 30;
Pred. No.
  Score
Pred.
   ADP-GLUCOSE (BY SIMILARITY).
84C584F6E0564097 CRC64;
   PRT;
   Mlamatches
  ₩ 30
   Glycosyltransferase;
   480
   DB
42;
  DB
   ζ
   ..
   0
  ..
   Length 480;
  Length 393;
   glycogen]
   ADP-glucose
  ..
  0
   S
   Gaps
  Gaps
  ់<u>ម</u>
   0
   0
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RESULT 11
YGC1_ECOLI
ID YGC1_ECOLI
AC 046898;
   RESULT
RL3_PIC
       RANCOCCO CONTRACTOR OF THE CON
   В
   δÃ
   Query Match
Best Local :
   Matches
   _PIG
   RL3_PIG
Q29293;
15-DEC-1998
15-DEC-1998
15-DEC-1998
 SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617: PubMed-9278503;
Blattner F.R., Plunkett G. III, B
Riley M., Collado-Vides J., Glasn
  This SWI
between
  Eukaryota;
Mammalla; I
   16-OCT-2001
16-OCT-2001
16-OCT-2001
  the European Biolnformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles regulzes a license agreement (See http://www.lsb-sib.ch/announce/
   NON_TER
   Escherichia coli.
Bacteria, Proteobacteria,
   SEQUENCE
  Sus scrofa
   NCBI_TaxID-562;
   Escher 1chia
   Hypothetical
   PROSITE; PS00474; |
Rlbosomal protein.
  EMBL; F14648; CAA23176.1;
  or send an emall to license@lsb-slb.ch).
  Evaluation and characterization library: analysis of 839 clones. damm. Genome 7:509-517(1996).
  Interoe A.K., Fredholm
  FISSUE-Small Intestine;
MEDLINE-96327607; PubMed-8672129;
   GCI OR B2757
   111
  fam; PF00297;
  EQUENCE FROM
  roDom; PD001374;
  nterPro;
   Local Similarity
hes 5; Conserv
   10
   1 IRPVGRF 7
  CYTOPLASMIC RIBOSOMES.
SUBCELLULAR LOCATION: C
SIMILARITY: BELONGS TO
  FUNCTION: THE L3 PROTEIN 1S
  SWISS-PROT entry 1s copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
   INPLGRE
  PS00474; RIBOSOMAL_L3:
  Eutheria;
  IPR000597; R1bosomal_L3.
   130
130 AA;
  (P1g).
  (Rel. 37,
(Rel. 37,
(Rel. 37,
   (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation)
protein ygcl precursor.
   Conservative
  M N.A.
Intestine;
  00059/; nll.; 1.; 1.
; Rlbosomal_L3; 1.
.374; Rlbosomal_L3; 1.
  protein
   STANDARD;
   STANDARD;
   130
  Chordata; Cranlata; Vertebrata; Cetartiodactyla; Suina; Suldae;
   14766 MW;
   76.38;
71.48;
  Last sequence up Last annotation L3 (Fragment).
   Created)
  clones.";
  Cytoplasmic.
   gamma
     Glasner
  Davles
   ب.
   Score
Pred.
   PRT;
   PRT;
   ACA48F9D3437A4BF CRC64;
                       Bloch
   subdivision;
   Mismatches
  A COMPONENT
  Ģ,
   29;
  Σ
ch C.A.,
  FAMILY OF RIBOSOMAL PROTEINS
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   update)
   130
   224
  porcine
   update)
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19:
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     Rode
                       Perna
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   Enterobacteriaceae;
   1
  small intestine
   C.K.,
  THE
   Length 130,
                     N.T.
   Indels
  LARGE
  Euteleostom1;
     Mayhew
   Burland V
  SUBUNIT
   0;
  CDNA
  outstation
   Gaps
                     <
   0
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THIR CHICK
ID THIR CHICK
AC P25324;
AC P25324;
AC P25324;
DT 01-MAY-1992
DT 01-MAY-2000
DE Thisulfate
GN TSI
OC Archosauria
QC Archosauria
QC Archosauria
QC Archosauria
QC Archosauria
QC Archosauria
QC FISUE-Live
RP SEQUENCE.
RN [1]
RA KOMANEK!
RT J. Protein
CC -!- FUNCTIO
CC -!- FUNCTIO
CC -!- SUBCELL
CC -!- SUBCELL
CC -!- SUBCELL
CC -!- SUBCELL
CC -!- SUBCELL
CC -!- SUBCELL
CC -!- SUBCELL
CC -!- SUBCELL
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  50
   STEE BERCCCCCCCCCCRRRA
   Query Match
Best Local
   Matches
  01-MAY-1992
01-MAY-1992
30-MAY-2000
  MEDLINE=91113289; PubMed=2275748;
Kohanski R.A., Heinrikson R.L.;
*Primary structure of avian hepatic rhodanese.";
J. Protein Chem. 9:369-377(1990).
-!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES
  the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   Mau B., Shao Y.;
*The Complete genome sequence of Escherichia Science 277:1453-1474(1997).
  SMART; SM00450; RHOD; 2.
PROSITE: PS00380; RHODANESE_I; 1.
PROSITE: PS00683; RHODANESE_2; 1.
  InterPro: IPR001307; Rhodanese.
InterPro: IPR001763; Rhodanese_domain.
Pfam; PF00581; Rhodanese; 2.
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of signiformatics and the EMBL outstation -
  Transferase; Mitochondrion.
   PIR; A37209; A37209.
HSSP; P00586; 1RHS.
   TISSUE-Liver
  NCBI_TaxID=9031;
  Archosauria;
   Gallus gallus (Chicken)
   Thiosulfate
   SEQUENCE
  - 1 - SIMILARITY: BELONGS
   Hypothetical protein;
   25
   2 RPVGRF 7
  CATALYTIC ACTIVITY: Thiosulfate + cyanide - sulfite + thiocyana SUBGUIT: MQNOMER.

SUBCELLULAR LOCATION: Mitochondrial matrix.

TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.

DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR COMPORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER, THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.

SIMILARITY: BELONGS TO THE RHODANESE FAMILY.
  DETOXIFICATION
   FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
  RPTCRF
   AE000359; AAC75799.1; ALT_INIT.
ne; EG13116; ygcI.
  U29579; AAA69267.1; ALT_INIT
  Similarity
5; Conserv
  Metazoa;
  Davis N.W., Kirkpatrick H.A.,
  (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 39, Last annotation update)
(Rel. 39, Last annotation update)
   224 AA;
   Conservative
   ВІ
   Aves;
   STANDARD;
   224
25209
  Neognathae;
  Chordata;
  17
  76.3%;
83.3%;
   Signal; Complete proteome
   ¥
   0
     A DOMAIN.
  Pred.
   HYPOTHETICAL PROTEIN YGCI
1C42CC009B317D68 CRC64;
   Score
   POTENTIAL.
  Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
  core 29; DB
red. No. 33;
Mismatches
   289
  . 33;
  Goeden M.A.,
   ۲.
  coli K-I2.";
   Length 224;
  sulfite + thiocyanate
   Indels
   Rose
  Phasianinae;
  D.J.,
   0
   Gaps
  0
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RESULT 13
AR72_HUMAN
ID AR72_HUMAN
AC 043488; 07574
DT I5-JUL-1999 (
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   S
  E E E E E E E E E B
   Query Match
Best Local S
Matches 5
  use by non-profit institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-corsend an email to license@isb-sib.ch).
  This SWI
between
the Euro
   "Molecular cloning, expression and catalytic activity of a human member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homolof rat aflatoxin BI-aldehyde reductase.";

Blochem. J. 332:21-34(1998).
   I5-JUL-1999 (Rel. 38, Created)
I6-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aflatoxin BI aldehyde reductase I (EC I.-...) (AFBI-AR (Aldoketoreductase 7).
AKR7A2 OR AFAR. OR AKR7.
   ACT_SITE
   Prami C., Savelyeva L., Perri P., Schwab M.;
"Cloning of the human aflatoxin B1-aldehyde reductase gene at IP36.1 in a region frequently altered in human tumor cells.";
Cancer Res. 58:5014-5018(1998).
   SEQUENCE
  Submitted (FEB-2000)
  SEQUENCE FROM N.A.
   MEDLINE-99040634; PubMed-9823300;
  SEQUENCE FROM N.A.
  MEDLINE-98244807; PubMed-9576847;
  SEQUENCE FROM N.A.
  Mammalla; Eutheria;
NCBI_TaxID=9606;
  Eukaryota; Metazoa;
  ACT_SITE
   TISSUE-Brain
  Homo sapiens (Human)
  ACT_SITE
  DOMAIN
  182 RPAGRF 187
  2 RPVGRF
  s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict
  mitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
  SIMILARITY: BELONGS
  SUBCELLULAR LOCATION:
  Similarity
5; Conserv
  289
  ~1
  244
245
  186
  Conservative
  ۶
   STANDARD;
  244
  289
186
  Chordata;
Primates;
  32286
   76.3%;
83.3%;
   TO THE ALDO/KETO REDUCTASE 2 FAMILY.
  Cytopiasmic
  ĭ
  ..
  Score 29;
Pred. No.
   B DOMAIN.

MAY PLAY A ROLE IN SUBSTRATE BI
SIMILARITY).
BY SIMILARITY.
SUBSTRATE (THIOSULFATE) BINDING
(BY SIMILARITY).
   SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).
  Catarrhini;
   Craniata;
  8BFCF671DE0B2BA4 CRC64;
  Mismatches
   330
  DB
42;
   Vertebrata; Euteleostomi;
  Hominidae;
                                     http://www.isb-sib
  ŗ
  Ţ,
  Length 289
  SUBSTRATE BINDING
  Indels
   Homo
   restrictions
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  collaboration -
   outstation
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9
  SQ PT SQ DR
   RESULT 14
AR73_HUMAN
  밁
   Matches
   Query Match
Best Local
   AR73_HUMAN STANDARD
O95154; O9NUC3;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
Aflacoxin BI aldehyde r
  EMBL, AF040639, AAD02195.1; --
EMBL, AL035413, CAB72322.1; --
EMBL, AL035413, CAB72322.1; --
TnterPro, IPR001395; Aldo_ket_red, I.
   ACT_SITE
CONFLICT
SEQUENCE
   CONFLICT
   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
   Oxidoreductase.
ACT_SITE 112
CONFLICT 113
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  Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   EMBL; Y16675; CAA76347.1; -.
EMBL; AL035413; CAB7232I.1;
MIN; 603418; -.
  *cDNA cloning, expression and activity of a second human aflatoxin Bl-metabolizing member of the aldo-keto reductase superfamily,
   MEDLINE-99315412;
   InterPro; IPR001395; Aldo_ket_red
Pfam; PF00248; aldo_ket_red; 1.
    CONFLICT
  PRINTS;
   SEQUENCE
  Carcinogenes1s 20:1215-1223(1999).
  AKR7A3.°;
  Knight L.P., Primiano T.,
   TISSUE-Liver;
   SEQUENCE FROM N.A., AND CHARACTERIZATION
   NCBI_TaxID-9606;
  AKR7A3.
                           CONFLICT
  ACT_SITE
  217 OPVGRF 222
   2 RPVGRP 7
  SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
   EFFECTS OF AFLATOXIN BI.
   Similarity
5; Conserv
   PR00069;
  330 AA;
                             113
51
138
201
   Conservative
   STANDARD;
   ALDKETRUTASE.
  PubMed=10383892;
   112
113
                             113
51
138
201
   36618 MW;
   76.3%;
83.3%;
  Created)
   Last sequence update)
Last annotation update)
reductase 2 (EC 1.-.-)
  Groopman J.D., Kensler T.W., Sutter T.R.;
HYDROGEN-BOND DONOR (PROBABLE).
E -> D (IN REF. 1).
V -> M (IN REF. 1).
A -> ADQSPEGCGSFWGTLGPGAOCCFPS (2).
N -> D (IN REF. 1).
   <u>سر</u>
  Score 29; DB
Pred. No. 48;
1; Mismatches
   HYDROGEN-BOND DONOR (PROBABLE).
A -> T (IN REF. 1).
, 3BBFB7ED0CAF4D54 CRC64;
   PRT;
                              ADQSPEGCGSFWGTLGPGAOCCFPS (IN
  33I
   DB
48;
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    Length 330,

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   Indels
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RESULT 15
RPA2_PYRAB
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  Query Match
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   Query Match
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16-0CT-2001
16-0CT-2001
  RPA2_PYRAB
Q9VII3;
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  *Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
  16-OCT-2001 (Rel. 40, Last sequence update)
18-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase subunit A" (EC 2.7.7.
RPOAZ OR PAB0425.
  Complete proteome. SEQUENCE 397 AA;
   EMBL; AJZ48284; CAB49538.I; -.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF01B54; RNA_pol_A2; 1.
  SEQUENCE FROM STRAIN-ORSAY;
   Transferase; Transcription; DNA-directed RNA polymerase;
  ÷
   Archaea; Euryarchaeota;
NCBI_TaxID-29292;
   Pyrococcus abyssi.
   Heilig R.;
  218 QPVGRF 223
320 VRPIGR 325
                        1 IRPVGR 6
   2 RPVGRF 7
   SUBSTRATES.

CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
   SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN PAMILY.
   OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
  Similarity
5; Conserv
   323
331 AA;
   (Rel. 40,
(Rel. 40,
  Conservative
   Conservative
  2
  STANDARD;
  40, Created)
   323 T
37206 MW;
  44594 MW;
  76.3%;
83.3%;
  76.3%;
66.7%;
  Thermococcales; Thermococcaceae; Pyrococcus.
  <u>ب</u>
  Score 29;
Pred. No.
   Score 29;
Pred. No.
   T -> A (IN REF. 1).
; B9C32C33C7102AB3 CRC64;
  PRT;
  E459658EAE9CI5CB
   Mismatches
   Mismatches
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  sp_bacteria:*
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sp_human:*
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sp_vertebrate:*
   sp_phage: *
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  sp_mamma1:*
  sp_archea: *
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   SUMMARIES
   : Search time 311.85 Seconds (without alignments)
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074584 synechocyst
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  Kormanec J., Bistakova J., Novakova R., Homerova D., Rezuchova "Cloning and characterization of a new polyketide gene cluster streptomyces aureofaciens CCM3239.";
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"Cloning of the catalase gene from Pleurotus sajor-caju.";

"Cloning of the catalase gene from Pleurotus sajor-caju.";

"Submitted (JUL-2000) to the EMBL/GenBank/DOBJ databases.

R EMBL; AF286097; AAK15159.1;

R HSSP; P15202; IA4E.

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01-JUN-1998
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   Satake H., Minakata H., Fujimoto M.,
"Carassius RPamide (C-RP amide).";
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Carassius auratus (Goldfish).
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Actinopterygil; Neopterygil; Teleostel;
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  Pleurotus sajor-caju (Oyster mushroom).
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  Redenbach M., Kieser H.M., Denapaite D., Eichner A
Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic an
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Moi. Microbiol. 21:77-96(1996).

EMBL; AL009204; CAA15814.1; .

InterPro; IPR001575; Oxid_FAD_bind.
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Dacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St. ACBI_TaxID-1902;
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  "A set of ordered cosmids and a detailed genetic a the 8 ktreptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
EMBL: AL049763; CAB42080.1:
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Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RCS 3:109-136(1995). EMBL; D90916; BAA18691.1; -...
  Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi N., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Moi. Microbiol. 21:77-96(1996).
EMBL; ALO21530; CAA16482.1;
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2E2414F099C8B2F7
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Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Chenk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Thoologis A., Davis R.W.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR386997, AAK621432.1; -.
EMBL, AR386997, AAK62442.1; -.
   Arabidopsis thailana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;

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Lenz C.,
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   Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., S
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
*NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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   Gonzalez A., Liu A., Liu K., Sakano H., Koo T., Pham P., Howng B., Chin C., Choi E., Chiou J., Altafi H., Brooks S Conn L., Conway A., Hansen N., Johnson-Hopson C., Khan S. Lam B., Nguyen M., Palm C., Shinn P., Tambunga G., Davis Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopals thaliana chromosome 1 BAC F23A5 sequence.",

"Arabidopals thaliana chromosome 1 BAC F23A5 sequence.",

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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NCE 274 AA; 31200 MW; 6D59588003C6C9CC CRC64;
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1 T., Shibahara
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  Davis R.W.,
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RA AIZAWB K., Ishia K., Yoshino M., Itoh M., Ishii Y.,
RA AIZAWB K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawb K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Firunon M., Aono H., Baldarelli R., Barsh G.,
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hlll J.N., Burr P.C.,
Hslao J., Zismann V., Pal G., Bowman C.L., Fujli C.Y., VanAken S.!
Bowman C.L., Craven B., Utterback T.R., Khalak N., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBA093B11 genCh.";
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EMBL, AC024594; AAK21337.1; "...
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
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Search completed: September 13, 2002, 09:29:26 Job time: 1071 sec

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Perfect score:
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  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   Minimum DB seq length: 0
Maximum DB seq length: 2
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  OM protein -
  Result
   Total number of hits satisfying chosen parameters:
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  Pred. No. is the number of results predicted by chance to have
score greater than or equal to the score of the result being pr
and is derived by analysis of the total score distribution.
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AAW31374
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1.945 Million cell updates/sec
Peptide PrRP8 frag
Murine pituitary-d
Synthetic ligand 1
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Human type G protein
Bovine G protein-
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| 77 10              | 22 18 |                    |                   |                    |                    | 21 21    |          |       |                    |                    |         |         |          |         |      |      |      |                    |                    |                    |      |           |        |      |                    |          |            |         |            |          |           |                |                    |
| AAWJIJBY           |       |                    |                   | AAG6252            |                    | AAB10359 |          |       |                    |                    | AAW3137 |         |          |         |      |      |      |                    |                    |                    |      |           |        |      |                    |          | AAB1036    | AAB1035 |            | AAW95175 |           |                | AAW97234           |
| kat type 6 protein |       | Human CRH releasin | Rat CRH releasing | Bovine CRH releasi | Human oxytocin sec | Ħ        | oxytocir | uitar | Mammalian 19P2 iig | Partial ligand pol | ne G pr | pe G pı | e G prot | c G pro | Ħ    |      |      | Proiactin releasin | CRH releasing prot | Human CRH reieasin | CRH  | ine ČRH r | ligand | gand | 19P2 ligand peptid | n secret | an öxytoci | H       | oxytocin s |          | ituitary- | an type Ilgand | Rat type ilgand po |

# ALIGNMENTS

AAB46955 RESULT

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AAB46955 standard; Protein;

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GPR10; UHR-1: PTRP receptor; prolactin-releasing peptide: pain: central nervous system disorder; autonomic regulation: analgesic; hypotensive: blood pressure.
WPI; 2001-182941/18
                Panula PAJ, Pertovaara A,
  03-AUG-1999; 99US-0365756.
20-MAR-2000; 2000US-0531567.
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                                   (JUVA-) JUVANTIA PHARMA LTD OY
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   Peptide PrRP8 fragment.
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                 Korp1 E;
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RESULT
AAW95178
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   C-terminal fragments of projections regulating sutonomic functions for regulating blood pressure
  Pitultary-derived llgand polypeptide: G-protein coupled orphan receptor; GPR10; UHR-1: modulator; pitultary; central nervous system; pancreas; tlssue: screen; therapeutic; binding: senile dementia: iligand; murine: Alzhelmer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
   the central nervous system, by administering an agonist or antagonist to the receptor; and (5) treating blood pressure, by blocking of receptors of PrRP or its C-terminal fragment GlyileArgProValdlyArgPhe-NH.2 ($2). The products of the invention have analgesic and hypotensive sctivity. (I) is useful for regulating autonomic functions, such as increasing blood pressure. (I) is useful for treating psin, for manufacturing a medicament for regulating blood pressure, and for tresting psin. Agonist snd antagonist of (II) are useful for treating each inflammatory pain and neuropathic psin, for regulating autonomic functions and treating high blood pressure.
   prolactin-releasing peptide (PrRP), referred to as PrRP20 and having a sequence (S1). The invention also describes (i) a therapeutic composition (C1) comprising (I) or s C-termins! fragment of PrRP referred to as PrRP8 and comprising (I) or s C-termins! fragment of PrRP referred to as PrRP8 and comprising a sequence (S2); (2) a diagnostic method based on antisera against PrRP20 for identification of disorders involving the central nervous system, including those associated with pain or autonomic regulation, where specific sntisers against the N-and/or C-terminal domains of PrRP is used to identify alterations in PrRP synthesis or levels; (3) a rst or human receptor encoded by a 1122 nucleotide sequence (S3), fully defined in the specification; (4) treating a person suffering from a disorder regulated by a receptor (II) encoded by a sequence of the control of the specification, located in the specification of the specifi
   AAW95178
  AAW95178 standard; Protein; 10 AA
   Murine pituitary-derived iigand poiypeptide antigenic
   10-MAR-1999
  Sequence
   This invention describes a novel C-terminal fragment (I) of an isolated
   Ciaim 2;
                       (TAKE ) TAKEDA
  28-APR-1997;
  27-APR-1998;
   05-NOV-1998.
   W09849295-A1
   secretion; diabetes; cancer; rheumatold arthritis;
  1 RPYGRE 6
   3 rpvgrf 8
  N
  therapy;
   Page 10; 40pp; English.
  8 AA:
   Conservative
   (first entry)
   transgenic
                          CHEM IND LTD
  97JP-0109974
  98WO-JP01923
   of prolactin-releasing peptide useful functions and in the msnufacture of a
  97.1%; Score 33; DB
100.0%; Pred. No. 6.
tive 0: Mismatches
   animal; epitope
  DB 22; 1
. 6.4e+05;
hes 0;
  Length 8;
   Indels
  epliepsy;
   ep1tope
   medicament
   ior
  0
   vasopressor,
  Gaps
  .0
```

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AAW31400
ID AAW3
  Query Match
Best Local Similarity
""tohes 6; Conserv
   밁
   S
   GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing Ct the ligand polypeptide. The ligand polypeptide, and its fragments, modulate ligand polypeptide. The ligand polypeptide, and its fragments, modulate Ct function of the pitultary, central nervous system, pancress and other Ct tissues and can be used to screen for agents that modulate binding of Ct the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therspectically, CC e.g. to treat senile dementia: Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jskob disease; polsoning by heavy metals or drugs: CC diseases; creutzfeld-Jskob disease; polsoning by heavy metals or drugs: CC operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its muten) are used to corrying the function of the polypeptide-expressing genes, as models of cidease, for drug screening and as source of cell lines. The ligand CC oplypeptide DNA is used as source of cell lines. The ligand CC oplypeptide DNA is used as source of cell ines. The ligand CC related sequences; in receptor-binding assays; for production of Ab and CC transgenic animals. Sequences AMW95174 to AAW95178 represent antiqenic contains.
  RESULT
                18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
   The Invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
  New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pitultary and pancress, and for drug screening
   Synthetic ligsnd 19P2-L31 peptide II.
  transgenic animals. Sequences AAW95174 to AAW95178 represent antigenic epiotpes which can be used for the preparation of anti-ligand polypeptide
   26-DEC-1996:
  W09724436-A2
   Synthetic
  therapeutlo
   modulator;
  06-APR-1998
   AAW31400;
  AAW31400 standard: Peptide; 15 AA
   Sequence
  Disciosure; Page 26: 206pp; English.
   Fukusuml S,
  10-JUL-1997.
  protein-coupled receptor; ligand binding: pharmaceutlcai; iodulator; pituitary: central nervous system: pancreas; prophylactic; herapeutlc agent; antigen.
   (J)
   1 RPVGRF 6
  w
  rpvgrf 10
   10
  Conservative
   Hlnuma
  (first entry)
   ۶
              96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
   96WO-JP03821
   Ś
   97.1%;
  0
   Score 33;
Pred. No.
  Mlsmatches
   DB 20; Length 10; 0.92;
  Ö
  Indels
  0
  Gaps
  naed
```

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S
   This peptide contains the partial C-terminal sequence of the synthetic CC ligand polypeptide 1992-131 which is capable of binding to a GC protein-coupled receptor protein. This peptide is used as an antigen to CC prepare rabbit anti-bovine 1992-131 antibodies which are used in binding CC assays. Pharmaceutical compositions containing this ligand may be used CC as a pituitary function modulator, a central nervous system modulator CC or a pancreatic function modulator. This ligand could have specific CC applications as a prophylactic or therapeutic agent for dementla, CC depression, hyperkinetic syndrome, disturbance of consciousness, anxiety CC syndrome, achizophrenia, trauma, growth hormone secretory disease, CC hyper-and polyphagia, hyperripidaemia, hypercholesterolaemia, containing the secretory disease, CC hyperglyceridaemia, hyperrolactinaemia, dishetes, cancer, pancreatitis, CC spinal disease, Turner's syndrome, neurosis, asthma, rheumatold arthritis, CC spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral CC elecosis, acute myocardial infarction, infertility, spinocerebellar CC end/or oligogaiactia. Asaays can also be developed to screen compounds which are capable of altering the binding activity of the ligand CC which are capable of altering the binding activity of the ligand
  Query Match
Best Local S
Matchea 6
  G protein-coupled receptor; GPCR; hypoovarlanlsm; gonecyst cacogenesis; menopausal syndrome; euthyrold; hypometabolism; lactation; modulation; pituitary adenomatoais; brain tumour; emmeniopathy; autolmmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaiy; Chiarl-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyazoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia; projectin aecretion.
   C-terminal ligand polypeptide derived antigen.
   AAW97230 standard;
  Ligand peptide for G protein-coupled receptor - acts function in the central nervous ayatem, pancreas and
   23-JUN-1997;
                               22-JUN-1998;
   WO9858962-A1
  06-MAY-1999
  Sequence
  Example 43; Page 151; 258pp; English.
   WPI; 1997-363672/33
  30-DEC-1998
  (TAKE ) TAKEDA CHEM 1ND
   Local Similarity
  10 rpvgrf 15
   1 RPVGRF 6
  -
  =
=
  ç
   Y, Kltada
   Fukuaumi S,
  15
   97.1%; Score 33; DB
llarity 100.0%; Pred. No. 1.
Conservative 0; Mismatches
  (first entry)
  A,
 97JP-0165437
                               98WO-JP02765
   Peptlde;
  ü
   Haba ta
   ĸ,
   Hinuma
   DB 18; Length 15;
1.4;
  ço
  Новоув М;
   0
  Indels
  by modulating pituitary gland
   0
   Gapa
   0
문
  Q
   XXX
```

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AAY49293
   RESULT
  AAW97229-31 represent a ligand polypeptide derived fragmenta used to produce antibodies. The specification describes an agent for modulating product antibodies. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a mait, for a grotein-coupled receptor (GPCR) protein. The agenta for promoting prolactin secretion can be used for treating or preventing thypocovarianism, gonecyst cacegenesis, menepausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodialac. The agents for inhibiting prolactin accretion can be used for treating or preventing pituitary adenomatosis, infertility, impotence, amenorabes, galactorabes, acromegaly, brain tumour, emmenlopathy, autolamune disease, prolactionma, charlest can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing contractions, hydatid mode, irruption mode, abortion, unthrifty absorbed as contraceptives. The agents for modulating placental function can be used for treating or preventing.
  Query Match
Best Local S
Matchea 6
  Use of G protein-coupled receptor ligands - for modulating prolactin accretion or placental function, e.g. for treating menopausal syndrome, tumoura, autoimmune disease or abnormal pregnancy
   Monoclonal antibody; 1992 ligand; diagnosis; projectin secretion; pitultary; regulatory mechanism; central nervous system; pancreat
   Sequence
  WPI; 1999-105614/09
(TAKE ) TAKEDA CHEM IND LTD
                                    21-MAY-1998;
  Homo sapiens
   AAY49293;
  AAY49293 standard; peptide;
  (TAKE ) TAKEDA CHEM IND LTD
  25-NOV-1999
   W09960112-A1
   Key
Modifled-site
   19P2 11gand
  22-FEB-2000
   Example 43;
   20-MAY-1999;
  etua, abnormai saccharometabolism, abnormal lipidmetabolism or
  10 rpvgrf 15
  Locai Similarity
ea 6; Conserv
   1 RPVGRF 6
   UI
   Hinuma S,
   15
  97.1%; Score 33; ilarity 100.0%; Pred. No. Conservative 0; Miamatc
   Page 123; 241pp; English.
   peptide fragment.
  (first entry)
   Ą
                                       98JP-0140293
   99WO-лР02650
   Location/Qualiflers
  /note= "C-terminal amide"
   Kawamata Y,
  15
   Mataumoto
   DB 20; Length 15;
   Ή;
  0
  0
  Gaps
```

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RESULT
AAY49295
õ
  용
   Query Match
Best Local
  Matches
  The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central narvous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative Sequences AAY49290-302 represent peptide fragments of the 1992 ligand.
                           New monoclonal antibodies, u
studying diseases related to
   New monoclonal antibodies, studying diseases related
        Disclosure;
  21-MAY-1998;
  20-MAY-1999;
  25-NOV-1999.
  909960112-A1
   Modified-site
   Modified-site
   Modified-site
   Homo Sapiens
  pituitary;
   Monoclonal
  19P2 ligand peptide fragment.
   22-FEB-2000 (first entry)
  AAY49295 standard; peptide; 15
   Scquence
  Disclosure; Page 26; 73pp; Japanese.
   Matsumoto
   (TAKE ) TAKEDA CHEM IND
   1 RPVGRF 6
||||||
10 rpvgrf 15
  hes 6; Conserv
  10
  σ
   2000-039381/03
   Ħ,
  15
  regulatory
  antibody;
       Page
  Conservative
  5
   Kitada
  Kitada
  98JP-0140293
  99WO-JP02650
   /note-
15
   /note-
   /note-
  Location/Qualifiers
        26;
  Ç
   19P2 ligand; diagnosis; prolactin secretion;
y mechanism; central nervous system; pancreatic.
   97.1%;
  ņ
     73pp; Japanese
  "acetylated Tyr".
  "C-terminal amide"
   "N-terminal acetylation"
  LTD.
  Hinuma
   Hinuma
   6
                           useful in dlagnosis, o ligand abnormality
  useful in diagnosis,
o ligand abnormality
  0
   Score 33;
Pred. No.
  Ā
  ŝ
  S
  Mismatches
   L B
   21;
  0
   Length 15;
                                     85
   as drugs
  Indels
                                      drugs
  its derivative.
                                      and
  and
  0
                                      ij
  'n
  Gaps
   0
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RESULT
AAY49296
នននិន្ននិន្ននិង
  밁
   Ş
   Matches
   Query Match
Best Local
                    The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pliuitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
  The invention provides a monocional antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunous ray can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences ANY49290-302 represent peptide fragments of the 19P2 ligand.
  WPI;
   AAY49296 standard; peptide; 15
   Sequence
  Disclosure; Page 27; 73pp; Japanese.
  New monoclonal antibodies,
  Matsumoto H,
   21-MAY-1998;
  25-NOV-1999.
  W09960112-A1
   Homo sapiens
   pituitary;
  Monoclonal
   19P2 ligand
  AAY49296;
  (TAKE ) TAKEDA CHEM IND
   20-MAY-1999;
  Modified-site
  22-FEB-2000
  1 RPVGRF 6
   10 rpvgrf 15
  Local Similarity
  2000-039381/03
   6
   diseases related
  antibody; 19P2 iigand; diagnosis; prolactin secretion;
regulatory mechanism; central nervous system; pancreatic.
   15 AA;
   pept1de
  Conservative
   (first entry)
  Kitada
   98JP-0140293
  99WO-JP02650
   Location/Qualifiers
  /note-
  97.1%; 500
100.0%; Pr
   fragment.
  ú
   "C-terminal amide"
   LTD.
  Hinuma
  , useful in diagnosis,
to iigand abnormality
   Score 33;
Pred. No.
   ζ
  Ç
   Mismatches
   DB 2:
   21;
  <u>.</u>
   Length
  . 8
   Indels
  drugs
                                       its derivative
  and
  0
  b
  Gaps
  0
```

Sequence

S

밁 20

100.0%;

Pred. No. 1.8:

0

ij

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RESULT
AAW31394
 Ş
   밁
  This sequence represents a peptide fragment from a novel human type CC ligand polypoptide corresponding to amino acid residues 34 to 53 of the CS sequence represented in ANW31390 and is used in an assay to monitor CC ligand binding to the G protein-coupied receptor protein. Pharmaceutical C compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapcutic agent for dementia, depression, hyperkinetic prophylactic or therapcutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schicophrenia, trauma, growth hormone secretoxy disease, hyper and polyphagia, con hyperiolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperiolactinaemia, diabetes, cancer, pancreatitis, renal disease, concurrer's syndrome, neurosis, asthum, rheumatoid arthritis spinal injury, transient brain ischacmia, epilepsy, amylotrophic laters sclerosis, acute myocardiai infarction, infertility, spinocerebeilar degeneration, conception of altering the binding activity of the ligand affecting activity activities activity.
   Query Match
Best Local S
Matches 6
   18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
  G protein-coupled receptor; ligand binding; pharmaceutical;
  Claim
   Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
  WPI; 1997-363672/33.
N-PSDB; AAV02431.
  10-JUL-1997
   W09724436-A2
  Homo sapiens
   therapeutic
  modulator;
   Human type G
  06-APR-1998
   AAW31394;
  AAW31394 standard;
Sequence
  Kawamata
  Fujii R,
   (TAKE ) TAKEDA
  Local Similarity
   10
  1 RPVGRF 6
   00
   rpvgrf 15
   6
  Page 185;
  Fukusumi S,
                                   altering of the G
  pituitary;
20
   agent.
   Conservative
  Kitada
   protein-coupled
  (first
  96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
  CHEK
   96WO-JP03821
  258pp; English.
  Peptide;
   HND
  ü
                                   protein-coupled
  97.1%;
100.0%;
  central nervous system; pancreas; prophylactic;
  Habata
   0
  20
   Score 33;
Pred. No.
   receptor ligand fragment
  K
   Mismatches
  Hinuma
                                   receptor protein.
  DB 21;
  Ś
  Hosoys M;
   0
  Length 15;
   Indels
   0
   Gaps
   0
```

Query Match

97

.1%

Score

ω ω

밂

18

Length

20

Query Match Best Local Similarity

97.1%;

Score :

. No.

DB 18;

Length 20;

```
RESULT
AAW31387
                                  This sequence represents a peptide fragment from a novel rat type CC ligand polypeptide corresponding to amino acid residues 33 to 52 of the CC sequence represented in AAW31383 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function CC modulator. This sigand could have specific applications as a modulator. This sigand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic Syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, CC trauma, growth hormone secretory disease, hyper- and polyphagia, CC hyperlipidaemia, hypercholesterolaemia, hypergiycerideemia, hyperprolactinaemia, diabetes, cancer, pencrentitis, renal disease, CC Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, caute myocardial infarction, infertility, spinocerebeilar degeneration, colisopalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting CC activation of the G protein-coupled receptor protein.
   Best Local Similarity
Matches 6; Conserv
   18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
  G protein-coupled receptor; ligand binding; pharmaceuticai; modulator; pituitary; central nervous system; pancreas; pro
   WPI; 1997-363672,
N-PSDB; AAV02424.
   AAW31387 standard; Peptide;
Sequence
   Claim 2; Page 180;
  Fujii R,
  W09724436-A2
   Rat sp.
  Rst type G
  06-APR-1998
   AAW31387;
   function in
   Ligand peptide for G protein-coupled receptor - acts
   Kswamata Y,
   (TAKE ) TAKEDA CHEM IND LTD
   26-DEC-1996;
  10-JUL-1997.
  therapeutic
   15 rpvgrf 20
  1 RPVGRF 6
  9
  Fukusumi S,
20
  protein-coupled
  the central nervous system,
   agent.
  Conservative
   (first entry)
  Kitada
Š
   96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
  96WO-JP03821
   258pp; English.
  ü
  central nervous system; pancreas; prophylactic;
  Habata
   receptor iigand fragment
   20 AA
   0;
  K
   Mismatches
  Hinuma S,
  pancreas
  нозоуа
   0
   and
   Indels
   by modulating pituitary gland
   0
  Gaps
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8
  å
   CC This sequence represents a peptide fragment of a novel bovine pituitary CC derived ligand corresponding to amino acid residues 34 to 53 of the CS sequence in AAM3136B and is used in an assay to monitor ligand binding CC to the G protein-coupled receptor protein. Pharmaceutical compositions CC containing this ligand may be used as a pituitary function modulator, a CC central nervous system modulator or a pancreatic function modulator. CC This ligand could have specific applications as a prophylactic or CC therapeutic agent for dementia, depression, hyperkinetic syndrome, CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, CC functiones secretory disease, hyper-and polyphagia, CC hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia, hypercrolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, CC funcer's syndrome, neurosis, rheumatoid arthritis, spinal injury, CC transient brain ischaemia, amylotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, CC trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertiiity CC and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
   RESULT 10
      Bost Local Similarity
Matches 6; Conserv
  Matches
                                       Query Match
  18-SEP-1996;
28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
  G protein-coupled receptor; ligand binding; pharmaccutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
   Sequence
   Claim
   Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
   N-PSDB; AAV02397.
   26-DEC-1996;
  10-JUL-1997
   H09724436-A2
   Bovine G
  06-APR-1998 (first entry)
   AAW31374;
  AAW31374 standard; Peptide;
   (TAKE
   15
  1 RPVGRF 6
   ||||||
|| rpvgrf 20
  2; Page 161; 258pp; English
   ) TAKEDA CHEM IND LTD
   6;
  protein-coupled receptor ligand peptide fragment 4.
   Fukusumi S,
Y, Kitada C;
   ೪
   Conservative
   ξ
  96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
   96WO-JP03821.
97.1%; 5c.
100.0%; Pr
  Habata Y,
                      Score 33; pred. No.
  20
   0
   Mismatches
  Hinuma
                                       DB 18; Length 20;
                      1.8;
  ķ
  Hosoya M;
   ç,
   Indels
   0
   Gaps
   0
```

Conservative

Mismatches

0;

Indels

0

Gaps

0

Ouery Match Best Local S Matches 6

Similarity 6; Conserv

Conservative

97.1%; Score 33; 100.0%; Pred. No. tive 0; Mismatc

1.8; Ö 20;

Length 20; Indels

Mismatches

0

0

0;

Sequence

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RESULT I
AAW97232
ID AAW9
당
   Ş
                              The present sequence represents a bovine pituitary-derived ligand CC fragment. It is used in the course of the invention. The specification CC describes an agent for modulating prolactin secretion which comprises a CC ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) CC protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocovarianism, genecyst cacogenesis, menopausal Syndrome, euthyroid or hypometabolism. They can by used for promoting Lactation in a domestic mammal and as an aphrodisiac. The agents for CI lactation in a domestic mammal and as an aphrodisiac. The agents for CI clasting prolactin secretion can be used for treating or preventing CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, CC probes-Albright syndrome, lymphoma, Argonz-del Castilo syndrome, CC acromegaly, Chiari-Fronmel syndrome, Argonz-del Castilo syndrome, CC robbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. Tha agents for modulating placental function can be used for treating or praventing CC choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abortion, abortion, unthrifty fetus,
  menopausal syndrome; euthyroid; hypometabolism; lactation; pltultary adenomatosis; brain tumour; emmeniopathy; autolmmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid moie; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia.
  Use of G protein-coupled receptor ligands - for modulating pr
secretion or placental function, e.g. for treating menopausal
  G protein-coupled receptor;
  AAW97232 standard; peptide; 20
   Ciaim 3; Page 136; 241pp; English
   syndrome, tumours, autoimmune disease or abnormai pregnancy
  WPI; 1999-105614/09.
   Fujii R, Hinuma S,
  W09858962-AL
  Bovine pituitary-derived ligand; modulation; projectin secretion;
   06-MAY-1999
  (TAKE ) TAKEDA CHEM IND LTD.
  23-JUN-1997;
   22-JUN-1998;
   30-DEC-1998.
   Bos sp.
   Bovine pitultary-derived ligand polypeptide fragment
  1 RPVGRF 6
||||||
15 rpvgrf 20
   (first entry)
   98WO-JP02765
   Kawamata
  GPCR; hypoovarianism; gonecyst cacogenesis;
  ۲
   Matsumoto
  for modulating prolactin
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밁 S

1 RPVGRF 6 |||||| 15 rpvgrf 20

```
Is used in the course of the invention. The specification describes

an agent for modulating prolactin secretion which comprises a

ligand polypeptide or a salt, for a g protein-coupled receptor (GPCR)

crotein. The agents for promoting prolactin secretion can be used for

treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal

syndrome, enthyroid or hypometabolism. They can by used for promoting

cut treating or preventing hypometabolism. They can by used for promoting

cut actation in a domestic mammal and as an aphrodisiac. The agents for

cut inhibiting prolactin secretion can be used for treating or preventing

cut pituitary adenomatosis. brain tumour, emmeniopathy, autoimmune disease,

prolactinoma, infertility, impotence, amenorrhea, galactorrhea,

cut cromegaly, Chiari-Frommel syndrome, Argonz-dei Castilio syndrome,

cut cromegaly, Chiari-Frommel syndrome, Sheehan syndrome or dyszoospermia.

cut for inhibitory agents can also be used as contraceptives. The agents for

cut modulating placental function can be used for treating or preventing

cut choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

cut approximate the contraction of the contracti
  Query Match
Best Local S
Matches 6
   Rat type ligand; modulation; prolactin secretion; gonecyst cacogenesis; gorotein-coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid: hypometabolism: lactation; pituitary adenomatosis; brain tumour: emmenlopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; kargonz-del Castilo syndrome; Forbea-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthilfty fetus; abnormal saccharometabolism;
  Use of G protein-coupled receptor ligands - for modulating projectin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
   AAW97234 standard; peptide;
  The present sequence represents a rat type ligand fragment. is used in the course of the invention. The specification d
  30-DEC-1998
   WD9858962-A1.
  abnormal lipidmetabolism; oxytocia.
   Rat type ligand
  06-MAY-1999
   Sequence
   Claim
   WPI; 1999-105614/09
  Fujii R,
  22-JUN-1998;
  12
   w
     Similarity
6; Conser
  TAKEDA CHEM IND
   Page 154; 241pp; English.
  Hinuma S,
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97.1%; Score 33; DB Llarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
  (first entry)
   $
   97JP-0165437
  98WO-JP02765
  polypeptide fragment.
  Kawamata
   20
   Y,
   ۶
  Matsumoto
                           DB 20
  20; Length 20;
     0
  0;
  Gaps
0
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Query Match Best Local Similarity Watches 6: Conserve

97.1%; Score 33; llarity 100.0%; Pred. No. Conservative 0; Mismatc

Mismatches

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В 1.8; 20;

Length 20; Indeis

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RESULT J
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                         The present sequence represents a human type ligand fragment. It

CC is used in the course of the invention. The specification describes

CC an agent for modulating prolactin secretion which comprises a

CC ligand polypeptide or a salt, for a G protein coupled receptor (GPCR)

CC protein. The agents for promoting prolactin secretion can be used for

CC treating or preventing hypoovarianism, gonecyst cacogenesis, menopausal

CC syndrome, euthyroid or hypometabolism. They can by used for promoting

CC lactation in a domestic mammal and as an aphrodistac. The agents for

CC inhibiting prolactin secretion can be used for treating or preventing

CC pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,

CC protes-Albright syndrome, lymphome, Argonz del Castilo syndrome,

CC rorbes-Albright syndrome, lymphome, Argonz del Castilo syndrome,

CC modulating placental function can be used for treating or preventing

CC chorlocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,

CC abnormal saccharometabolism, abnormal ilpidmetabolism or oxytocia.
   G protein-coupled receptor; GPCR; hypocovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyscoospormia; contraceptive; placental function; choriocarcinoma; hydatid mole; abortion; unthrifty fetus; abnormal saccharometabolism; oxytocia.
   Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
  Claim 3; Page 166: 241pp; English.
   06-MAY-1999
   AAW97236 standard;
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  (TAKE ) TAKEDA CHEM
   23-JUN-1997:
  22-JUN-1998;
   30-DEC-1998
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  Homo sapiens
  Rat type ligand: modulation; prolactin secretion;
   Human type ligand
  15
  13
  i RPVGRF
  rpvgrf 20
  Hinuma S,
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   (first entry)
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   97JP-0165437
  98WO-JP02765
  polypeptide fragment.
   peptide;
  IND LTD
  Kawamata
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  Matsumoto
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AAW95191
which is a ligand for the G-protein coupled orphan receptor designated CC GPRIO (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding but are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the CC polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; chizophrenia; disorders of growth hormone secretion; cancer; CC operative nutritional status and as vasopressor. Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC polypeptide DNA is used as a source of cell lines. The ligand CC related sequences; in receptor-binding assays; for production of Ab and continued to the colon of Ab and continued to the colon of Ab and colon of the colon of
  8
   New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
   Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
  GPR10; UHR-1; modulator; pitultary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senlle dementia; ligand; murine; Alzhelmer's disease; Parkinson's disease; Huntington's disease; drug;
  AAW95191 standard; peptide; 20 AA
   The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated
  Example 19; Page 151; 206pp; English
  (TAKE ) TAKEDA CHEM IND
  28-APR-1997;
   27-APR-1998;
  05-NOV-1998.
  WO9849295-A1
   gene therapy; transgenic animal; bowine
   Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor,
   Bovine pituitary-derived
  10-MAR-1999
   15 rpvgrf 20
  14
   1 RPVGRF
  1999-009423/01
   ; in drug development; for gene therapy and to develop transgenic The present sequence represents a bovine genome-derived ligand ide fragment which is similar to the murine ligand-polypeptide.
  Hinuma
   (first entry)
  97JP-0109974
   98WO-JP01923
   ligand polypeptlde fragment
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Query Match

97 .18;

Score 33;

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Length

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Sequence

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AAW95175
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   The invention relates to a murine pituitary-derived ligand polypeptide CC which is a ligand for the G-protein coupled orphan receptor designated CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing CC the ligand polypeptide encoding DNA are used to produce a recombinant CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate CC function of the pituitary, central nervous system, pancreas and other CC tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a CC sample and to raise antibodies. They may also be used therapeutically, CC e.g. to treat senile dementia; Alzhalmer's, Parkinson's or Huntington's CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; CC diseases; contributed and as vasopressor, Transgenic animals CC carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of CC disease, for drug screening and as source of cell lines. The ligand CC related sequences; in receptor-binding assays; for production of Ab and CC related sequences; in receptor-binding assays; for production of Ab and CC antisera; in drug development; for gene therapy and to develop captor before which can be used for the preparation of anti-ligand polypeptide.

CC captibodes which can be used for the preparation of anti-ligand polypeptide.
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   Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor (GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; muring; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeid-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopress
  New polypeptide ligand for orphan G protein coupled receptors for treating disorders of central nervous system, pituitary ar pancreas, and for drug screening
  gene therapy; transgenic animal; epitope.
   Disclosure; Page 26;
   WPI; 1999-009423/01
  Fukusumi S, Hinuma
   28-APR-1997;
  27-APR-1998;
   Murine pituitary-derived ligand polypeptide antigenic epitope
  10-MAR-1999
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| US-09-421-208-8   | 421-208           | US-08-776-971-97  | 776-97            | US-08-776-971-47  | US-08-776-971-5   | US-09-172-353-4   | US-09-105-678A-43 | US-09-105-678A-37 | US-09-105-678A-31 | US-09-105-678A-9 | US-09-105-678A-8  | US-09-105-678A-7  | US-09-421-208-48 | US-09-421-208-42  | US-09-421-208-36 | US-08-776-971-73 | US-08-776-971-66  |
| Sequence 8, Appli | Sequence 7, Appli | Sequence 97, Appl | Sequence 61, Appl | Sequence 47, Appl | Sequence 5, Appli | Sequence 4, Appli |                   | Sequence 37, Appl | Sequence 31, App1 |                  | Sequence 0, Appli | Sequence 7, Appli | •                | Sequence 42, Appl |                  | •                | Sequence 66, Appl |

# ALIGNMENTS

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                  INFORMATION FOR SEQ
  CONPUTER READABLE FORM:

NEDIUM TYPE: Diskette
COMPUTER: IEM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-197
CLASSIFICATION: <UNknown>
              NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 93:
  APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996 ATTORNEY/AGENT INFORMATION:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, B
STREET: 130 Water
   PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS
  APPLICANT:
  APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
  ZIP: 02109
   COUNTRY:
  STATE: MA
   CITY: Boston
   Application US/08776971B
  Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Nasaki
   Fujii, Ryo
  EE: DIKE, BRONSTEIN,
130 Water Street
   USA
   for Windows Version
   ROBERTS & CUSHMAN, LLP
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; FRAGMENT TYPE: Internal
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US-08-776-971-93
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  Sequence 34, Application US/09105678A Patent No. 6103882
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Best Locai Similarity
Matches 6; Conserv
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATE: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION:
  APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   TELEPHONE: 617-523-3400
   MOLECULE TYPE: peptide
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  PPLICANT:
   Local Similarity hes 6; Conserv
   NAME: Conlin, David G.
REGISTATION NUMBER: 27,026
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   i RPVGRF 6
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  LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
  TOPOLOGY: linear
  130 Water Street
  20 amino acids
   USA
  Suenaga, Masato
   Conservative
   Conservative
   97.1%; Score 33; DB 3;
100.0%; Pred. No. 0.52;
Live 0; Mismatches
   97.1%; Score 33; 100.0%; Pred. No.
   0
   Mismatches
   DB 4;
   0; Indels
   Length 15,
  Length 20;
   Indels
   0
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   Gaps
   Gaps
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STRANDEDNESS:
TOPOLOGY: iin
MOLECULE TYPE:
US-09-105-678A-40
   밁
  US-09-105-678A-40
   US-09-105-678A-46
   Sequence 40,
Patent No. 61
GENERAL INFO
   Sequence 46, Application US/09105678A Patent No. 6103882
   Query Match
Best Local Similarity
Matches 6; Conserv
  APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION DATA: JP 172118/1997 FILING DATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: CONLIN, DAVId G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342
   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
   GENERAL INFORMATION:
   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING
NUMBER OF SEQUENCES: 52
   ZIP: 02109
COMPUTER READABLE FORM:
  APPLICANT: Tanaka, .....
APPLICANT: Nishimura, Osamu
APPLICANT: Nishimura, Osamu
TTTT OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
   CORRESPONDENCE ADDRESS:
   SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION DATA:
   NUMBER OF SEQUENCES: 5
   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
  · i RPVGRF 6
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
   TELEPHONE: 617-523-6440
   15 RPVGRF
   TYPE: amino acids
  MEDIOM TYPE:
  COUNTRY: USA
ZIP: 02109
   STREET: 130 N
                                  CITY:
  STREET:
   ADDRESSEE:
   ADDRESSEE:
COUNTRY:
   INFORMATION:
             Boston
: MA
  6103882
   š
  Application US/09105678A
  130 Water Street
  130 Water Street
US.A
   20
   Conservative
   iinear
  DIKE, BRONSTEIN,
  DIKE, BRONSTEIN,
  Floppy disk
  peptide
   97.1%; Score 33; DB 3;
100.0%; Pred. No. 0.52;
Live 0; Mismatches
  40:
   ROBERTS & CUSHMAN, LLF
   ROBERTS & CUSHMAN, LLI
  A 19P2 LIGAND
   ç
  Length 20;
   Indels
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   Gaps
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US-08-776-971-8
; Sequence 8, Application
; Patent No. 6228984
; GENERAL INFORMATION:
  밁
  RESULT
   US-09-105-678A-46
  NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3440
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 46:
  Matches
   Query Match
Best Local Similarity
   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
   APPLICATION NUMBER: JP 1
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA:
   TOPOLOGY: 11
   MEDIUM TYPE:
COMPUTER: I
  15 RPVGRF 20
   STRANDEDNESS:
  1 RPVGRF 6
  LENGTH:
  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SQFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: D1skette
   HOSOYA, MASAKI
Fujii, Ryo
Fukuumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND DSE
NUMBER OF SEQUENCES: 140
  APPLICANT: Hinuma, Shuji
   amino acid
  Application US/0877697IB
   READABLE FORM:
  COUNTRY: USA
  STATE: MA
   CITY: Boston
  Conservative
   iinear
   peptide
   Floppy disk
  labata, Yugo
Kawamata, Yuji
   97.1%;
  JP 172118/1997
   0.
   Score 33;
Pred. No.
  48466-342
  Mismatches
   Version #1.30
   DB 3;
   0
   Length 20;
   Indels
   0
   Gaps
   0
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  Ş
   US-08-776-971-50
  US-08-776-97I-8
   Sequence 50, Applicati
Patent No. 6228984
GENERAL INFORMATION:
  Query Match
Best Local (
  Matches
   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3440
INFORMATION FOR SEQ ID NO: 8:
                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/76,971B
FILING DATE: 06-Feb-1997
CIASSIFICATION INMBER: PCT/JP96/0382I
FAPPLICATION NUMBER: PCT/JP96/0382I
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
PTING DATE: 15-MAR-1996
  APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
   ||||||
15 RPVGRF 20
  1 RPVGRF 6
  Local Similarity es 6; Conserv
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
   FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 8:
   MOLECULE TYPE: FRAGMENT TYPE:
   SEQUENCE CHARACTERISTICS:
   CITY: Boston
STATE: MA
   LENGTH: 20 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
   ZIP: 02109
   STREET: 130 Water Street
   COUNTRY:
   Application US/08776971B
                           PPLICATION NUMBER:
  Conservative
  Hinuma, Shuji
  Kawamata, Yuji
  Habata, Yugo
   20 amino acids
   USA
   protein
  97.1%; Score 33; DB 4;
100.0%; Pred. No. 0.52;
Live 0; Mismatches
NUMBER: JP 8/211805
I2-ADG-1996
  Masaki
  47176
  Length 20;
  ..
  Gaps
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DB 4:

0; Indeis Length 20;

9

Gaps

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Query Match
Best Local Similarity
6; Conserve
  밁
  ş
   ; SEQUENCE DESCRIPTION: SEQ ID NO: 50: US-08-776-971-50
   3-08-776-971-64
Sequence 64, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
                               COMPUTER: IDM COMPATIBLE
COMPUTER: IDM COMPATIBLE
OPENATING SYSTEM: DOS
SOFTWARE: RASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,9713
FILING DATE: 06-Feb-1997
CLASSIFICATION VINDER: US/08/776,9713
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 11-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 11-SEP-1996
  15 RPVGRF 20
  I RPVGRF 6
  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
  Fukusumi, shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
  TOPOLOGY: linear HOLECULE TYPE: proteln FRAGMENT TYPE: internal
                           ATTORNEY/AGENT INFORMATION:
  ATTORNEY/AGENT INFORMATION:
  TYPE: amino acid
STRANDEDNESS: single
  COUNTRY: USA
ZIP: 02109
   STATE: MA
  CITY: Boston
  STREET: 130 Water Street
   APPLICATION NUMBER: JP 8/246573 FILING DATE: 18-SEP-1996
   ENGTH: 20 amino acids
   Conservative
   : Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
  Hosoya, Masaki
  97.1%;
   Ryo
  Score 33; DB 4; Pred. No. 0.52;
   0
   Mismatches
   0
  Length 20;
   Indels
   0
   ç
  RESULT 8
US-08-776-971-98
   밁
   Query Match
Best Local Similarity
"---has 6; Conserve
  Ş
   ; SEQUENCE DESCRIPTION: US-08-776-971-64
  Patent No. 6228984
GENERAL INFORMATION:
  -08-//-
Sequence 98, Appra-
Sequence 98, Appra-
No. 6228984
   INFORMATION FOR SEO ID NO: 64:
SEQUENCE CHARACTERISTICS:
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| 15 RPVGRF 20
  1 RPVGRF 6
  NUMBER OF SEQUENCES: ...
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
   ATTORNEY/AGENT INFORMATION:
  APPLICANT: Hinuma, Shuji
Habata, Yugo
   MOLECULE TYPE: protein FRAGMENT TYPE: internal
  APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
   COMPUTER: IEM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
   TYPE: amino acld
STRANDEDNESS: slngle
  CITY: Boston
  TELEFAX: 617-523-6440
   COUNTRY: USA
  STATE: MA
  TOPOLOGY: linear
  LENGTH: 20 amino acids
  REGISTRATION NUMBER: 27,026
   Application US/08776971B
  Conservative
   Kawamata, Yuji
Hosoya, Masaki
  97.1%; Score 33;
100.0%; Pred. No.
Live 0; Mismatc
  SEQ ID NO:
  Mismatches
  64
```

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  မှ
  RESULT 9
US-09-421-208-34
   US-08-776-971-98
   ; MOLECULE TYPE: peptlde
US-09-421-208-34
  Query Match
Best Local Simliarity
Matches 6; Conserv
                              Query Match
Best Local Similarity
Matches 6; Conserv
  -09-411
Sequence 34, Appr
Sequence 34, Appr
Sequence 34, Appr
Sequence 34, Appr
  TELEPNONE: 617-523-340
TELEFAX: 617-523-6440
INFORMATION FOR SEQ IO NO:
   TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 98: SEQUENCE CHARACTERISTICS:
   NAME: COnlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPNONE: 617-523-3400
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING OATE: 26-UUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING OATE: 27-UUN-1997
ATTORNEY/AGENT INFORMATION:
  COMPUTER REACABLE FORM:
MEOIUM TYPE: Floppy disk
  APPLICANT: Suenaga, Masat
APPLICANT: Morlya, Takeo
APPLICANT: Tanaka, Yoko
   SEQUENCE CNARACTERISTICS:
   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
ADORESSEE: DIKE, BRC
   APPLICANT: N18h1mura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
  1 RPVGRF 6
|||||
| 15 RPVGRF 20
  APPLICATION NUMBER: FILING OATE:
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
   TOPOLOGY:
   STRANDEDNESS:
  COUNTRY:
   LENGTN:
 1 RPVGRF 6
   SEQUENCE DESCRIPTION: SEQ ID NO: 98:
   INFORMATION:
  02109
  Boston
  amino acid
   MA
  STRANDEDNESS: single
   TYPE: amino acid
  Application US/09421208
  LENGTN: 20 amlno acids
  130 Water Street
  20 amino acids
  USA
                                  Conservative
   Conservative
   linear
   BRONSTEIN, ROBERTS & CUSHMAN, LLP
   97.1%;
                           97.1%; Score 33; OB 100.0%; Pred. No. 0.5 tlve 0; Mlsmatches
  Masato
  US/09/421,208
   34:
   0
   Score 33; OB 4;
Pred. No. 0.52;
   Mismatches
  OB 4;
0.52;
                                ..
  0; Indels
   Length 20
  Length 20;
                                Inde15
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   0
                              Gaps
   Gaps
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   0
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   F
  ; TOPOLOGY: 11
; MOLECULE TYPE:
US-09-421-208-40
   US-09-421-208-40
  US-09-421-208-46
  Sequence 46, Applicat.
Patent No. 6258561
GENERAL INFORMATION:
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   Query Match
  TELECOMMUNICATION INFORMATION:
TELEPAX: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ IO NO: 40:
   PILING OATE:

PROOR APPLICATION UMBER: US 09/
APPLICATION NUMBER: US 09/
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172
FILING OATE: 27-JUN-1997
ATTORNET/AGENT INFORMATION:
NAME: CON111, David G.
REGISTRATION NUMBER: 27.02
REFERENCE/DOCKET NUMBER: 4
  GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishlmura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGANO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
   MEOIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MECOIUM TYPE: Floppy (
COMPUTER: IBM PC com
   APPLICANT: Tanaka, Yoko
APPLICANT: Nishlmura, Osamu
TITLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
   CORRESPONDENCE AODRESS:
  SEQUENCE CNARACTERISTICS:
  Local Similarity
nes 6; Conserv
   TYPE: amlno acid
STRANDEONESS:
   COUNTRY: US
ZIP: 02109
  15
   15
  CITY: Boston
   1 RPVGRF 6
   APPLICATION NUMBER:
   ADORESSEE:
   RPVGRF
   RPVGRF
   6, Application US/09421208 6258561
  ), Application US/09421208 6258561
  ቻ
   E: DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP 130 Water Street
  Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
   20 amino acids
  USA
   20
  20
  Conservative
  llnear
  97.1%; bred. nc.
100.0%; Pred. nc.
1ve 0; Mismatches
   JP 172118/1997
  US 09/105,678
   US/09/421,208
   27,026
  48466-342
   OB 4;
   Length 20;
  Inde1s
  0
  Gaps
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RESULT 12
US-09-105-678A-28
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   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-46
   Sequence 28, Application US/09105678A Patent No. 6103882
   Best Local Similarity Matches 6; Conserv
  Query Match
   GENERAL INFORMATION:
  TELEFAX: 617-523-6440
INFORMATION FOR SEQ IO NO:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-OOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION OATA:
ADDITION TOWNERS. IS COMPATON STATEMENT APPLICATION OATA:
   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
  MEOIUM TYPE: Floppy dlsk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-00S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  TITLE OF INVENTION: METNOO OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Yoko
APPLICANT: Nishinura, Osamu
  SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
              PRIOR APPLICATION DATA:
  COMPUTER READABLE FORM:
MEOLUM TYPE: Floppy
  1 RPVGRF 6
||||||
15 RPVGRF 20
  NAME: Conlin, David G. REGISTRATION NUMBER: 27 REFERENCE/DOCKET NUMBER:
   TYPE:
STRANDEDNESS:
11near
 APPLICATION NUMBER:
                                 APPLICATION NUMBER: U$/09/105,678A FILING DATE: 26-JUN-1998
  COUNTRY:
  STATE:
   STREET:
   APPLICATION NUMBER:
  COUNTRY:
  ADORESSEE: Din.,
   ZIP: 02109
   ELEPHONE:
   02109
   Boston
   Boston
  ¥
  Ś
  130 Water Street
  20 amino acids
  USA
   Conservative
  DIKE, BRONSTEIN, ROBERTS & CUSNMAN, LLP
   97.1%;
100.0%;
   US/09/421,208
JP 172118/1997
   27,026
   0; Mismatches
   Score 33;
Pred. No.
   48466-342
   DB 4;
   ..
  Length 20;
   Indels
   0
   Gaps
   0
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  Š
   Query Match
Best Local Similarity
6; Conserva
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US-09-105-678A-35
   US-09-105-678A-28
   Sequence 35, Application US/09105678A Patent No. 6103882
APPLICATION NUMBER: US/09/105,678A FILING DATE: 26-JUN-1998 PRIOR APPLICATION DATA: APPLICATION UMBER: JP 172118/1997 FILING OATE: 27-JUN-1997 ATTORNEY/AGENT INFORMATION: NAME: Coniin, David G. REGISTRATION NUMBER: 27,026 REFERENCE/DOCKET NUMBER: 48466-342
   INFORMATION FOR SEQ IO NO:
SEQUENCE CHARACTERISTICS:
   GENERAL INFORMATION:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-OOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION OATA:
  APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
  CORRESPONDENCE ADORESS:
ADDRESSEE: OIKE, BRO
   APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
  FILING OATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
  FEATURE:
  FEATURE:
   NUMBER OF SEQUENCES:
  MOLECULE TYPE: peptide
  TITLE OF INVENTION: METHOO OF PRODUCING A 19P2 LIGAND
  15 RPVGRF 20
  NAME/KEY: Modified-site
LOCATION: 21
COTHER INFORMATION: /product- "Gly-OH or Gly-Arg"
  TELEPHONE: 017-523-6440
  REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
  NAME: Conlin, David G. REGISTRATION NUMBER: 2
   COUNTRY:
  CITY:
  STREET:
   OTHER INFORMATION:
  OTNER INFORMATION: /product-
  TYPE: amino acid
STRANDEONESS:
   LOCATION:
   NAME/KEY: Modified-site LOCATION: 10
  TOPOLOGY:
  1 RPVGRF 6
   NAME/KEY: Modified-site
   CENGTH:
   02109
   Boston
: MA
  130 Water Street
   21 amino acids
   USA
  Conservative
  linear
   97.1
100.0%; r.
  BRONSTEIN, ROBERTS & CUSHMAN, LLF
   /product- "Gly or Ser"
  Score 33;
Pred. No.
  48466-342
  "Ala or Thr"
   Version #1.30
  DB 3;
  Length 2I;
   0; Indels
   0
   Gaps
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o,

TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:

35:

TELEPNONE:

: 617-523-3400 617-523-6440

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  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-35
                 S
   US-09-105-678A-41
  RESULT 14
US-09-105-678A-41
  Query Match 97.1%; Subst Local Similarity 100.0%; Matches 6; Conservative 0;
  Ouery Match 97.1%; Score 33; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 6; Conservative 0; Mismatches
  Sequence 41, Application US/09105678A Patent No. 6103882
  APPLICATION NUMBER: US/09/:
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 172:
APPLICATION UMBER: JP 172:
ATTORNEY/AGENT INFORMATION:
   GENERAL INFORMATION:
  TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
  NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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MEDIUM TYPE: Floppy disk
COMPUTER: HAM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  SEQUENCE CHARACTERISTICS:
LENGTN: 21 amino acids
  SEQUENCE CNARACTERISTICS:
  SOFTWARE: Patentin Relicurrent APPLICATION DATA:
  APPLICANT: Suenaga, Masato
APPLICANT: MOTIYa, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osam
TITLE OF INVENTION: METHOD
  CORRESPONDENCE ADDRESS
   MOLECULE TYPE:
   APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
WHBER OF SEQUENCES: 52
  TYPE: amino
STRANDEDNESS:
I RPVGRF 6
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TOPOLOGY: 11
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  STREET:
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   ADDRESSEE:
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   1 RPVGRF 6
  Boston
  amino acid
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  ž
  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
  21 amino acids
   617-523-6440
   USA
  Patentin Release #1.0, Version #1.30
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Search completed: September I3, 2002, 09:20:59 Job time: 624 sec
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  PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 172118/1997
FILING DATE: 27 JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON1In, Dav1d G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
REFERENCE/DOCKET NUMBER: 49466-342
REFERENCE/DOCKET NUMBER: 47,026
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TELEPHONE: 617-523-3400
TELEPAN: 617-523-6440
INFORMATION FOR SEQ ID NO: 47:
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Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 26-JUN-1998
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   APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METNOD OF PRODUCING A 19P2 LIGAND
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run September 13, 2002, 09:24:04; Search time 172.41 Seconds (without alignments)
3.901 Million cell updates/sec

US-09-446-543A-73\_COPY\_15\_21 34

Seguence: Title: Parfect score: 1 RPVGRFX 7

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

283138 segs, 96089334 residues

Total number of hits satisfylng chosen parameters: 283138

Minimum DB seq length: 0 length: 2000000000

Post-processing: Minlmum Match 0% Maximum Match 100% Listing first 45 su

summaries

Databasa - u n -PIR\_71:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| DB ID  Description  JC7607  T35893  T40334  AC3538  AC3538  AC3538  ANPothetical  AC3538  ANPothetical  APPOthetical  APPOTHETIC | 82.4          | 82.4   | 82.4         | ٢              | 82.4   | ۲             | 82.4          | 82.4          | 82.4          |              | •              | 85.3   | 85.3   | 85.3   | •      | •       | •      | •              |               | •      |        |        |        | •      | •      | ۳.     | .7     | 97.1          | 97.1          | •             |
| JC7607  JC7607  prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel proporthetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical probable ment prolactin-rel probable ment prolactin-rel probable prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin-rel prolactin- | 299           | 299    | 294          | 260            | 257    | 251           | 246           | 246           | 239           | 193          | 138            | 379    | 367    | 362    | 315    | 308     | 289    | 226            | 172           | 170    | 559    | 501    | 173    | 154    | 149    | 107    | 511    | 445           | 83            |               |
| prolactin-rel<br>FAD-dependent<br>hypothetical<br>hypothetical<br>hypothetical<br>hypothetical<br>hypothetical<br>hypothetical<br>hypothetical<br>hypothetical<br>hypothetical<br>protein BVJI<br>hypothetical<br>probable memb<br>hypothetical<br>probable prol<br>proline-rich<br>butyryl-coa c<br>envelope prot<br>hypothetical<br>MotA/TolQ/Ext<br>3-oxoscyl-(ac<br>probable den)<br>probable den)<br>probable den)<br>probable den)<br>probable den)<br>probable den)<br>probable den)<br>probable den)<br>probable den)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | N             | N      | N            | N              | N      | Ŋ             | N             | N             | N             | N            | Ν              | N      | N      | N      | Ŋ      | Ŋ       | _      | Ŋ              | N             | 2      | N      | N      | Ŋ      | N      | N      | N      | N      | Ŋ             | Ŋ             | B             |
| prolactin-relevante prolactin-relevante prolactin-relevante protectical phypothetical phypothetical phypothetical phypothetical phypothetical protein ByJ5 protein ByJ5 protein ByJ5 probable membhypothetical probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proline-rich probable proth probable deny probable deny probable deny probable deny probable prophypothetical probable prophypothetical probable deny probable deny probable prophypothetical probable prophypothetical probable probable deny probable probable deny probable probable prophypothetical phypothetical phypothetical probable prophypothetical phypothetical phypothetical phypothetical phypothetical probable probable probable probable deny probable prophypothetical phypothetical phyp | в86770        | C70643 | F84922       | T36846         | F83104 | AB3392        | AI2990        | H98292        | AB1887        | T44148       | S24102         | T45286 | T04521 | G96735 | T46156 | AC1053. | A37209 | A65057         | T02229        | S76067 | G83897 | 866763 | S76779 | T34825 | AH2262 | AC3538 | T40334 | T35893        | JC7607        | ID            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | UDP-N-acetyle |        | hypothetical | probable dehyo |        | phosphotyrosy | 3-oxoacy1-(ac | 3-oxoscy1-(ac | MotA/TolQ/Exb | hypothetical | envelope proto |        | rich   | prol   | CBl    | men     | w      | hypothetical p | protein BrJ15 |        |        | _      | _      | _      | _      |        |        | FAD-dependent | prolactin-rel | :             |

| ě.<br>U           | 4                  | 43                | 42                 | 41                 | 40                 | 9E                 | 38                 | 37                 | 36                 | 35                 | E<br>A             | 33                 | 32                 | 31                 | 30                 |  |
|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
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| 82.4              | 82.4               | 82.4              | 82.4               | 82.4               | 82.4               | 82.4               | B2.4               | 82.4               | 82.4               | 82.4               | B2.4               | 82.4               | B2.4               | 82.4               | 82.4               |  |
| 585               | 580                | 522               | 497                | 458                | 457                | E<br>E<br>E        | 424                | 409                | 367                | 325                | 325                | 316                | 316                | 305                | 300                |  |
| N                 | N                  | Ν                 | 2                  | ν                  | N                  | 2                  | N                  | N                  | N                  | Ŋ                  | N                  | N                  | N                  | N                  | _                  |  |
| C69336            | A96683             | н97509            | D98347             | AC2935             | AG2728             | B47041             | D69399             | T47470             | T44687             | AE2991             | D98292             | F98027             | G95161             | G96962             | S08244             |  |
| probable electron | hypothetical prote | probable glycosy1 | hypothetical prote | conserved hypothet | polysaccharide bio | hypothetical prote | 3-ketoacyl-CoA thi | lsovaleryl-CoA deh | cobalamin blosynth | ABC transporter, m | ribose ABC transpo | UDP-N-scetylmurama | UDP-N-scetylenolpy | UDP-N-acetylenolpy | conserved hypothet |  |

## AL I GNMENTS

A; Molecule type: DNA A; Residues: 1-83 < YAM> A; Residues: 1-83 < YAM> A; Cross-references: DDDJ: AB040612; DDBJ: AB040613 C; Comment: This peptide induces arachidonic acid metabolita release from rst anterior release, and stimulation of ACTH secretion from the pituitary. C:Accession: JC7607

R:Ysmsda, M.; Ozaws, A.; Ishil, S.; Shibusawa, N.; Hsshids, T.; Ishizuka, T.; Hosoya, Blochem. Blophys. Res. Commun. 281, 53-56, 2001

A:Title: Isolation and characterization of the rat projectin-releasing peptide gene: A:Reference number: JC7607; MUID:21092785; PMID:11178959

A:Accession: JC7607 prolactin-releasing peptide - rat
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FAD-dependent oxidoreductase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000 C;Accession: T35893 R;Oliver, K.; Harris, D.; Parkhlll, J.; Barrell, B.G.; Rajsndream, M.A. submitted to the EMBL Data Library, November 1997

A; Reference number: 221592 A; Accession: T35893

A:Status: preliminsry; translated from GB/EMBL/DDBJ A:Molecule type: DNA A:Residues: 1-445 <OLI> A:Cross-references: EMBL:AL009204; PIDN:CAA15814.1;

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Query Match

97.18; Score 33; B <u>ب</u> Length 445;

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A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
  A;Cross-references: EMBL:AL022244; PIDN:CAA18295.1; GSPDB:GN00067; SPDB:SPBC3B8.06
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   R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; submitted to the EMBL Data Llbrary, March 1998
   hypothetical protein SPBC3B8.06 - fission yeast (Schizosaccharomyces pombe)
C;Specics: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequencc_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40334
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  A; Experimental source: strain
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 synonym of
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   DNA Res. 8, 205-213, 2001
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  R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Mio, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
   C; Accession: S76779 R; Kaneko, T.; Sato,
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EMBL:D90916;
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  J.; Barrell,
January 1998
  Streptomyces coelicolo:
NID:g1653715; PIDN:BAA18691.1; PID:d101 to the EMBL Data Library, June 1996
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S76067
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  R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, Nucieic Acids Res. 28, 4317-4331, 2000
A;Tille: Complete genome sequence of the slkaiiphilic bacterium Baciilus haiodus A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: G83897
  uroconase (urocanste hydratase) hutU (imported] - 8acillus haiodurans (strain C;Species: Bacillus haiodurans (strain C;Date: 01-Dec-2000 *sequence_revision 01-Dec-2000 *text_change 15-Jun-2001 C;Accession: G83897
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  A;Gene: hutU
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   A; Moiecule type: DNA
A; Rcsidues: i-559 <STO>
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   A;Gene: MIPS:YDL070c
A;Map position: 15L
   A; Molecule type: DNA
A; Residucs: 1-501 <ALE>
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hypothetical protein b2757 - Escherichia coli (strain K-12)
c;Specias: Escherichis coli
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c;Specias: Rose, D.7; Mau, D.; Shao, Y.
science 277, 1453-1462, 1997
A;Fifte: The complete genome sequence of Escherichia coli K-12.
  A; Molecule type: mRNA
A; Residues: 1-172 <KOZ)
A; Cross-references: EMBL: AB005878; NID:dll12079; PID:dl022465
A; Experimental source: strain Bright Yellow 2
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A;Accession: T02229
A;Ststus: preliminary; translated from GB/EMBL/DDBJ
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A:Variety: PCC 6803
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C:Accession: S76067
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C; Date: 05-Mar-1999 #sequence_revision 05-Mar
C; Accession: T02229
   B
  R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nskamura, Y.; Miysjima, o, K.; Okumurs, S.; Shimpo, S.; Tskeuchi, C.; Wada, T.; Watsnabe, A.; Yamsds, M.; Ys DNA Res. 3, 109-136, 1996
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   A;Cross-references: EMBL:D63999; GB:AB001339; NID:91001396; PIDN:BAA10045.1; PID:d101
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A; Accession: S76067
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  protein ByJ15
  A; Status: preliminary
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Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quaii, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Ruthers aguence of a multiple drug resistant Salmonella enterica sero; A; Reference number: ABOSO2; PMID:11677608

A; Accession: AC1053
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A; Residues: 1-289 <KON>
A; Residues: 1-289 <KON>
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C; Keywords: liver; mitochondrion; sulfoprotein; sulfurtransferase
F; 244/Active site: Cys (sulfocysteine intermediate) #status predicted
  probable membrane protein STY4751 [Imported] - Salmonella enterica subsp. enterica serov C; Species: Salmonella cnterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C; Accession: AC1033 C; Accession: AC1033 R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Plckard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
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J. Protein Chem. 9, 369-377, 1990
A;Title: Primary structure of avian hepatic rhodanese.
A;Reference number: A37209; MUID:91113289
A;Accession: A37209
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A; Rcsidues: 1-308 < PAR>
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A37209
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hypothetical protein T4D2.30 -
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A;Note: T4D2.30
C;Superfamily: myrosinase-associated protein MyAP
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  A; Map position: 3
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Ti  n-profit institutions as long  d this statement is not removes  quires a license agreement (See  email to license@isb-sib.ch).  418; BAA29026.1; -  418; BAA29026.1; -  121 BY SIMILARITIN-REI  22 52 PROLACTIN-REI  23 52 PROLACTIN-REI  23 52 PROLACTIN-REI  24 PROLACTIN-REI  25 PROLACTIN-REI  26 AMIDATION (G  83 AA; 9215 MW; DOC75A264EEE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Fuj<br>Fuj<br>San<br>O.<br>98).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | STANDARD;  1. 39, Created. 1. 39, Last set. 1. 41, Last and 1. 11, Last and 1. 11, Last and 1. 12, Last and 2. 13, Prolactin de prrp20]. de prrp20]. de (Rat). 2.00; Chordata; zoa; Rodentia; | 552<br>552<br>552<br>552                                                                                                                      |
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in the brain."; in the brain."; Kawamata Y., wa T., Nishimura                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Pote 93                                                                                                                                                                                       | HUMAN P.AQUAE L.DROME L.DROME L.DROME L.DROME A.ORYSA A.ORYSA L.ORDE L.ADNSP L.ADNSP L.ADNSP L.ADNSP L.ADNSP                                  |
| ) release and receptor GPR10 d, with highest is produced thrumatics and the There are no ng as its continued by See http://www.  pair of basic arty.  pair of basic pair of basic pair of basic pepT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1: RELEASING PEPT1:                                                                                                                                       | ., Hosoya ! ., Sekiguc' M.; n."; r., Nabat.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | AA.<br>lite)<br>date)<br>YRP) (Prolactin<br>peptide PrRP31;<br>peptide PrRP31;<br>Pertebrata; Eut                                                                                             |                                                                                                                                               |
| PP11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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| regulates to 0. May stim to leveis in the EMBL our restriction tent is 1 yand for is b-sib.ch. isb-sib.ch. incresidues. The PRRP31.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Fukusumi<br>L.,<br>Ninuma<br>H.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | in-reieasing<br>1; Prolactin<br>uteieostomi;<br>Murinae; Rati                                                                                                                                 |                                                                                                                                               |
| egulates the May stimulate leveis in cough a collabor e EMBL outstat restrictions on ent is in no and for comme isb-sib.ch/anno residues. DE PRRP31. DE PRRP31. DE PRRP31.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | જં જ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | sing<br>ctin-<br>ctin-<br>mi;                                                                                                                                                                 | baciilus ha homo sapien aquifex aeo drosophila pseudomonas pseudomonas thermotoga curyza sativ cucurbita grea may8 (m aphanocapsa mus musculu |
| ion<br>iton<br>itcia                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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| · / - 4 8 - 5 -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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  RESULT 2
PRRP_HUMAN
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Best Local S
Matches 6
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   This SWISS-PRDT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
  MOD_RES
   MEDLINE-98266781: PubMed-9607765:
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fu
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.,
"A prolactin-releasing peptide in the brain.":
Nature 393:272-276(1998).
   PubMed-10498338:
Fujil R., Fukusumi S
Sekiguchi M., Kitada
  Nature
[2]
  Homo sapions (Human).
Eukaryota: Metazoa; Chordata;
Mammalia: Eutheria; Primates;
   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAR-2002 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
  PEPTIDE
PEPTIDE
  "Tissue distribution
   TISSOE SPECIFICITY.
  TISSUE-Brain
   PRRP_HUMAN
P8I277;
   SIGNAL
   Hormone:
  receptor
  SEQUENCE FROM N.A.
   NCBI_TaxID=9606;
   releasing peptide PrRP20].
   ŝ
4B
            1 RPVGRF
  н
  TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS
  FUNCTION: Stimulates
  RPVGRF
   expression of prolactin
   lactotrophs directly
RPVGRF
   RPVGRF
  AB015419: BAA29027.1;
  Pept. 83:1-10(1999).
  6; Conserv
   requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@lsb-sib.ch).
   Similarity
6; Conserv
   Amidation;
  Fukusumi S., Hosoya M.,
M., Kltada C., Kurokawa
53
                    6
   52
  Ø
   Conservative
  Conservative
   34
4
   Š
   STANDARD:
   9639
  Signal.
22
53
53
53
   97.1%:
  of projectin-releasing
   97.1%: Score 33; 100.0%: Pred. No.
   Ž
  prolactln (PRL) release and regulates
tin through its receptor GPRIO. May sti
   to secrete PRL.
  0
   0
   Score 33:
Pred. No.
   BY SIMILARITY.

PROLACTIN-RELEASING PEPTIDE PRRP31.

PROLACTIN-RELEASING PEPTIDE PRRP20.

AMIDATION (G-54 PROVIDE AMIDE GROUP

229A2F3F50CF981B CRC64;
  Craniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo
  PRT:
   Mismatches
   Mismatches
   Kawamata Y., I
T., Nishimura
  87
  DB 1:
0.93:
   DB 1;
0.89;
  3
  peptide
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   Habata
a O., On
   Length 87
  Length 83:
  Indels
  (PrRP)
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  Fukusumi
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   Query Match
Best Local S
Matches 6
   GLG_RHIME STANDARD;

GLG_RHIME STANDARD;

p5833;

Ol-MAR-2002 (Rel. 41, Last seq

Ol-MAR-2002 (Rei. 41, Last seq

Ol-MAR-2002 (Rei. 41, Last ann

Glycogen synthase 1 (EC 2.4.I.

synthase 1);

GLGAl OR R02846 OR SMC03924.

Rh1zobium meilloti (Sinorhizob
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  Hinuma S., Habata Y., Fujii R., Kawamata Y., H. Kitada C., Masuo Y., Asano T., Matsumoto H., S. Kurokawa T.. Nishimura O., Onda H., Fujino M.; "A proiactin-releasing peptide in the brain."; Nature 393:272-276(1998).
                       NCBI_TaxID-382;
                                  Bacteria; Proteobacteria; alpha
Rhizobiaceae; Sinorhizobium.
SEQUENCE
  48
  ب
  FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
  RPVGRF
  RPVGRF
  Slmilarity
  6
  53
  Conservative
   (Sinorhizoblum mellloti)

    Last sequence update)
    Last annotation update)
    (EC 2.4.I.21) (Starch [bacterial glycogen]

  Chordata; Craniata; Vertebrata; Eutel Cetartiodactyla; Ruminantia; Pecora;
   97.1%;
   Created)
   0
   Score 33:
Pred. No.
   PROLACTIN-RELEASING PEPTIDE PR
PROLACTIN-RELEASING PEPTIDE PR
AMIDATION (G-54 PROVIDE AMIDE
08AC35Al3B0FA908 CRC64;
  PRT;
  subdivision;
  Mismatches
  480
   DB 1;
1.1;
   peptide
  Ž
   (Prolactin-releasing ide PrRP31; Prolactin-
  Rhizobiaceae group,
  of.
   Sekiguchi M.,
   Hosoya M.,
   0
  Length
  basic
  Euteleogtomi:
  98
  residues
   Fukusumi
  PRRP31.
   Bovoidea;
  GROUP)
   0
   Gaps
   0
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RESULT 5
YGCI_ECOL1
9
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  Query Match
Best Local S
Matches 5
   Capela D., Barloy-Nubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

A Bolstard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masyy D.,

A Pohl T., Porteteile D., Puehler A., Purnelle B., Ramsperger U.,

A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symblont

"Sinorhizobium meliloti strain 1021.",

"Inc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

"I FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.

"I CATALYTIC ACTIVITY: ADP-glucosy 1-(1,4)-alpha-D-glucosy) (N+1).

"C -1- PATNWAY: Glycogen blosynthesis; second step.

"I SIMILARITY: BELONGS TO TNE BACTERIAL/PLANT GLYCOGEN SYNTNASE
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 the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A.
STRAIRW 12 / MG1655;
STRAIRW 142617; PubMed = 9278503;
MEDILINE = 97426617; PubMed = 9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Buriand Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhev G.F. Riley M., Collado - Vides J., Glasner J.D., Rode C.K., Mayhev G.F. Gregor J., Davis N.W., Kirkpatrick N.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
  16-OCT-2001
16-OCT-2001
16-OCT-2001
   Complete proteome.
BINDING 15
SEQUENCE 480 AA;
  EMBL; AL591792; CAC47425.1; -. Glycogen biosynthesis; Transferase;
  This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
  "The complete genome sequence of Escherichia coli K-12.", Science 277:1453-1474(1997).
   Q46898;
  STRAIN-1021;
MEDLINE-21396507;
  Escherichia coli,
Bacteria; Proteobacteria,
  Hypothetical
YGCI OR B2757
   NCBI_Tax1D-562;
   55 KPVGRF
  1 RPVGRF
   LECOLI
   'n
   Similarity
   (Rel
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   60
  σ
   Conservative
  protein
  STANDARD;
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  PubMed-11481430;
  51408
   yell precursor.
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  88
  Created)
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   WW.
  gamma
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   Score
Pred.
  ADP-GLUCOSE (BY SIMILARIT 84C584F6E0564097 CRC64;
   ght. It is produced through Bioinformatics and the Ex
   subdivision;
  Mismatches
   30;
  Glycosyltransferase,
  224 AA
   update)
  Enterobacteriaceae,
  SIMILARITY).
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  Length 480
  1ndels
   ADP-glucose.
  EMBL
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  D.J.,
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  collaboration
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   RESULT
   Query Match
Best Local S
Matches 5
  Query Match
Best Local :
   01-MAY-1992
01-MAY-1992
30-MAY-2000
Thiosulfate
  ACT_SITE
  DOMAIN
DOMAIN
ACT_SITE
   CNICK
   EMBL;
  Kohanski R.A., Heinrikson R.L.;
"Primary structure of avian hepatic
J. Protein Chem. 9:369-377(1990).
   EcoGene; EG13116; ygc1.

Hypothetical protein; Signal; Complete
SIGNAL 17
NVBOTHETIAL
NVBOTHETIA
  PROSITE;
  InterPro: 1PR001307; Rhodu
InterPro: 1PR001763; Rhodu
Pfam; PF00581: Rhodunese;
  -I- SIMILARITY: BELONGS
PIR; A37209; A37209.
HSSP; P00586; 1RNS.
   TST
  SEQUENCE
  DETOXIFICATION.
-1- CATALYTIC ACTIVITY: Thiosulfate + cyanide -
   SEQUENCE
   CNAIN
  ACT_SITE
  DOMA1N
  Transferase; Mitochondrion.
  SMART;
  MEDL1NE-91113289; PubMed-2275748;
   SEQUENCE.
   NCBI_TaxID-9031;
   Archosaurla; Aves; Neognathae;
   Eukaryota;
   Gallus galius (Chicken).
   INTR_CHICK
   SSUE-Liver;
   25 RPTGRF
   1 RPVGRF
  TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.

DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR CONFORMATION, SUGESTING A COMMON EVOLUTIONARY ORIGIN. NOWES THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
  SUBCELLULAR LOCATION: Mltochondrial matrix.
  FUNCTION: FORMATION OF
   d
   U29579; AAA69267.1; ALT_INIT.
AE000359; AAC75799.1; ALT_INIT
ee; EG13116; Y9CI.
  SM00450;
   5; Conserv
  PS00380; RNODANESE_1:
PS00683; RNODANESE_2;
   Metazoa;
   224 AA;
  289
   6
   (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 39, Last annotation update)
sulfurtransferase (EC 2.8.1.1) (Rhodanese).
  244
545
   Conservative
  246
  143
159
186
   30
   18
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   STANDARD;
  RNOD;
   224
25209
  244
  246
  142
158
289
186
   Chordata; Cranlata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
  32286
  Rhodanese_domain.
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  Rhodanese.
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  DOMAINS ARE VERY DIFFERENT.
THE RNODANESE FAMILY.
  IRON-SULFUR COMPLEXES AND CYANIDE
  SIMILARITY).
BY SIMILARITY.
SUBSTRATE (THIOSULFATE) |
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SUBSTRATE (THIOSULFATE) |
(BY SIMILARITY).
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  B DOMAIN.
   Score
Pred.
    Score
Pred.
   NYPOTHETICAL PROTEIN YGCI; 1C42CC009B317D68 CRC64;
  A DOMAIN
   PRT;
  8BFCF671DE0B2BA4
   Mismatches
   No :
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9
  rhodanese.";
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   proteome
26;
  ROLE
   Phasianidae; Phasianlnae;
  IN SUBSTRATE BINDING
                    Length 289
   Length
  CRC64;
  sulfite + thiocyanate
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   Gaps
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Similarity

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RESULT 7
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ID AR72_HIMAN
ID COA3488
DT 16-OCT
DE AFIATO
DE (Aldok
GN AKR7A2
QS Homo se
OC Eukary
QC Eukary
QC Mammal
QX NCSI_T
RN [1]
RN [2]
RP SEQUEN
RC TISSUE
RX MEDLIN
RA ITCLAR
RT STOCK
RT SEQUEN
RC TISSUE
RX MEDLIT
RX PERMIC
CC TISSUE
RX PERMIC
CC -1- SI
CC -1- SI
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   Oxidorcductase.
ACT_SITE 112
CONFLICT 113
SEQUENCE 330
  entitles
or aend a
   MEDLINE-98244807; PubMed-9576847; Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.; "Molecular cloning, expression and catalytic activity of a human AKR7 member of the alido-keto reductase auperfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin B1-aldehyde reductase."; Blochem. J. 332:21-34(1998).
  0.43488; 075/45;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last annotation
16-OCT-2001 (Rel. 40, Last annotation
   the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
  Prami C., Savelyeva L., Perri P., Schwab M.;

*Cioning of the human aflatoxin B1-aidehyde reductase
1p36.1 in a region frequently altered in human tumor c
Cancer Res. 58:5014-5018(1998).
   Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
   Aflatoxin Bl aldehyde reductase (Aldoketoreductase 7).
AKR7A2 OR AFAR OR AKR7.
   AR72_HUMAN
043488; 07
   submitted (FEB-2000) to -1- FUNCTION: CAN METABO
   SEQUENCE FROM N.A.
   MEDLINE-99040634; PubMed-9823300;
   SEQUENCE FROM N.A.
   MIM; 603418;
  Hail R
  TISSUE-Brain:
  InterPro;
   182
  SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
   nitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
DINYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINGGENIC
EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
   . RPVGRF
  REDUCTASE.
   RPAGRE
  Pro; IPR001395; Aldo_ket_red.
PF00248; aldo_ket_red; 1.
  AF026947; AAC52104.I; -.
   Y16675; CAA76347.1; -
AL035413; CAB72321.1;
   s requires a license agreement (So an email to license@isb-sib.ch).
   5
    Similarity
  112
113
330
   187
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   Conservative
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  STANDARD;
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36618
   Chordata;
Primates;
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  Cytoplasmic.
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3BBFB7ED0CAF4D54 CRC64;
  Craniata; Vertebrata;
Catarrhini; Hominidae;
  PRT;
  ALDO/KETO REDUCTASE
   Mismatches
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  29;
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   Hominidae;
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   Indels
  2 FAMILY
   Euteleostom1;
   gene at cells.";
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Matches 5
   Matches
   Oxidoreductase.
ACT_SITE 113
CONFLICT 51
CONFLICT 138
CONFLICT 201
   AR73_HUMAN
O95154; Q9N
   CONFLICT
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SEQUENCE
   16-OCT-2001 (
16-OCT-2001 (
Aflatoxin Bl
   EMBL;
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   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CAN METABOLIZE THE AFLATOXIN B1 (AEB1) PROTEIN-BINDING -I- EUNCHOLD SE DIHUDRODIOL BY CORMING NONBINDING AFBI DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGEN.
   entitles
  B1-metabolizing member AKR7A3.";
  MEDLINE-99315412;
  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
   HOmo sapiens (Human).
   095154; Q9NUC3;
16-OCT-2001 (Re
  PRINTS;
   Pfam; PF00248; aldo_ket
   SEQUENCE FROM
   Carcinogeneaia
   Knight L.P., Primiano
   SEQUENCE FROM N.A.,
  NCBI_TaxID-9606;
  TISSUE-Liver;
   cDNA cioning, expression
  217
218 OPVGRF 223
  send
                   μ
  SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE
   EFFECTS OF AFLATOXIN BI.
SUBCELLULAR LOCATION: Cytoplasmic
   RPVGRF
                  RPVGRF
   AF040639;
AL035413;
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  s requires a llcense agreement (See http://www.isb-aib.ch/announce/an email to licenae@isb-aib.ch).
  Similarity
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   IPR00I395; Aldo_ket_red
0248: aldo_ket_red; 1.
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   Conservative
  Conservative
  aldehyde
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  B
  20:1215-1223(1999).
  STANDARD;
  AAD02I95.1;
CAB72322.1;
  ALDKETROTASE.
  PubMed-I0383892;
   215
323
37206
   113
51
138
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   AND
  85.3%;
83.3%;
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reductase 2 (EC 1.-..
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   CHARACTERIZATION.
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  the aldo-keto
  Groopman J.D., I and activity of
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E -> D (IN REF. 1).
V -> M (IN REF. 1).
  Craniata; Vertebrata;
Catarrhini; Hominidae;
   PRT:
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  B9C32C33C7I02AB3
   Mismatches
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   D (IN REF. 1)
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   D (IN REF. 1).
M (IN REF. 1).
ADOSPEGCGSFWGTLGPGADCCFPS
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  29;
  reductase superfamily,
   Kensler T.
of a second
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   Hominidae;
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  CRC64;
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   human
  2 FAMILY.
   Indels
  Euteleostom1;
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   RESULT 10
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Matches 5
  P55351;
01-NOV-1997
01-NOV-1997
15-JUL-1998
   MURB_LACIA STANDARD; PRT; 299 AA. 99CGD5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last acquence update) 01-MAR-2002 (Rel. 41, Last annotation update) UDP-N-acetylenolpyruvoylglucosamine reductase acetylmuramate dehydrogenase). WURB OR LIL162.
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  Plaamid aym pNGR234a.
Bacteria; Proteobacteria;
Rhlzobiaceae; Rhizobium.
NCBl_TaxID=394;
  EMBL; AE000064; AAB91602.1: -.
Hypothetical protein; Plasmid;
SEQUENCE 292 AA; 32539 MW;
   Freiberg C.A., Fellay Perret X.;
   SEQUENCE FROM N.A. MEDLINE-97305956; PubMed-9163424;
  Hypothetical
   Bolotin A., Wincker P., Mauger S., Welssenbach J., Ehrlich S.D., Soro
  STRAIN-IL1403;
  SEQUENCE FROM N.A.
  NCBI_TaxID=1360;
  Lactococcua lactis (subsp. lactia) (Streptococcus
Bacteria; Firmicutes; Bacillus/Clostridium group:
  Bacteria; Firmicutes;
  "Molecular basis of symbiosis between Nature 387:394-401(1997).
  Rhizoblum ap.
   Y4AD.
  MEDLINE=21235186; PubMed=11337471;
  Lactococcus
  (4AD_RHISN
  127 PVGRF 131
   2 PVGRF 6
   SIMILARITY: SOME, TO PHYTO SIMILARITY: SOME, TO Y4AC.
  FUNCTION: PROBABLY PART OF
SYNTHESIS OF AN ISOPRENOID
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  Conservative
  (strain NGR234).
   STANDARD;
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  82.4%:
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  Last sequence up
  protein Y4AD
  Created)
   PHYTOENE
   alpha
   Bairoch A., Broughtón W.J., Rosenthal
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  Score 28;
Pred. No.
  Sorokin A.;
  PRT;
  COMPOUND.
  Isoprene blosynthesis.
1055E5E7F3614379 CRC64;
  Mismatches
   subdivision; Rhizobiaceae group;
   AND
  OPERON Y4AABCD
  Jaillon O.,
  292
             SIMILARITY)
  Rhizobium
  SQUALENE SYNTHETASES.
  DB 1; Length 292;
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  Malarme
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Matches 5
   SMART; SM0011
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InterPro; IPROVOCE
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
SMART; SM00116; CBS; 4.
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   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 33.4 kDa protein in ribosomal RNA operon.
Thermofilum pendens.
Archaea; Crenarchaeota; Thermoproteales; Thermofillace
NCBI_TaxID-2269;
  InterPro; IPR003170; MurB.

Pfam; PF02215; MurB; 1.

Pfam; PF02873; MurB_C; 1.

Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;

Peptidoglycan synthesis; Complete proteome.

Peptidoglycan synthesis; Complete Proteome.
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   EMBL; X14835; CAA32944.1;
PIR; S08244; S08244.
InterPro; IPR000644; CBS.
   Thermofilum pendens.";
Syst. Appl. Microbiol. 13:117-127(1990).
-i- SIMILARITY: CONTAINS 4 CBS DOMAINS.
   Kjems J., Leffers H., Oleaen T., Ing "Sequence, organisation and transcriand the downstream tRNA and protein
  acety1-3-O-(1-carboxyviny1)-D-glucosamine + NADPH
--- COFACTOR: FAD (BY SIMILARITY).
--- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
--- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
--- SIMILARITY: BELONGS TO THE MURB FAMILY.
   entities requires a license agreement (S or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
2475;
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   YR33_THEPE
  EMBL; AE006348; AAK05260.1: -.
  or send an email to license@isb-sib.ch).
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  226 RPVGHF 231
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   1 RPVGRF 6
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  Thermoproteales; Thermofiliaceae;
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  Score 28;
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  PRT;
D811A313D37A4293 CRC64;
  Mismatches
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  , Garrett R.A.;
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   the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo cntitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
   SEQUENCE FROM M.A.
Ken C.F., Lin C.T.,
"Molecular cloning
   PRINTS; PRO0067; CATALASE.
PRODOM: PD0000510; CATALASE: 1.
PROSITE: PS00437; CATALASE: 1 1.
PROSITE; PS00438; CATALASE: 2; 1.
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
   CATA_BRARE
   ZFIN; ZDB-GEME-000210-20; cat.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
   Brachydanio rerio (Zebrafish)
   Gerhard G.S.,
   SEQUENCE
  Molecular cloning
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  ده
  PEROXIDE.

CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.

COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).

SUBUMIT: HOMOTETRANER (BY SIMILARITY).

SUBCELLULAR LOCATION: Peroxisomal (By similarity).

SIMILARITY: BELONGS TO THE CATALASE FAMILY.
   Match
   p. Biochem. Physiol. 127:447-457(2000).
FUNCTION: OCCURS IM ALMOST ALL AEROBICALLY
SERVES TO PROTECT CELLS FROM THE TOXIC EFFE
  PVGRF
   AJ007505; CAB64949.1; -. AF170069; AAF89686.1; -. P00432; 4BLC.
   E FROM M.A.

C.S., Kauffman E
   Similarity 100 5; Conservative
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   NADP
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  STANDARD;
   Peroxidase;
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  E.J., Grundy M.A.,
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BY SIMILARITY PROXIMAL HEME LIGAND (
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V -> S (IN REF. 2).
T -> I (IN REF. 2).
S -> F (IM REF. 2).
MLQ -> NAA (IN REF. 2)
   EMBL/GenBank/DDBJ databases
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   Score :
   (Zebra
   Mismatches
   J.F.;
ng for catalase from zebrafish (Danio
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   of the Danio
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   Length 300;
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  peroxide,
   Indels
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  _ECOLI STANDARD; PRT; 847 AA MDOH_ECOLI STANDARD; PRT; 847 AA p3137; P77371; O1-OCT-1993 (Rel. 27, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation updat Periplasmic glucans biosynthesis protein md MDOH OR B1049 OR 21684 OR ECS1427.
   COMFLICT
SEQUENCE
                              SEQUENCE FROM M.A.

STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A. Posfai G., Hackett J., Klink S., Boutih A., Shao Y., Miller L. Grotbeck E.J., Davis N.W., Lim A., Dimaianta E.T., Potamousis Grotbeck E.J., Davis N.W., Lim A., Dimaianta E.T., Potamousis Nepodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H. Nature 409:529-533(2001).
   Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kitagawa M., Makino K., Masuda S., Miti T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito M. Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., Yano M., Horiuchi K., Yano M., Horiuchi K., Yano M., Horiuchi K., Yano M., Horiuchi K., Yano M., Yan
   28
   Science
   Mau B.,
  Gregor J., Davis M.W.,
  Biattner F.R., Plunkett
Riiey M., Collado-Vides
  syringae.";
  "Homology between a genetic locus (mdoA) involved in the osmoregulated biosynthesis of periplasmic glucans in Escherichia coli and a genetic locus (hrpM) controlling pathogenicity of Pseudomonas
  Escherichia
  Bacteria, Proteobacteria,
  Escherichia coli, and Escherichia coli 0157:H7.
  MEDLINE-97061202; PubMed-8905232;
   SEQUENCE
   MEDLINE~97426617; PubMed-9278503;
   SEQUENCE FROM N.A.
  MEDLIME-95020533; PubMed-7934824;
   312 PVGRF 316
   Ŋ
   complete genome sequence nce 277:1453-1474(1997).
  Microbioi.
   PVGRF
  Shao
  Similarity 100. 5; Conservative
   478
526 J
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  Debarbieux L., Bohin A.,
  ۲.,
   MG1655;
   N.A
   N.A.
   AA.
  10:329-340(1993).
   478 M
59654 MW;
  82.4%;
   t G. III, Bloch C.A., Perna N.T., Burland V
s J., Glasner J.D., Rode C.K., Mayhew G.F.,
Kirkpatrick H.A., Goeden M.A., Rose D.J.,
  gamma
  0,
  Score 28;
Pred. No.
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   of Escherichia coli K-12.";
   -> T (IM REF. 2)
E1120D3796522785
  subdivision; Enterobacteriaceae;
  Mismatches
  Lacroix J.-M.,
   update)
ein mdoH
   Escherichia coli 0157:H7.";
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  ۳.
  0,
  Length 526;
  CRC64;
  Bohin J.-P.;
  Ħ.A.,
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  Gaps
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RESULT 14
ANPA_MOUSE STANOARO;
DT 01-NOV-1990 (Rel. 16, Created)
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  á
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Matches 5; Conserv
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STRAIN-0157:H7 / RIMD 0509952;

MEDLINN-21156231; PubMed=I1258796;

Hapashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with aboratory strain K-12.";

DNA Res. 8:11-22(2001).

11- FUNCTION: NECESSARY FOR NORMAL GLUCOSYLTRANSPERASE ACTIVITY. I
  CONFLICT
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SEQUENCE
  DOMAIN
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  EcoGene; EG11886; mdoH.

EcoGene; EG11886; mdoH.

InterPro; IPR001173; Glycos_transf_2.

Pfam; PF00535; Glycos_transf_. Transf
   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
   EMBL; X64197; CAA45522.1; -. EMBL; AE000206; AAC74133.1; -. EMBL; 090742; BAA35848.1; -.
   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   Complete proteome.
  Transmembrane;
  DOMAIN
   TRANSMEM
  DOMAIN
  TRANSMEM
  DOMAIN
  86
  2 PVGRF 6
  PATHWAY: OPG (OSMOREGULATED PERIPLASMIC GLUCANS) BIOSYNTHESIS. SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. STRONG.
  TO P.SYRINGAE HRPM.
   COULD BE A GLUCOSYL TRANSFERASE
  S35418: S35418.
  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
  PVGRF 102
   AE005315; AAG55795.1;
AP002555; BAB34850.1;
   Conservative
  140
161
194
215
  Inner membrane;
   139
160
193
214
425
425
446
512
533
533
559
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679
745
  96937 MW;
   82.4%;
100.0%;
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Pred. No
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PERIPLASMIC.
POTENTIAL.
CYTOPLASMIC.
POTENTIAL.
   ס ⊳
   PERIPLASMIC
   PERIPLASMIC.
POTENTIAL.
  CYTOPLASMIC.
  CYTOPLASMIC (POTENTIAL).
  CYTOPLASMIC
  POTENTIAL.
   CYTOPLASMIC
   PERIPLASMIC.
  Transferase; Glycosyltransferase;
  -> G (IN REF. 1).
-> L (IN REF. 1).
7DCAF93640180944 CRC64;
  Mismatches
   OR.
  Ö.
   There are no restrictions
   SIMPLY A SUBUNIT
   1.3e+02
  DB 1;
                         À
   as its content
   Usage
   Length 847
  and the
  Indels
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   and for
   OF.
   Yokoyama K.,
Tobe T.,
  a collaboration
MBL outstation -
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  Gaps
   commercia;
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PFINITE: PS00459; ANT_RECEPTORS

NART; SM00458; ANT_RECEPTORS

PROSITE; PS00458; ANT_RECEPTORS

PROSITE; PS00459.
OOMAIN
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  the European Bioinformatics and the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
  This SWI
  Ol-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
A-type receptor).
MPRI OR NPRA.
Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  EMBL; J05504; AAA37670.1; -.
EMBL; L31932; AAA66945.1; -.
PIR; A36568; OYMSAR.
PIR; A30888; A39088.
NSSP; O02846; 1ANL.
   CGMP synthesis;
  InterPro; IPR001170; ANF_reptor.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
   SEQUENCE FROM N.A.
MEDLINE=95139994; PubMcd=7838126;
Scheenfeld J.R., Sehl P., Quan C., Burnier J.P., Lowe Scheenfeld J.R., Sehl P., Quan C., Burnier J.P., Lowe **Agonist selectivity for three species of natriuretic
  Pandey K.N., Singh S.;
"Molecular cloning and expression of murine natriuretic factor receptor cDNA.";
J. Bioi. Chem. 255:12342-12348(1990).
   MGD; MGI:97371; Nprl.
   -1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIOE. HAS GUANYLATE
   receptor-A."
  SEQUENCE FROM N.A.
  ÆEDLINE-90324219; PubMed-1973687;
   SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANBOUS: THERE SEEM TO BE AT LEAST THERE AND RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (AND-A AND AND-B) ANO ONE (AND-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
   SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
   SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
   CYCLASE ACTIVITY ON BINDING OF ANF.

CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP +
  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
   Pharmacol. 47:172-180(1995).
   PF01094; ANF_receptor; 1. PF00211; guanylate_cyc; 1.
   SM00044; CYCc; 1
PS00458; ANP_RECEPTORS; 1.
PS00458; GUANYLATE_CYCLASES_1;
PS50125; GUANYLATE_CYCLASES_2;
PS50011; PROTEIN_KINASE_DOM; 1.
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   29
.470
491
524
872
   Signal
1057
469
490
1057
1057
  Glycoprotein;
              CYTOPLASMIC (POTENTIAL)
PROTEIN KINASE-LIKE.
  ATRIAL NATRIURETIC PEPTIDE RECEPTOR EXTRACELLULAR (POTENTIAL).
  POTENT IAL

    phosphorylation; Lyase;

  moved. Usage by and for (See http://www.isb-sib.
  guanylate cyclase/atrial
   diphosphate
   0.6
  restrictions
   peptide
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  collaboration -
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  밁
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   RESULT
   Query Match
Best Local S
Matches 5
[3]
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SEQUENCE FROM H.A.
MEDLINE-91352095; PubMed-1679239;
MEDLINE-91352095; PubMed-1679239;
Duda T., Goraczniak R.M., Sharma R.K.;
Puda T., Goraczniak R.M., Sharma R.K.;
Site-directed mutational analysis of
"Site-directed mutational analysis of reveals the atrial natriuretic fa
  DISULFID
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   SEQUENCE FROM N.A.

MEDLINE-91056089; Pubmed-1978722;
Yamaguchi M., Rutledge L.J., Garbers D.L.;

"The primary structure of the rat guanylyl
natrluretic peptide receptor gene.";
J. Blol. Chem. 265:20414-20420(1990).
  p18910;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
   Chinkers M., Garbers D.L., Chang M.S., Lo
Goeddel D.V., Schulz S.,
"A membrane form of guanyIate cyclase is
peptide receptor.",
Nature 338:78-83(1989).
   MEDLINE-89143770; PubMed-2563900;
Chinkers M., Garbers D.L., Chang M.S.,
  Rattus norvegicus (Rat).
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  82.4%;
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INTERCHAIN (PROBABLE).

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  SIMILARITY.
   Mismatches
                       factor
  a membrane
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   DB 1; L
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  an atrial natriuretic
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                    mbrane guanylate cyclase signaling site.";
  cyclase A/atrial
   D.G.,
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  Length 1057;
   Chln
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  (POTENTIAL).
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(POTENTIAL).
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  Euteleostomi;
Murinae; Rat
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8 8

2 PVGRF ||||| |120 PVGRF

124

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InterPro; IPRO01828; ANF_receptor.

R InterPro; IPRO01828; ANF_receptor.

R InterPro; IPRO01054; Guanylt_cyclase.

R InterPro; IPRO01054; Guanylt_cyclase.

R Pfam; PF00201; guanylate_cyc; l.

R Pfam; PF00201; guanylate_cyc; l.

R Pfam; PF00069; pkinase; l.

R Pfam; PF00065; NATPEPTIDER.

R PRONTS; PR00255; NATPEPTIDER.

R PROSITE; PS00458; ANF_RECEPTORS; l.

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R PROSITE; PS50111; PROTEIN_KINASE_DOM; l.
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DOMAIN
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EMBL; J05677; AAA41200.1; -.
EMBL; M74535; AAA41202.1; -.
PIR; S03348; OYRTR.
HSSP; Q02846; LAVL.
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   entities requires a license agreement (S or send an email to license@isb-sib.ch).
  CGMP synthesis;
  mod1f1ed
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  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW Buropean Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
   SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
  Similarity
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  non-profit institutions as long and this statement is not removed
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100.0%;
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          Score 28;
Pred. No.
   BY SIMILARITY.
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INTERCHAIN (PROBABLE)
   -> H (IH REF. 3).
-> P (IN REF. 3).
; 9EA9AE6B5AC058I6
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  CRC64;
 Indels
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   Scoring table:
  Sequence:
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  562222 seqs, 172994929 residues
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  RPVGRFX 7
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sp_human:*
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   sp_rvirus:*
ap_bacteriap:*
sp_archeap:*
   ap_mhc: *
   sp_rodent:*
   %p_invertebrate:*
  sp_unclassified:*
   sp_vertebrate:
   sp_plant:*
   Length
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Q9P195
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   Q93LZ7
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Q50531
Q59714
Q9W624
Q9C1M8
Q9C1M8
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Q9C1M8
   summaries
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   Compugen Ltd
          Q08229 saccharomyc
Q9kbe5 bacillus ha
Q90y59 paralichthy
Q90y57 paralichts cy
Q91p17 hepatitis c
Q9p155 homo sapien
Q55547 synechocyst
  Q9w624 carassius a
Q9c1m8 pleurotus s
Q9c139 streptomyce
p74584 synechocyst
  Q931z7 streptomyce
O50531 streptomyce
O59714 schizosacch
   Q9u8b2 hexamita sp
Q96115 drosophila
   Description
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| 82.4   | •      |                   | 82.4   | •      | •                  | •      |        | •      | 82.4   | •      | •          | 82.4   | •      | •      | •                  | •      | •                  | •      | 85.3   | •              |                    | •      | •      | •      |        | •      | •                  | •                  |
| 294    | 294    | 266               | 260    | 258    | 257                | 257    | 200    | 198    | 193    | 163    | 163        | 161    | 141    | 106    | 605                | 605    | 379                | 378    | 378    | 367            | 366                | 366    | 362    | 355    | 315    | 315    | 303                | 200                |
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| Q92UB5 | 006001 | OHUV60            | 088068 | Q921C1 | Q98NM6             | Q9HW71 | Q9NPN7 | Q9VNSB | Q9QJ59 | Q92T10 | Q9H7F5     | Q92221 | Q96W56 | 067984 | Q96MB9             | Q9BQ21 | P97088             | Q9HLL7 | Q9FI48 | <b>Q9SVU</b> 5 | Q9D157             | Q9M8Y5 | 29C996 | Q9FSS1 | Q9DCM1 | 09SCQ1 | Q92PD8             | Q9HM02             |
| S      |        | Q9vuh0 drosophila | stre   |        | Q98nm6 rhizobium i | -      |        | Q.     |        | 0 rhi  | Omo        | -      |        | rhod   | Q96mb9 homo sapien |        | P97088 clostridium | ٦      | ш      | ara            | Q9d157 mus musculu |        | -      | -      | •      | •      | Q92pd8 rhizobium m | Q9hm02 thermoplasm |

## ALIGNMENTS

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01-JUN-1998
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01-DEC-2001 (TremBLrel. 19, Created)
01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
CHAIN LENGTH FACTOR-LIKE PROTEIN.
  Kormanec J., Bistakova J., Novakova R., Homerova D., Rez "Cloning and characterization of a new polyketide gene c streptomyces aureofaciens CCM3239.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY033994; AAK61719.1;
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
  Bacteria; Firmicutes; Actinobacteria; Actinobacteridze; Actinomycetales; Streptomycineae; Streptomycea. ACBI_TaxID-1894;
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Conservative 0; Mismatci
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  K MEDLINE-97000351; PubMed-8843436;
R Redenbach M., Kleser H.M., Denapaite D., Elchner A., Cull
R Kinashl H., Hopwood D.A.;
The 8 set of ordered cosmids and a detailed genetic and phys
The 8 kb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1956).
R EMBL; AL009204; CAA15814.1;
R InterPro, IPR001575; Oxid_FAD_bind.
R Ffam; PF01565; FAD_binding_4, 1.
R PRDSITE; PS00862; OX2_COVAL_FAD; UNKNOWN_1.
SEQUENCE 445 AA; 49067 MW; BCOAEFBB74E38CF5 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 57.7 KDA PROTEIN C3B8.06 IN CHROMOSOME
   -i- SUBCELLULAR LOCATION: INTEGRAL MEM-
-i- SIMILARITY: IN C-TERMINAL TO YEAST
EMBL; AL022244; CAA18295.1; -.
   Eukaryota; Fungi; Ascomyo
Schizosaccharomycetales;
Schizosaccharomyces.
  Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Schizosaccharomycetea:
   Dliver K., Harria D.;
Submitted (DEC-1997)
  Actinomycetales;
NCBI_Tax1D=1902;
  01-JUN-2001 (TIEMBLIE1 17, I
FAD-DEPENDENT DXIDOREDUCTASE.
SC9B10.24C.
   Lyne M., Rajandream M.A., Pohl T.;
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Submitted (NOV-1997)
   STRAIN-A3(2);
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llarity 100.08;
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  Streptomycineae;
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A Jeong M.-J., Park S.-C.;
A Jeong M.-J., Park S.-C.;
T "Cloning of the catalase gene from Pleurotua daj...
I Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
PREMBL, AF286097; AAX15159.1; -.

DR HSSP; P15202; lA4E.
DR HSSP; P15202; lA4E.
DR Pfints; PR0002226; Catalase; l.
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DR PRODOM; P0000510; Catalase; l.
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01-JUN-2001 (TremBirel. 17, G:
01-JUN-2001 (TremBirel. 17, L:
01-DEC-2001 (TremBirel. 19, L:
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Q1-NOV-1999
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  Pleurotus sajor-caju (Oyster mushroom)
Eukaryota; Fungi; Basidiomycota; Hymen
Agaricales; Pleurotaceae; Pleurotus.
   Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB020024, BAA76662.1, -.
SEQUENCE 117 AA: 12879 MW: D5DC4CB22038C2B0 CRC64;
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01-DEC-2001 (TrEMBLrel.
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TISSUE-BRAIN;
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511 AA;
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   97.1%; S
llarity 100.0%;
Conservative 0;
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57703 MW;
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  12,
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   score 33; DB
s; Pred. No. 29;
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   054139
  Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Nopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 MD Streptomyces coalicolor A3(2) chromosome.",
Mol. Microbiol. 21:77-96(1996).
EMBL; AL021530; CAA16482.1;
SEQUENCE FROM N.A.

MEDLINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani N., Tai

Miyajima N., Nirosawa M., Sugiura

Hosouchi T., Matsuno A., Muraki A
  Synechocystis sp. (strain Bacteria; Cyanobacteria; (CBL_Tax1D=1148;
   974584;

01-FEB-1997 (TrEMBLrel. 02, Cr

01-FEB-1997 (TrEMBLrel. 02, La

01-JUN-2000 (TrEMBLrel. 14, La

NYPOTNETICAL 20.5 KDA PROTEIN.
  Parkhill J., Barrell
Submitted (JAN-1998)
   Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last Bequence update)
01-JUV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTNETICAL 16.9 KDA PROTEIN.
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SEQUENCE 154 AA; 1
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Redenbach M., Kieser H.M., Donapaite D.,
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  KPYGRF
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  16884 MW;
   88.2%;
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ni N., Tanaka A., Asamizu E., Nakamura Y.,
, Sugiura M., Sasamoto S., Kimura T.,
Muraki A., Nakazaki N., Naruo K., Okumura
   n PCC 6803).
Chroococcales;
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Last sequence Last annual
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EMBL/GenBank/DDBJ databases
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Pred. No. 42;
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PRINTS; PR00474; GLU5KINASE.
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01-DEC-2001
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GH17930P.
          Drosophila me
Eukaryota; Me
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Ephydroidea;
   .....amita sp.
Eukaryota; Diplomonadida;
NCBI_TaxID=28003;
[1]
  Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;

"Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions.";

DNA Res. 3:109-136(1996).

EMBL; D90316; BAA18694.1; ...

Hypothetical protein; Complete protcome.

SEQUENCE 173 AA; 20509 MW; 2E2414F099C8B2F7 CRC64;
  01-MAY-2000 (TrEMBLrel. 13, Creatêd)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CARBAMATE KINASE (EC 2.7.2.2).
  Dimopoulos M., Bagnara A.S., Edwards M.R.
"Characterisation and sequence analysis o
from the diplomonad Hexamita inflata.";
J. Bukaryot, Microbiol, 47:499-503(2000).
   Q961L5
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  CG8278
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  Q9U8B2;
   Q9U8B2
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94 KPYGRF 99
  1 RPYGRF 6
   1 RPVGRF 6
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  Similarity
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          melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Nexapoda; Inse
Neoptera; Endoptergyota; Diptera; Brachycera;
a; Drosophilidae; Drosophila.
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  Score 30; DB
Pred. No. 47;
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Submitted (JUL-1996) to the EME
EMBL; 274812; CAA99080.1; -.
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SROUENCE 501 AA; 55923 MW;
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SEQUENCE FROM N.A.
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STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
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Nunco J., Paclab J., Paragas V., Park S., Phouanenavong S., Wa
Yu C., Lewis S.E., Rubin G.M., Ceinlker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, NYOS1522, AAK92946.1; -.
SEQUENCE 369 AA: 41753 MW; 676CE63BB03F465D CRC64;
   O9KBE5 PRELIMINARY; PRT;
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O1-OCT-2000 (TrembLrel. 15, Created)
O1-OCT-2000 (TrembLrel. 15, Last seq
O1-JUN-2001 (TrembLrel. 17, Last annotation)
UROCONASE (UROCANATE HYDRATASE) (EC
   008229
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   HUTU OR BH1983.
Bacillus halodurans.
Bacteria; Firmicutes;
  SEQUENCE FROM N.A.
Alexandraki D., Kats
Submitted (JUL-1996)
  Eukaryota; Fung1; .
Saccharomycetales;
NCBI_TaxID=4932;
  Saccharomyces cerevisiae (Baker's yesst).

Eukaryots; Fung1; Ascomycota; Saccharomycotina; Sacciaromycetales; Saccharomycetaceae; Saccharomyces
SEQUENCE FROM N.A. STRAIN=C-125 / JCM
                              Bacillus/Staphylococcus
NCBI_TaxID=86665,
  YOL070C
   SEQUENCE FROM N.A.
   170
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9153;
   88.2%;
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  Bacillus,
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  Score 30; DB
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O1-DEC-2001 (TIEMBLITE1. 19, Last
GENOME POLYPROTEIN [CONTAINS: EN(
(NG1)] (FRAGMENT).
Hepatitis C virus.
Viruses; ssrNA positive-strand v.
  Takami H., Nak
Fuji F., Hiram
Horikoshi K.;
   O90Y59 PRELIMINARY; PRT; 109 AA.
O90Y59: O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
   MEDLINE=21435923; PubMed=11551708; Lee E.Y., Park H.H., Kim Y.T., Chung "Cioning and sequence analysis of the (Paralichthys Olivaceous)."; Gene 274:237-243(2001). Gene 274:237-243(2001). SEQUENCE 109 AA; 12117 MW; C7CE18
  Paralichthys olivaceus (Fiounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pieuronectoidel; Paralichthyidae; Paralichthys.
NCBI_TaxID-8255;
  MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Fuji F., Hirama C., Nakamura Y., O
Hepacivirus.
NCBI_TaxID=11103;
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   InterPro; IPR000193; Urocanase. Pfam; PF01175; Urocanase; 1. ProDom; PD025423; Urocanase; 1. PROSITE; PS01233; UROCANASE; 1.
   "Complete genome sequence of the aikaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtili: Nucleic Acids Res. 28:4317-4331(2000).
EMBL, AP001513; BAB05702.1;
  SEQUENCE
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   C7CE18986C50A6ED CRC64;
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  J.K., Choi T.J
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  Tomaru U., Sugiyama K., Matsuno Y., Kato N.;
"Splenic Malignant Lymphoma with Hepatitis C viru
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ dat
-!- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLY
EMBL; AB044725; BAB03672.1;
-EMBL; AB044725; BAB03672.1;
-Interpro; IPR002519; HCV_env
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  *Functional prediction of the coding sequences of 79 by analysis of cDNA clones from human fetal liver.*; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databas EMBL; AF119851; AAF69605.1; . B6716A242C773055 CRC64
   Zhang
He F.;
Synechocystis sp. (strain Bacteria; Cyanobacteria; NCBI_TaxID-1148;
  TISSUE=LIVER;
Zhang C., Yu
  Eukaryota; Metazoa;
Mammalla; Eutheria;
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   SEQUENCE FROM N.A.
   PRO1722
  Coat protein; Envelope protein;
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  Polyprotein; Transmembrane.
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Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Mlyajima N.,
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the I Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
   [1]
SEQUENCE FROM N.A.
STRAIN-PCC 6803;
   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.":

DNA Res. 3:109-136(1996).

EMBL, D63999; BAA10045.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 170 AA; 18583 MW; 6BC7097A9BB3CBF3 CRC64;
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MEDLINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nak

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura

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Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,

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